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Word or phrase: ge	ne	Search
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## We found 64 dictionaries with English definitions that include the word gene:

Tip: Click on the first link on a line below to go directly to a page where "gene" is defined.

### General (19 matching dictionaries)

- 1. <u>gene</u>: Merriam-Webster's Online Dictionary, 10th Edition [home, info]
- 2. -gene, gene: Encarta® World English Dictionary, North American Edition [home, info]
- 3. <u>gene</u>: Cambridge International Dictionary of English [home, info]
- 4. gene: The Wordsmyth English Dictionary-Thesaurus [home, info]
- 5. <u>gene</u>: The American Heritage® Dictionary of the English Language [home, info]
- 6. gene: Infoplease Dictionary [home, info]
- 7. <u>-gene, gene, gene-</u>: Dictionary.com [home, info]
- 8. Gene, gene: UltraLingua English Dictionary [home, info]
- 9. gene: Cambridge Dictionary of American English [home, info]
- 10. Gene: Wikipedia, the Free Encyclopedia [home, info]
- 11. gene: Rhymezone [home, info]
- 12. <u>gene</u>, <u>gene</u>: AllWords.com Multi-Lingual Dictionary [home, info]
- 13. gene: All About Homonyms [home, info]
- 14. gene: Columbia Encyclopedia, Six Edition [home, info]
- 15. gene: The New Dictionary of Cultural Literacy [home, info]
- 16. Gene: Encarta® Online Encyclopedia, North American Edition [home, info]
- 17. gene: WordNet 1.7 Vocabulary Helper [home, info]
- 18. <u>gene</u>: LookWAYup Translating Dictionary/Thesaurus [home, info]
- 19. gene: Encyclopedia.com [home, info]

### Art (1 matching dictionary)

### Quick definitions (Gene)

- noun: (genetics) a segment of DNA that is involved in producing a polypeptide chain; it can include regions preceding and following the coding DNA as well as introns between the exons; it is considered a unit of heredity (Example: "Genes were formerly called factors")
- name: A male given name (common: 1 in 1149 males; popularity rank in the U.S.: #200)
- name: A female given name (rare: 1 in 20000 females; popularity rank in the U.S.: #1299)
- name: A surname (very rare: popularity rank in the U.S.: #40659)

Encyclopedia article

The word "gene" is shared by many

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299 GYTFNKYDIN 308
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                                                                                                April 21, 2004, 17:26:23; Search time 26.6667 Seconds (without alignments) 118.319 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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1.4 140 11 0924R2 1.4 141 11 0924Q4 1.4 142 11 0924Q2 1.4 143 11 091VA2 1.4 143 11 091VA2 1.4 143 11 0924R7 1.4 143 11 0924R7 1.4 143 11 0924R7 1.4 143 11 0924R7 1.4 143 11 0924R9 1.4 145 11 0924R9 1.4 145 11 0924R4 1.4 145 11 0924R4 1.4 145 11 0924R8 1.4 146 11 0924R8 1.4 146 11 0924R8 1.4 146 11 0924R8 1.4 146 11 0924R8 1.4 4 82 11 0924R1 1.4 4 88 11 0921K1 1.4 4 88 11 081C07 1.6 6 18 6 19 081C07	ALIGNMENTS	PRELIMINARY; PRT; 448 AA.	ted) sequence annotatio	chetaiotaomicron. teroidetes; Bacteroides (class) ae; Bacteroides. 18;	8; Deng S., J.I.; tteroides t	Leome. 48 AA; 51254 MW; E4DA4539991DFB	ore 47; DB cd. No. 3.4; Mismatches	TPTSYDIN 10
11187 1222222222222222222222222222222222222		RESULT 1 Q8A516 ID Q8A516	AC 08A516; DT 01-UN-2003 DT 01-CTN-2003 DT 01-OCT-2003 DE PUTATIVE OUT	GN BT2253. OS Bacteroides t OC Bacteroidace. OX NCBI_TaxID=8.	RN [1] RP SEQUENCE FROM N.A. RC STRAIN=VDI-5482 / ATCC 29148; RX MEDLINE=22550858; PubMed=1266392 RA Xu J., Bjursell M.K., Himrod J., RA Chiang H.C., Hooper L.V., Gordon RT "A genomic view of the human-Bac RI Science 299:2074-2076 (2003). DR EMBL, AE016935, AAO77360.1; DR GO; GO:0005215; F:transporter ac DR GO; GO:0006810; P:transporter ac DR GO; GO:0006810; P:transporter ac DR HILEE-PROFIT INFO.	KW Complete pro	Query Match Best Local Simi Matches 8;	Qy 1 GYT

QBK0Z4

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STRAINBALBY:

Cui D., Zeng G., Yan X., Li X., Su C.;

Cui D., Zeng G., Yan X., Li X., Su C.;

Cui D., Zeng G., Yan X., Li X., Su C.;

Cloning of mouse genes related to repairing of intestinal epithelium of then irradiated mice by treatment with the intestinal RNA of mice of the same strain.";

Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).

EMBL, AF240166; AAK43731.1;

EMBL, AF240166; AAK43731.1;

InterPro; IPR007110; Ig-11.

Pfam; PF00047; ig; 1.

PFam; PF00047; ig; 1.

PROSITE; PS50835; IG LIKE; 1.

PROSITE; PS50835; IG LIKE; 1.

SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;
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STRAIN-CSTBL/6J; TISSUE=Pancreas;
STRAIN-CSTBL/6J; TISSUE=Pancreas;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavan T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice."; World J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c;
PubMed=11819679;
Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MRP3.
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01-OCT-2003 (TrEMBLrel. 25, La
1810060009Rik protein.
IGH-1 OR 181006009RIK.
Mus musculus (Mouse).
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45 GYTFIAYDIN 54
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                                                   QBKOZ4;
QBKOZ4;
QBLOZT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence AI893585.
Bus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1012 TaxID=10090;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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80.0%; Pred. No. 3.8;
vative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUB-Breast tumor;
Straubberg R.;
Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC029188; AAH29188.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.cl.
InterPro; IPR003599; Ig.cl.
InterPro; IPR003596; Ig.cl.
InterPro; IPR003596; Ig.cl.
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                       PRELIMINARY;
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Q8WY24; **Q8WY24** 

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OBWYZ 4
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Gaps

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Query Match
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                            RESULT 7
2019TM
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RC TIESO
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X Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
Chung J.H., Choi S.J., Kim H.G., Kim I.J., Choi I.H., Lee S.D.,
X Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
T. "Cloning and characterization of cDNAs encoding VH and VL of a monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and generation of a single-chain FV molecule (sCFV).";
I mol. Cells 7:s16-819(1997).
R EMBL; U88067; AB48044.1; -.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR007110; Ig-like.
R Pfam; PF00047; ig; 2.
SMART; SM00406; IGV; 2.
R PFAM; SM00406; IGV; 2.
R POSTITE; PSS0835; IG_LIKE; 2.
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Winshigh B., Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                         Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
BMBU: AXO07918: BAB25349.1; -.
PIR; S26746; SA6746.
HSSP; P01842; 7FAB.
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                                                                                                                                                                                                                                                                                                                                                                76.8%; Score 43; DB 11; Length 473; 80.0%; Pred. No. 19; 2; Indels tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                        MGD; MGI:96443; Igh-1.
InterPro; IRR007110; Ig-like.
InterPro; IRR003006; Ig_MHC.
InterPro; IRR003066; Ig_v.
Pfam; PF00047; ig; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00836; IG_MHC; 1.
SRQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 241
241 AA; 26086 MW; 0276887248E9C771 CRC64;
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Last sequence update)
Last annotation update)
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01-DEC-2001 (TERMELrel. 19, Created)
01-DEC-2001 (TERMELrel. 19, Last sequence update)
01-OCT-2003 (TERMELrel. 25, Last annotation updat
Anti-CEA 79 single chain Fv fragment (Fragment)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AA
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Best Local Similarity 80...
Best Local Similarity 80...
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SEQUENCE
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Gaps

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Indels

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Mismatches

222 GYTFTKYENN 231

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STRAIN=Berkeley, Pubmed=10731132,
Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Shburner M., Henderson S.N.,
Adams M.D., Celniker S.E., Holt R.A., Ashburner M., Henderson S.N.,
B. Baradon R.C., Rogers Y.-H.C., Marads R.G., Champe M., Pefeifer B.D.,
R. Baradon R.C., Bazer B.G., Helt G., Nelson C.R., Miklos G.L.G.,
R. Man K.H., Doyle C., Bazer B.G., Helt G., Nelson C.R., Miklos G.L.G.,
R. Baridon R.C., Baren B.P., Brandari D., Boseley E.M.,
Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Boseley E.M.,
Ballew R.M., Gong P. D., Deng E. Boxesen M. Cantorer J. Center A., Chardra I.
R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chardra I.
R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chardra I.
R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chardra I.
R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chardra I.
R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chardra I.
R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chardra I.
R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chardra I.
R. Barton K.J., Deng C., Mays D.D., Dew I., Dietz S.M.,
Achorary Ju., Harvey D., Helman T.C., Hernandez J.R., Houck J.,
R. Harris N.L., Harvey D., Helman T.C., Hernandez J.R., Houck J.,
Jalali M., Kalush F., Kodrel C.C., Ferrac C., Ferrac S., Dunn P.,
R. Harris N.L., Harvey D., Mchary C., Morris J., Month J. M., Match M. Murphy B., Murphy L., Murny D.M., Natherson D.L.,
R. Melson D.S., Nelson K.A., Mixon K., Mosser D., Santh T.,
R. Bartert K., Remington K.A., Mixon K., Mosser D.C., Scheeler F., Shen H.,
R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Sun E.,
R. Wang Z.-Y., Wassarman D.A., Weinsechbedh J.,
R. Wang Z.-Y., Wassarman D.A., Weinsechbed J., R.,
R. Wang Z.-Y., Wassarman D.A., Weinsech J.C.,
R. Wang Z.-Y., Wassarman D.A., Weinsechbed J., Shingson M.,
R. Whillame S.M., Worley E.W., Shull M., Wang Z., Zhan M.,
                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Haxapoda, Insecta, Pterygota,
Bukaryota, Endopterygota, Diptera, Brachycera, Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
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PROSITE; PS00150; ACYLPHOSPHATASE 1; 1.
SEQUENCE 102 AA; 11765 MW; 3CDC09E7FF96FBDE CRC64;
                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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GO; GO:0003998; F:acylphosphatase activity; IEA.
InterPro; IPR001792; Acylphosphatase.
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PRINTS; PR00112; ACYLPHPHTASE.
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                                                                           PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             CG18505 protein.
ACYP2 OR CG18505
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                                                                           Q9VF36
Q9VF36;
RESULT 9

109 VF3 6

109 VF3 6

109 VF3 6

100 DT 001 - M

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Length 102;

71.4%; Score 40; DB 5; 87.5%; Pred. No. 13;

Local Similarity

Best

Query Match

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MEDLINE=20448942; PubMed=10992488;
MEDLINE=20448942; PubMed=10992488;
MT-Call-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9GYZ2
Q9GYZ2,
Q9GYZ2,
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SONG X.T., Feng Z.O., Guan X.H.;

Song X.T., Feng Z.O., Guan X.H.;

"Amplification, cloning and sequence analysis of the heavy chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum.",
Schistosoma japonicum.",
Schistosoma japonicum.",
EMBL, AFS82622; AAG01452.1;
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                     09JL75;
01-0CT-2000 (TYEMBLYEL 15, Created)
01-0CT-2000 (TYEMBLYEL 15, Last sequence update)
01-0CT-2003 (TYEMBLYEL) 25, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 AA; 12118 MW; FF65E441BBF936A6 CRC64;
                                                                                                                         109 AA.
                                                                                                                                                                                                                                                                                                                                                                                    Infect. Immun. 68:5803-5808 (2000).
EMBL; AP206031; AAF69329.1; -
PIR, S26313; S26313.
HSSP; PO1810; 2FBJ.
InterPro; IPR007110; IG-11ke.
InterPro; IPR007110; Ig-11ke.
Fam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                       PRT;
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Best Local Similarity 100...
7; Conservative
                                                                                                                       PRELIMINARY;
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93 YTFTSFDI 100
                                                                                                                                                                                                                       Mus musculus (Mouse)
                          2 YTFTSYDI 9
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Q9GYZ2
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09JL75
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PIR; PH1152; PH1152.
PIR; PH1153; PH1153.
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STRAIN=C57BL/6;
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PH1147;
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Q924R6
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"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells.";
Bunnitted (SEP-2006).
ENBL, AR307936; AAL09420.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-11ke.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS0835; IG_IKE; 1.
                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0920E8 PRELIMINARY; PRT; 120 AA.
0920E8; CTEMBLED. 19, Created)
01-DEC-2001 (TrEMBLED. 19, Last sequence update)
01-DEC-2003 (TrEMBLED. 25, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable region
                                                                                                                                                                                                                                                            Query Match 71.4%; Score 40; DB 5; Length 119; Best Local Similarity 70.0%; Pred. No. 15; Matches 7; Conservative 1; Mismatches 2; Indels
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NON TER 120 120
SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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STRAIN=C3H/HeJ-lpr/lpr;
MEDLINE=96409289; PubMed=8814271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-DNA heavy chain (Fragment). J558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam, PP00047; ig; 1.
SMART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NOW_TER 1.9
SEQUENCE 119 AA; 13567 MW; E
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                                                                                                                                                                                                                                                                                                                                                                                    1 GYTFTSYDIN 10
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GYSFTGYNMN 35
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EX. Widoh MK. Alaxander Al., Pippa M. W. Dieserby D. S. Glikksenn G.S., and the control of the c
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A KOZONO Y., KOZONO H., Azuma T.;
T Direct Betimation of Relative Affinity by Flow Cytometry Reveals
T "Direct Betimation of B Call Antigen Receptors in Response to (4-
Affinity Maturation of B Call Antigen Receptors in Response to (4-
RT Affinity Maturation of B Call Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitropheny]) Acetyl (NP).";
Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.

BR EMBL; AB067784; BA863269.1;
DR FMR; PH1137.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR Ffam; PR00047; Ig'l.
DR SMART; SM00406; Ig_v.
DR PROSTT; PS50835; IG_LIKE; 1.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
Whis musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 11
TaxID=10090;
                                                     Query Match 71.4%; Score 40; DB 11; Length 137; Best Local Similarity 100.0%; Pred. No. 17; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 71.4%; Score 40; DB 11; Length 139; Best Local Similarity 100.0%; Pred. No. 18; Matches 7; Conservative 0; Mismatches 0; Indels
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SQ SEQUENCE 137 AA; 15171 MW; 5C38D966DC6A4124 CRC64;
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0; Gaps

Search completed: April 21, 2004, 17:37:13 Job time: 28.6667 secs

26 GYTFTSY 32

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 21, 2004, 17:25:48; Search time 5.07246 Seconds (without alignments) 102.653 Million cell updates/sec Run on:

SBQ1 56 1 gytftsydin 10 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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* Query	Match	100.0	87.5	87.5	73.2	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	9.69	69.6	9.69	9.69	67.9	67.9	61.9	66.1	66.1	66.1	64.3	64.3	64.3	64.3	64.3	64.3	62.5
	Score	56	49	49	41	40	40	40	40	40	40	40	40	40	40	40	40	39	39	39	39	38	38	38	37	37	37	36	36	36	36	36	36	35
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Query Match
100.0%; Score 56; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels

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P18526 mus musculu Q66154 cucumber mo P37638 escherichia Q923Q2 rhizobium m Q04489 saccharomyc P12616 actinomyces P40912 hansenula a Q03966 cryphonectr P2470 saccharomyc Q18017 caenorhaboli P01766 homo sapien Q81ki3 bacillus an	ALIGNMENTS  PRT; 117 AA.  uence update)  octation update)  Al/A4 precursor.  Craniata; Vertebrata; Buteleostomi;  Sciurognathi; Muridae; Murinae; Mus.  21;  dd tissue-specific expression of  ";  ight. It is produced through a collaboration- isht. It is produced through a collaboration- isht bloinformatics and the EMBL outstation- isht bloinformatics and the EMBL outstation- isht inot removed. Usage by and for commercial inot removed. Usage by and for commercial inoth Announce!	al.  IG HEAVY CHAIN V REGION VH558 A1/A4.  FRAMEWORK-1.  COMPLEMENTARITY-DETERMINING-1.  FRAMEWORK-3.  COMPLEMENTARITY-DETERMINING-2.  FRAMEWORK-3.  BY SIMILARITY.  8BOBC138856DFC9D CRC64;
HV55 MOUSE COAT_CRVAS YHIW ECOLI EGLC RHIME YMJ6 YEAST FWZ ACTNA ILACI TRYPA MUSI YEAST MUSI YEAST HY3Ē HUMAN MOAB_BLM ČAREL	ALIGNMENTS  T.1  MOUSE PRT, 117 AA.  PH052 MOUSE PRT, 117 AA.  10-JAN-1988 (Rel. 06, Created) 10-JAN-1988 (Rel. 06, Created) 10-JAN-1988 (Rel. 06, Last sequence update) 11-JAN-1988 (Rel. 06, Last sequence update) 12 heavy chain V region VH558 Al/A4 precursor.  Mus musculus (Mouse).  MUSTATORIS METAZOS; Chordata; Craniata; Vertebra Markaryote; MetaZos; Chordata; Craniata; Vertebra Markaryote; MetaZos; Chordata; Craniata; Vertebra Markaryote; Redentia; Rodentia; Sciurognathi; Muri NCBI_TAXID=10090;  SEQUENCE FROM N.A.  MEDLINE=85099340; PubMed=2578321;  Vancopoulos G.D., Alt F.W.;  SEQUENCE FROM VH Gene segments.";  "Developmentally controlled and tissue-specific currearranged VH gene segments.";  This SWISS-PROT entry is copyright. It is produced the European Bioinformatics Institute of Bioinformatics the European Bioinformatics Institute. There as use by non-profit institutions as long as is modified and this statement is not removed. Use modificed and this statement is not removed. Use	ise@isb-sib.ch).  ike.  ike.  ig HEAVY CHAIN V RE FRAMEWORK-1.  COMPLEMENTARITY-DET FRAMEWORK-2.  COMPLEMENTARITY-DET FRAMEWORK-3.  BY SIMILARITY.  IMW, BEOECI38856DFC9D
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	MOUSE POUSE POUSE POUSE POUSE POUSE POUSE POUSE O1-JAN-1988 (Rel. 06, Cas O1-JAN-1989 (Rel. 06, Las IS-UTL-1999 (Rel. 38, Las IS heavy chain V region V mammalia; Retaca; Chord Mammalia; Eutheria; Roden (NEL TaxID=10090; (1) SEQUENCE FROM N.A. MEDLINE=85099340; PubMeda Yancopoulos G.D., Alt F.W. "Developmentally controlly "Developmentally contr	or send an email to lic EMBL; M13787; AAA38499- PIR; A02029; HVMSA1. HSSP; P01810, 2784. INCEPTO; IPRO07110; IS INCEPTO; IPRO07110; IS INCEPTO; IPRO07110; IS INCEPTO; IPRO0710; IS INCEPTO; INCEPTO
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                                                                                                                                                                                                                                                                                MEDLINE=83131846; PubMed=6186498; MEDLINE=83131846; PubMed=6186498; MEDLINE=83131846; PubMed=6186498; MEDLINE=83131846; PubMed=6186498; Marshak-Rothstein A.; Midle genetic basis of antibody production: the dominant anti-arsonate ididotype response of the strain A mouse...; Immunol. 12:1023-1032(1982)...

-I. MISCELLANBOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS SEGMENT, JH2.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                         Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=83152818; PubMed=6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Somatic mutation in genes for the variable portion of the immunoslobulin heavy chain."; Science 216:309-311(1982).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49, DB 1; Length 120;
Pred. No. 0.027;
0; Mismatches 1; Indels
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120 AA; 13307 MW; FF04E4A167B654AF CRC64;
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HSSP, P01789; 1MCP.
InterPro; 1RR007110; 1g-like.
InterPro; 1RR003596; 1g-v.
Pfam; PF00047; ig; 1.
SWARY; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Hybridoma.
DOMAIN
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 36-65.
Mus musculus (Mouse)
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                                                             PRT;
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Best Local Similarity 90.v.,
Best Local Si Conservative
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10-OCT-2003 (Rel. 42,
Ig heavy chain V regio
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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P01746;
                                                         HV03 MOUSE
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Hatzenbuhler N.T., Nulf S.C.;
"Cloning and sequence analysis of the gene encoding invertase from
"Cloning and sequence occidentalis.";
Curr. Genet. 16:145-152(1989).
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-
fructofuranoside residues in beta-D-fructofuranosides.
-!- SIMILARITY: Belongs to family 32 of glycosyl hydrolases.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
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1-WAR-1992 (Rel. 21, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Invertase precursor (EC 3.2.1.26) (Beta-fructofuranosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 1; Length 140;
Pred. No. 0.032;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   20 140 IG HEAVY CHAIN V REGION 93
20 139 IG-LIKE.
140 140 MW, 25A4CBBE31DA5CE8 CRC64,
                                                                                        EMBL; J00493; AAA38128.1; -.
PIR; A94264; HYWSG7.
HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
PR081TE; PS50835; IG LIKE.
Immunoglobulin V region; Hybridoma; Signal.
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PIR, 813528; S33528.
PIR, 813529; S33528.
PIR, PR001362; Glyco_hydro_32.
Pfam; PF00251; Glyco_hydro_32; 1.
SMART; SM00640; Glyco_32; 1.
Hydrolase; Glycosidase; Glycoprotein; Signal.
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BY SIMILARITY
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MEDLINE=90090692; PubMed=2688929;
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90.0%;
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"Structural studies on induced antibodies with defined idiotypic
"Structural studies on induced antibodies with defined idiotypic
"Structural studies on induced antibodies from A/J
T specificities. VII. The complete amino acid sequence of the heavy
AT chain variable region of anti-pazophenylarsenate antibodies from A/J
T inmunol. 123:279-284 (1979).

J immunol in a ross -reactive idiotype.";
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GGLCKAC. . . (FOTENTIAL).

GGLCKAC. . (FOTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metrzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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0
                                                                                                                                                                                                                                Score 41, DB 1; Length 533;
Pred. No. 4.1;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.4%; Score 40; DB 1; Length 114; 66.7%; Pred. No. 1.2; 1.2; 1.4e 3; Mismatches 0; Indels
N-LINKED (GLCNAC. ..) (POTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1G heavy chain V region (Anti-arsonate antibody).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A/J;
MEDLINE=79195438; PubMed=109536;
                                                                                                                                                                                         60839 MW;
                                                                                                                                                                                                                                        73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 66.7%;
les 6; Conservative
                                                                                                                                                                                                                                                            Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                            ||||| |: |
158 GYTFTKYENN 167
                                                                                                                                                                                                                                                                                                                                 1 GYTFTSYDIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 GYTFSSYEL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GYTFTSYDI 9
                                                                                                                                                                                         533 AA;
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21-JUL-1986 (
15-JUL-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
HV00 MOUSE
AC P01741; 986
DT 21-JUL-1986
DT 21-JUL-1986
DT 10-OCT-2003
DE 19 heavy cha
OC Bukaryotei M
Musmmalia; EU
OC Bukaryotei M
OC STRAINB-7919
RR GERINB-7919
RR GERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
HV04 MOUSE
ID HV04 MOUSE
AC P01748;
DT 21-JUL-1986
DT 15-JUL-1996
                        CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                   CARBOHYD
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    CARBOHYD
    SPITE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Theavy call 24:625-637(1981).

Call 24:625-637(1981).

Call 24:625-637(1981).

RELATED GENES THIS GENELINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.

PIRE, AOZOSI, HYWAS.3.

RICEPPRO; IPR007310; Ig-like.

RICEPPRO; IPR007306; Ig-v.

RICEPPRO; IPR007306; Ig-v.

RICEPPRO; IPR007306; Ig-v.

RICEPPRO; IPR007006; IG-v.

RICEPPRO; IRR0, SP0040; IRR0, SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                              STRAIN=CS7BL/6;
MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MuSB_TaxID=10090;
                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSE! RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.4%; Score 40; DB 1; Length 117; 100.0%; Pred. No. 1.2; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V REGION 23.
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
1g heavy chain V region 3 precursor.
IGH-VJ558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK-1
Ig heavy chain V region 23 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.7; Conservative
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20 50
50 55
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117 1
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                             NCBI_TaxID=10090;
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ID HV05 MOUSE
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NON TER
SEQUENCE
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Best Local S
Matches 7
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Gaps

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117 117 117 Aa; 12867 MW; 740A65DD851FCA8C CRC64;

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Query Match
71.4%; Score 40; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  45 GYTFTSY 51
                                                                                                                                                                                               1 GYTFTSY 7
  NON TER
SEQUENCE
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DISULFID
NON TER
SEQUENCE
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DOMAIN
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AC P01754,
AC P01754,
DT 21-UUL-
DT 01-JUL-
DT 28-FEB
DF IGH-VUI
OS IGH-VUI
OS MUS MUS MUS
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HV09_MOUSE
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981).
- I- MISCELLANBOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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MEDLINE-81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1996 (Rel. 01, Created)
15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last amocation update)
16 heavy chain V region 102 precursor.
18 heavy chain V region 50 precursor.
19 heavy chain V region 60 precursor.
19 heavy chain W region 80 precursor.
19 heavy chain W region 102 precursor.
20 heavy chain V region 102 precursor.
30 heavy chain V region 102 precursor.
31 heavy chain V region 102 precursor.
32 heavy chain V region 103 heavy chain V 
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0
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-1.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%; Score 40; DB 1; Length 117; 100.0%; Pred. No. 1.2; 0; Indels rative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13016 MW; 427C861C53975EDC CRC64;
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HSSP, P01810, 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR00356; Ig-v.
Pfam; PP00047; Ig; 1.
SMART; SM0406; IGv; 1.
PR051TR; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
                                                                                                      EMBL; J00536; AAA38605.1; -..
PIK; AQC031; HVM33.
PIKSP; P01810; ZFB3.
MGD; MGI:96486; Igh-vJ558.
InterErc; IPROO7110; Ig-like.
InterPrc; IPROO3565; Ig-v.
Pfam; PP00047; ig; 1.
SMART; SMO0406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
Les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GYTFTSY 7
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P01750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
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DOMAIN
DOMAIN
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HV06 MOUSE
TO PU1750,
DT 21-UUL-
DT 21-UUL-
DT 21-UUL-
DE 15-UUL-
DE 16-UUL-
DE 16-UUL-
DE 16-UUL-
DE 16-UUL-
DE 16-UUL-
DE 16-UUL-
DE NORBLIN
RA MEDLINI
RA
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-!- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
HISSP; D90809; HVMS61.
HSSP; P01810; 2FBJ.
InterPro; IPR003596; Ig.v.
InterPro; IPR003596; Ig.v.
FROMET; SP00047; ig; 1.
FROM; SWART; SW00406; IGv; 1.
FROSITE; PS50835; IG LIKE; 1.
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                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
STRAIN=CS7BL/6;
BUDINES-1234548; PubMed=6788376;
BOChwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
Baltimore D.;
HV09 MOUSE STANDARD; PRT; 117 AA.
P0175; P11271;
21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12890 MW; 16191A088CB17F5A CRC64;
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BY SIMILARITY.
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EMBL; M13788; AAA38506.1; -.
PIR; A02035; MHMSB4.
HSSP; PO1310; ZFBJ.
InterPro; IPR001110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF0047; ig; 1.
SMART; SM00406; IGv; 1.
IMMRT; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          First, P01789; IMCP. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig_v.
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SMART; SMO406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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ilarity 70.0%;
Conservative
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68
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1115
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118
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Best Local Similarity
7; Conserve
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Best Local Similarity
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P06330;
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DISULFID
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SEQUENCE
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                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                          "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-i- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                    MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
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MEDLINE=8809340; PubMed=2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally, controlled and tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING-1
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COMPLEMENTARITY-DETERMINING-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION 145. FRAMEWORK-1.
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01-07N-1988 (Rel. 06, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
16-Mus heavy chain V region VH558 B4 precursor.
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100.0%; Pred. No. 4.-.
0; Mismatches
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MGD; MGI:96486; Igh-VJ558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003566; Ig-V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
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Cell 40:271-281(1985).
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Best Local Similarity luv.
7; Conservative
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54
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                                                                           STRAIN=C57BL/6
                                                                                                                  Baltimore D.;
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P06328;
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SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@lsb-sib.ch).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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FRAMEWORK-1.
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12934 MW; 94F7BEE4C762A018 CRC64;
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Pred. No. 1.3;
1; Mismatches
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01-07NN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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100.0%; Pred. No. 1.-.
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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BY SIMILARITY
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"Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981).

-!- MISCELIANDEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
(NPB ANTIBODIES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=84182519; PubMed=6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
"Imphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
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MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
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21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last amoctation update)
16-dul-1999 (Rel. 38) Last amoctation update)
17-JUL-1999 (Rel. 38) Precursor.
18 heavy chain V region S43 precursor.
19 heavy chain V region S43 precursor.
20 heavy chain V region S43 precursor.
21 heavy chain V region S43 precursor.
22 heavy chain V region S43 precursor.
23 heavy chain V region S43 precursor.
24 heavy chain V region S43 precursor.
25 heavy chain V region S43 precursor.
26 heavy chain V region S43 precursor.
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21 heavy chain V region V regio
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Pred. No. 1.3;
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Last annotation update)
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100.0%; Pred. No. ...
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                          120 AA
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Mus musculus (Mouse)
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HSSP; PO1810, 2FBJ.
InterPro; IPR007110, Ig-like.
InterPro; IPR003596; Ig_v.
Pfan; PP0047; ig; 1.
SMART; SMO0406; IGv.; 1.
PROSITE; PS50835; IG LIKE; 1.
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01-JAN-1988 (Rel. 06, Last seq
15-JUL-1999 (Rel. 38, Last ann
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                                     1 GYTFTSYDIN 10
                                                                                           GYTFTDYYMN 35
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120 120 1
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P01755;
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DISULFID
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HV11_MOUSE
DD 1755,0
DT 21-JUL.
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P06329;
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-!- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAXING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDLINE=81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P01751; P01752;
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last anocation update)
10-007-2003 (Rel. 42, Last anocation update)
Ig heavy chain V region B1-8/186-2 precursor.
Buka musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 1; Length 137; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V REGION S43. FRAMEWORK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15200 MW; ADD5881BF44B8EC9 CRC64;
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100.0%; Pred. No. ....
0; Mismatches
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JH2 SEGMENT.
BY SIMILARITY.
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SMART; SM0046; ig; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                         EMBL; J00539; AAA38172.1; -.
PIR; A02038; G2MS43.
HSSP; P01810; ZFBJ,
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J00529; AAA38170.1; -.
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1es 7; Conservative
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137 AA;
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SEQUENCE
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IG HEAVY CHAIN V REGION B1-8/186-2.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
D SEGMENT.
JT SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          15419 MW; 1B57DD4FD0C9F465 CRC64;
PIR; A90809; MEMS18.

PDB; 1A6U; 27-MAY-98.

PDB; 1A6U; 27-MAY-98.

InterPro; IPR00310; Ig-like.

InterPro; IPR003596; Ig_v.

Ffam; PR00407; Ig; 1.

SMART; SM00406; Igv.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Signal; 3D-structure.

SIGMAL

CHAIN

20 139 FRAMEWORK-1.

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50 68 FRAMEWORK-2.
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Search completed: April 21, 2004, 17:33:56 Job time : 6.07246 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 21, 2004, 17:27:33 ; Search time 9.13043 Seconds (without alignments) 105.353 Million cell updates/sec Run on:

Title: SEQ1
Perfect score: 56
Sequence: 1 gyt

1 gytftsydin 10

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ល	Description	g heavy chain V	g heavy	g heavy chain pr	g heavy chain V	g heavy chain V		g heavy chain V	g gamma chain V	g heavy chain V																				
SUMMARIES	ID	\$26918	PH1670	HVMSA1	534014	S31600	PH0988	S31596	B28572	B24754	A28572	PH1490	PH1491	S42176	PH1522	PH1523	<b>S38565</b>	A24754	PH1517	PH1518	PH1504	PH1500	PH1502	PH1503	PH1505	PH1520	PH1510	A26405	A21854	PH1494
	DB	2	N	н	~	N	N	N	~	(7)	~	N	N	~	N	N	~	7	N	N	N	N	N	N	N	N	~	~	~	7
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d	Query	. 0	8	00	ö	00	94.6	ä	7	۲.	7	ζ.	7	۲.	۲.	ζ.	7	۲.	7	7	7	۲.	۲.	7	۲.	۲.	۲.	۲.	7.	7
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1 GYTFTSYDIN 10

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PH1492	HVMSG7	PH1482	PH1483	A32189	F48677	G48677	E48677	S68170	S17614	PH0982	PH0983	PH0981	PH0984	S26463	PH1519
7	н	7	Ŋ	Ŋ	N	N	N	N	0	7	N	~	N	7	0
135	140	140	140	110	123	123	123	125	96	101	101	104	107	111	119
87.5					85.7	85.7	85.7	83.9	82.1	82.1	82.1	82.1	82.1	82.1	82.1
49	49	49	49	4.00	48	48	48	47	46	46	46	46	46	46	46
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

Gaps

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PH0988
Ig heavy chain V region (clone 178-c3) - mouse (fragment)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house)
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C,Accession: PH0988
A;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cs
A;Ritle: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cs
A;Reterence number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH0988
A;Accession: PH0988
A;Accession: PH0988
A;Accession: PH0988
A;Accession: PH0988
C;Cyperfamint indleic acid sequence not shown
A;Residues: 1.111 cTIL
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S31596
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the {
A;Reference number: S31585
A;Accession: S31596
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-132 CGII:
A;Resid
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Wechanisms that generate human immunoglobulin diversity operate from the { A;Reference number: S31865
A;Reference number: S31865
A;Reference number: S31860
A;Reference preliminary
A;Rolecule type: mRNA
A;Residues: 1-136 cCUI>
A;Residues: 1-136 cCUI>
A;Coss-references: EMBL:214165; NID:g30994; PIDN:CAA78534.1; PID:g30995
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:214166; NID:g30996; PIDN:CAA78535.1; PID:g30997
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 136;
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Matches 9; Conserv
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If heavy chain precursor V region (Al/A4) - mouse
C;Species: Mus musculus (house mouse)
C;Accession: A02029
C;Accession: A02029
R;Yancopoulos, G.D.; Alt, F.W.
Cell 40, 271-281, 1885
A;Title: Developmentally controlled and tissue-specific expression of unrearranged V-H g
A;Reference number: A90860; MUD:85099340; PMID:2578321
A;Reference number: A90860; MUD:85099340; PMID:2578321
A;Reference number: BNA
A;References: GB:M13787; NID:g196006; PIDN:AAA38499.1; PID:g466291
A;Residues: 1-117 < YAN>
A;Coss-references: GB:M13787; NID:g196006; PIDN:AAA38499.1; PID:g466291
A;Coss-references: GB:M13787; NID:g196006; PIDN:AAA38499.1; PID:g466291
A;Coss-references: GB:M13787; Immunoglobulin homology
C;Keywords: heterotertamer: immunoglobulin to region (A1/A4) #status predicted <XIG>F;20-117/Product: Ig heavy chain V region (A1/A4) #status predicted <XIG>F;20-117/Product: Ig heavy chain V region (A1/A4) #status predicted <XIG>F;20-54/Region: complementarity-determining 1
F;50-54/Region: complementarity-determining 2
F;69-88/Region: complementarity-determining 2
F;69-117/Region: framework 3
F;41-115/Disulfide bonds: #status predicted
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334014
19 heavy chain V region - human
C'Species: Home sapiens (man)
C'Species: Home sapiens (man)
C'Species: Home sapiens (man)
C'Species: Home sapiens
C'Species: Accession: 534014; S30535
R'Mariette, X.; Tsapis, A.; Brouet, J.C.
R'Mariette, X.; Tsapis, A.; Brouet, J.C.
A'Title: Nucleotidic sequence analysis of the variable domains of four human monoclonal
A'Reference number: S34001; MUID:93209281; PMID:7681398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
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831600
IG heavy chain V region - human (fragment)
IS pecies: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 831600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-127 «MRR»
A; Cross-references: EMBL: Z18321
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
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Best Local Similarity 100.
Matches 10; Conservative
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15 GYTFTSYDIN 54
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Globes was musculus (clone XR6-1) - mouse (fragment)
Closecies: Mus musculus (house mouse)
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Closecies: Mus musculus (house mouse)
Closecies: Made. 177, 797-809, 1993
A,Title: Hypermutation is observed only in antibody H chain V region transgenes that have do for somatic mutation.
A,Reference number: PH1482; MUID:93171820; PMID:8436910
A,Recession: PH1480
A,Status: translation not shown
A,Status: translation not shown
A,Status: L-102 <GIU>
A,Astatus: L-102 <GIU>
CSUD-Affamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 03-Peb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1491
R;Giusti, A.M.; Manser, T.
B;Giusti, A.M.; Manser, T.
A;Athle: Hypermutation is observed only in antibody H chain V region transgenes that hav for somatic mutation.
A;Reference number: PH1482; MUID:93171820; PMID:8436910
A;Accession: PH1491
A;Accession ont shown
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C;Species: Wus musculus (house mouse)
C;Date: 28-Sep.1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: S42176
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A,Residues: 1-102 <GIU>
A,Experimental source: hybridoma cell
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
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Pred. No. 0.11;
0; Mismatches 1; Indels
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                                                                     Score 49; DB 2; Length 98;
Pred. No. 0.1;
0; Mismatches 1; Indels
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Pred. No. 0.11;
0; Mismatches
F;15-98/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 90.0%;
Matches 9; Conservative (
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Best Local Similarity 90.0%;
Matches 9; Conservative (
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Matches 9, Conservative
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C;Species Mus musculus (house mouse)
C;Species Mus musculus
C;Species Mus musculus
C;Species Mus Musculus
C;Accession: A28572
Eur. J. Immunol. 13, 123-132, 1983
A;Title: The genetic basis of antibody production: a single heavy chain variable region
A;Reference number: A91262; MulD:83157801; PMID:6403356
A;Accession: A28572
A;Accession: A28572
A;Accession: A28572
A;Accession: MulD:83157801; PMID:640336
A;Residues: 1-98 < SIE.
C;Residues: 1-98 < SIE.
C;Residues: 1-99 < SIE.
C;Reperfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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Ig heavy chain V regions (CR-Id 7, CR-Id 14) - mouse (fragment)
(5,Species: Mus musculus (house mouse)
(5,Species: Mus musculus (house mouse)
(5,Accession: B28572
(5,Accession: B28572
(6,Accession: M.; Huang, S.Y.; Gefter, M.L.
(7, Immunol. 13, 123-132, 1983
(7,Title: The genetic banis of antibody production: a single heavy chain variable region A,Reference number: A91262; MUD:83157801; PMID:6403356
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B24754
B24754
C; Pade V chain V region (SE1.3) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 28-Sep-1887 #sequence_revision 06-Nov-1992 #text_change 16-Aug-1996
C; Accession: B24784
J. Exp. Med. 164, 291-302, 1986
A; Reference number: A24754; MUID: 86253060; PMID: 3088196
A; Reference number: A24754
A; Accession: B24754
A; Accession: B24754
C; Superfaminary
A; Molecule type: mRNA
A; Residues: 198 A+MB>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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Matches 9, Conservative
        1 GYTFTSYDIN 10
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R;Mo, J.A.; Bona, C.A.; Holmdahl, R.

Bur. J. Immunol. 23, 2503-2510, 1993

A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with specta-
A;Reference number: 542176; MUID:94009207; PMID:7691608
A;Accession: S42176
A;Accession: S42176
A;Accession: S42176
A;Accession: S42176
A;Accession: S42176
A;Accession: S42176
A;Croser-references: MMID:25441; NID:9407810; PIDN:CAA80928.1; PID:9407811
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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J. Exp. Med. 177, 797-809, 1993
A.Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.
A.Reference number: PH1482; MUID:93171820; PMID:8436910
A.Recession: PH1522
A.Ratus: translation not shown
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1523
R;Giusti, A.M.; Manser, T.
J. Exp. Med: 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hay d for somatic mutation.
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PH1522
IG heary chain V region (clone PR14-3-3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Decies: O3-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1522
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A)Reperimental source: hybridoma cell
C)Superfamily: immunoglobulin v region; immunoglobulin homology
C)Keywords: heterotetramer, immunoglobulin
P;18-101/Domain: immunoglobulin homology <IMM>
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A/Molecule type: DNA
A/Residues: 1-114 <GIO
A/Reperimental source: hybridoma cell
C/Superfamily: immunoglobulin V region; immunoglobulin
C/Keywords: heterotetramer; immunoglobulin
F/18-101/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.11;
1; Mismatches 1; Indels
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Pred. No. 0.12;
0; Mismatches 1; Indels
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A;Reference number: PH1482; MUID:93171820; PMID:8436910
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Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
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Indels
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Mismatches
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April 21, 2004, 17:33:24; Search time 148.696 Seconds (without alignments) 65.641 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                    6019581 segs, 976053577 residues
                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                 Perfect score:
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                                                                                                          Sequence:
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                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB ID Description

Sequence 125, App Sequence 3125, App Sequence 3125, A Sequence 34903, A Sequence 34903, A Sequence 34115, A Sequence 34115, A Sequence 3, Appli Sequence 3, Appli Sequence 290, App Sequence 290, App Sequence 290, App Sequence 390, App Sequence 344, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 361, App Sequence 373, App	Sequence 3 Sequence 4 Sequence 4 Sequence 4 Sequence 5 Sequence 5 Sequence 6 Sequence 6 Sequence 6 Sequence 7 Sequence 7 Sequence 7 Sequence 7 Sequence 8 Sequence 8 Sequence 9 Sequence 9 Sequence 9 Sequence 9 Sequence 9	ASE A2 AND USES THEREOF
PCT-US03-38234-125 US-10-726-332-125 US-09-864-761-34182 US-09-864-761-34202 US-10-182-997-24903 US-10-03-135-33269 US-10-203-136-34115 US-10-203-137-34182 US-10-203-137-34182 US-10-203-137-34182 US-10-203-137-34182 US-10-104-975-3 US-104-975-3 US-104-975-3 US-104-975-3 US-104-975-3 US	US-09-674-752-31 US-09-751-181-45 US-09-791-537-7778 US-10-029-98B-45 US-10-029-98B-45 US-10-032-423A-45 US-10-032-423A-45 US-10-041-860-299 US-10-041-860-296 US-10-041-860-344 US-10-041-860-344 US-10-041-860-361 US-10-041-860-361 US-10-041-860-361 US-10-041-860-361 US-10-041-860-373 US-10-041-860-374 US-10-041-860-374 US-10-041-860-374 US-10-041-860-374 US-10-041-860-374 US-10-041-860-374 US-10-041-860-374 US-10-041-860-374	no PC/TUS0338234 ic. inetics Incorporated Landes Landes Lee ig ig introprose DIRECTED TO PHOSPHOLIPASE X.072A X.072A X.072A X.072A X.072A Windows Version 4.0
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67

OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39

OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUE 8.00e-48

PCT-US01-00663-34182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 56, DB 1, Length 92; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 10; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 99/608 408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 38837
SSOFTWARE: Molecular Dynamics Sequence Listing Engine 200 ILENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TILLE OF LAWARILON: GENE EXPRESSION ANALYSIS, PILE REPERENCE: ARONICa-X-1
CURRENT PILING DATE: 2001-05-23
PRIOR PELICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-06-26
PRIOR PELING DATE: 2000-06-06
PRIOR PELING DATE: 2000-06-03
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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## CENTRAL OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES:
## CENTRAL OF ILIANG DATE: 2001-01-30
## COURRENT FILING DATE: 04 February 2000 (04.02.00)
## PRIOR FILING DATE: 03 August 2000 (03.08.00)
## PRIOR FILING DATE: 04 February 2000 (03.08.00)
## PRIOR FILING DATE: 04 February 2000 (03.08.00)
## PRIOR FILING DATE: 03 AUGUST 2000 (03.08.00)
## PRIOR FILING DATE: 03 AUGUST 2000 (03.08.00)
## PRIOR PILING DATE: 04 February 2000 (03.08.00)
## PRIOR PILING DATE: 05 OCCODER 2000 (03.08.00)
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Best Local Similarity 100.0%; Pred. No. Matches 10; Conservative 0; Mismatch
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Best Local Similarity 100.
Matches 10; Conservative
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; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38234-125
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US-10-726-332-125
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US-10-726-332-125
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Sequence 33269, Application US/10203135
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Molecular David K.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN GENOME TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG
FILE REPERBANCE: PB 0004 W0 5
CURRENT APPLICATION NUMBER: US/0180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PLING DATE: OF PED-LAY 2000 (04.02.00)
PRIOR PLING DATE: OF MAGNING OF SECONDERING DATE: OF MAGNING M
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GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER
FILE REFERENCE: PB 0004 WO 3
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                                                                             0; Indels
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
                                  Pred. No. 0.11; Mismatches
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OTHER INFORMATION: MAP TO AB019440.1
100.08; Pr
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Best Local Similarity 100.
Matches 10; Conservative
                                                                             Conservative
                                                                                                                                                      1 GYTFTSYDIN 10
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ORGANISM: Homo sapiens
                                  Best Local Similarity
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                                                                             Matches
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US-10-182997.

GENERAL INFORMATION:

APPLICANT:

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BONDAL DAVIG R.

APPLICANT:

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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67

OTHER INFORMATION: EXPRESSED IN LUNG. 3510NAL = 0.73

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62

OTHER INFORMATION: SWISSPROT HIT: P23083, BVALUE 2.00e-39

US-09-864-761-47202
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US-10-182-997-24903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 56; DB 23; Length 92; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 10; Conservative 0; Mismatches 0; Indels
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FEATURE:
                     PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLIANG DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTRARE: Annomax Sequence Listing Engine vere: 1.1
SEQ ID NO 47202
LENGTH: 92
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                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 92
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                                                                                                                                                                                  OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67 PEATURE:
OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39 PEATURE:
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PCT-US02-22011-3
| Sequence 3, Application PC/TUS0222011
| Sequence 3, Application PC/TUS0222011
| GENERAL INPORMATION:
| APPLICANT: Foote, Jefferson
| TILLE OF INVENTION: Super Humanized Antibodies
| FILE REPERENCE: 501231.02
| CURRENT APPLICATION NUMBER: PCT/US02/22011
| CURRENT PELLON DATE: 2002-07-12
| PRIOR PILING DATE: 2001-07-12
| PRIOR PILING DATE: 2001-07-12
| NUMBER: OF SEQ ID NOS: 122
| SOFTWARE: Patentin version 3.1
| LENGIN OS
| TYPE: PRT
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Super Humanized Antibodies
TITLE OF INVENTION: Super Humanized Antibodies
FILE REPRENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
FRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin Version 3.1
IENGTH: 96
                                                                                           FEATURE:
OTHER INFORMATION: MAP TO AB019440.1
FEATURE:
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Best Local Similarity 100.
Matches 10; Conservative
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                            TYPE: PRT
ORGANISM: Homo sapiens
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PCT-US02-22011-3
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ORGANISM: Homo sapiens
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US-10-194-975-3
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GENERAL INFORMATION:
APPLICANT: Penn, Sharton G.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: AMALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
TITLE OF INVENTION: AMALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
FILLE REPERBNCE: PB 0004 WO 7
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,466
PRIOR PLING DATE: O3 August 2000 (03.09)
PRIOR PLING DATE: O3 August 2000 (03.09)
PRIOR PLING DATE: O3 August 2000 (03.00)
PRIOR APPLICATION NUMBER: US 60/234,687
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OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39

PEATURE:

OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUE 8.00e-48

US-10-203-136-34115
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CURRENT APPLICATION NUMBER: US/10/203,136

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 26 May 2000 (36.05.00)

PRIOR PELING DATE: 03 August 2000 (30.08.00)

PRIOR FILING DATE: 03 August 2000 (30.08.00)

PRIOR FILING DATE: 03 August 2000 (30.08.00)

PRIOR FILING DATE: 03 October 2000 (30.00)

PRIOR FILING DATE: 10 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR FILING DATE: 20 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 38578

NUMBER OF SEQ ID NOS: 38578

SEQ ID NO 34115

LENGTH: 92
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OTHER INFORMATION: MAP TO AB019440.1
FEATURE:
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ORGANISM: Homo sapiens
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Gaps

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APPLICANT: GAZIT, Gau.
APPLICANT: WEBER, Richard
APPLICANT: BEZABEN, BINYam
TITLE ON INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
FILE REFERENCE: ABGENIX.051VPC
CURRENT APPLICATION NUMBER: PCT/US03/00398
CURRENT PILLING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 377
SOFTWARR: FactSEQ for Windows Version 4.0
SEQ ID NO 290
LENGTH: 98
TYPER: PRT
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TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
FILE REFERENCE: ABGENIX.051VPC
CURRENT APPLICATION NUMBER: PCT/US03/00398
CURRENT FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 295
LENGTH: 98
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APPLICANT: BEZABEH, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
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100.0%; Pred. No. 0.12;
tive 0; Mismatches 0; Indels
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APPLICANT: CORVALAN, Jose, R.F.
APPLICANT: UIA, Xiao-Chi
APPLICANT: FENG, Xiao-Dong
APPLICANT: TANG, Xiao-Dong
APPLICANT: GHEN, Francine
APPLICANT: GAZIT, Gadi
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APPLICANT: CORVALAN, Jose, R.F.
APPLICANT: JIA, Xiao-Chi
APPLICANT: FENG, Xiao-Dong
APPLICANT: YANG, Xiao-Dong
APPLICANT: GAEN, Francine
APPLICANT: GAEN, Francine
APPLICANT: WEBER, Richard
APPLICANT: WEBER, Richard
APPLICANT: BEZABEH, Binyam
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
    CHEN, Francine
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ORGANISM: homo sapiens
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APPLICANT CORVALAN, JOSE, R.F.
APPLICANT FENG, Xiao-Chi
APPLICANT FENG, Xiao-Dong
APPLICANT GAZIT, Gadi
APPLICANT GAZIT, Gadi
APPLICANT GAZIT, Gadi
APPLICANT GAZIT, GAGI
APPLICANT GAZIT, GA
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Sequence 43, Application PC/TUSO238450

GENERAL INFORMATION:

APPLICANT: Rother, Russell

TITLE OF INVENTION: HYBRID ANTIBODIES

FILE REFERENCE: 1087-37

CURRENT PPLING DATE: 2003-03-21

NUMBER OF SEQ ID NOS: 195

SOFTWARE: Patentin version 3.1

SEQ ID NO 43

LENGTH: 98
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GENERAL INFORMATION:
APPLICANT: ABGENIX, INC.
APPLICANT: CORVALAN, Jose, R.F.
APPLICANT: JIA, Xiao-Chi
APPLICANT: FENG, Xiao-Chi
APPLICANT: YNG, Xiao-Dong
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 10; Conservative
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24 GYTFTSYDIN 33
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ORGANISM: homo sapiens
PCT-US03-00398-289
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; ORGANISM: human
PCT-US02-38450-43
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PCT-US03-00398-290
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PCT-US03-00398-289
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; FILE REFERENCE: ABGENIX.051VPC
; CURRENT APPLICATION NUMBER: PCT/US03/00398
; CURRENT FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 98
; TYPE: PRT
; ORGANISM: home sapiens
PCT-US03-00398-296
Query Match

Applicative 0; Mismatches 0; Indels 0; Gaps

Qy

I GYTFTSYDIN 10

Db

Z6 GYTFTSYDIN 35

Search completed: April 21, 2004, 17:57:21
JOb time: 148.696 secs
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Sequence 125, Appli
Sequence 2, Appli
Sequence 31, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 17, Appli
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Sequence 7, Appli
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Sequence 17, Appli
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Sequence 12, Appli
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                                                                                                                                                                                                   April 21, 2004, 17:34:09; Search time 7.10145 Seconds (without alignments) 39.310 Million cell updates/sec
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1: /cgn2 6/ptodata/2/paa/USO6 NEW COMB.pep:*

2: /cgn2-6/ptodata/2/paa/USO6 NEW COMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-926-323A-2
US-10-793-44122
PCT-US03-36870-3
PCT-US03-36870-5
PCT-US03-36870-6
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PCT-US04-05247-6
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No.
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Sequence 20, Appl Sequence 410, Appl Sequence 7, Appli Sequence 31, Appl Sequence 52, Appl Sequence 22, Appl Sequence 701, Appl Sequence 701, Application 101,	OLIPASE A2 AND USES THEREOF	Length 10; i Indels 0; Gaps 0;	
6 US-10-681-421-20 6 US-10-627-556-406 6 US-10-621-421-71 6 US-10-681-421-71 6 US-10-681-421-71 6 US-10-681-421-111 6 US-10-681-421-111 6 US-10-681-421-111 6 US-10-681-421-111 6 US-10-7556-242 6 US-10-7554-479-7801 6 US-10-881-479-7801 6 US-10-881-421-109 1 PCT-US03-32349-15 1 PCT-US03-32349-15 1 PCT-US03-32349-17 1 PCT-US03-32349-17 5 US-09-905-928A-6 5 US-09-905-928A-6 5 US-09-905-928A-6	RESULT 1 PCT-US03-38234A-125  Sequence 125, Application PC/TUS0338234A  Sequence 125, Application PC/TUS0338234A  GENERAL INFORMATION: APPLICANT: LEXICON GENETICS INCORPORATED APPLICANT: LIG Chen APPLICANT: Ling Chen APPLICANT: Ling Chen APPLICANT: Ling Chen APPLICANT: Mark R. Lee APPLICANT: Mark R. Lee APPLICANT: Xiao Feng APPLICANT: Xiao Feng APPLICANT: Xiao Feng APPLICANT: Xiao Feng APPLICANT: Mark R. Nocerini ITILE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 A: TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 A: TITLE OF INVENTION NUMBER: PCT/US03/38234  PRIOR FILING DATE: 2003-02-19 PRIOR FILING DATE: 2003-12-02  NUMBER OF SEQ ID NOS: 222  SOFTWARE: FEATSEQ for Windows Version 4.0  SEQ ID NO 125  LENGTH: 10  TYPE: PRI CREANISM: Homo sapiens PCT-US03-38234A-125	0%; Score 56; DB 1; 0%; Pred. No. 0.00083 0; Mismatches 0;	39926323A 1 0r 11e
76.8 1121 76.8 121 76.8 121 76.8 121 76.8 121 76.8 122 76.8 122 76.8 123 76.8 124 76.8 125 76.8 126 76.8 127 76.8	ULT 1 -US03-38234A-125 sequence 125, Application PC/TUS0338234A sequence 125, Application PC/TUS0338234A APPLICANT: LEXTON GENETICS INCORPORAT APPLICANT: LEXTON GENETICS INCORPORAT APPLICANT: Mary Haak-Frendscho APPLICANT: Mary Haak-Frendscho APPLICANT: Mary Haak-Frendscho APPLICANT: Mary Haak-Frendscho APPLICANT: Mary Hauk-Frendscho APPLICANT: Mary Hauk-Frendscho APPLICANT: Mary Haug APPLICANT: Mark R. Noceini APPLICANT: Mark R. Noceini APPLICANT: Mark R. Noceini APPLICANT: Mark R. Noceini APPLICANT: Mark P. Noceini APPLICANT: Mark P. Noceini APPLICANT: PARIOR DATE: 2003-02-19 PRIOR FILING DATE: 2003-12-02 CURRENT APPLICATION NUMBER: PCT/US03/3823 PRIOR FILING DATE: 2003-12-02 SUFTWARE: PASELSC for Windows Version 4 ILENGTH: 10 TYPE: PRT CURRANT: HOMO Sapiens	Similarity 100 0; Conservative GYTFISYDIN 10 [H	ATION ATION ATION ATION ATION AND COCK, Francadel, Francadel, Hen, Vadelf, Hen, Uther, Tholubrech, Suller, Mar.
7 8 0 0 0 1 0 8 8 8 8 8 8 8 8 8 8 8 8 8 8	REGULT 1 PCT-US03-38234 SEQUENCE 122 GENERAL INF APPLICANT: APPLIC	Query Match Best Local Matches 1 Qy 1	RESULT 2 US-09-926-323A-2 IS SEQUENCE 2, AD GENERAL INFORM APPLICANT: N APPLICANT: M

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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         COUNTRY: USA
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Matches 8; Conserva
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                     TITLE OF INVENTION: Diagnostic and Therapeutic Use of Antibodies Against The TITLE OF INVENTION: Drokinase Receptor FILLS OF INVENTION: Urokinase Receptor CURRENT APPLICATION NUMBER: US/09/926,323A CURRENT FILING DATE: 2002-03-05 PRIOR APPLICATION NUMBER: PCT/EPO0/03347 PRIOR APPLICATION NUMBER: PCT/EPO0/03347 PRIOR FILING DATE: 2000-12-13 PRIOR FILING DATE: 2000-12-13 PRIOR FILING DATE: 2000-12-13 PRIOR FILING DATE: 2000-13-13 PRIOR FILING DATE: 2000-
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Sequence 4122, Application US/10793479

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclett, A.
APPLICANT: Duclett, A.
APPLICANT: Giordano, J.Y.
APPLICANT: WINTERING: ESPONSE: S. US/10/793, 479
CURRENT FILING DATE: 2004-03-03
PRIOR FILING DATE: 2004-03-03
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SSOTIMARE: Patent.pm
SSO ID NO 4122
LIBRIGH: 127
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GENERAL INFORMATION:
APPLICANT: William M. Pardridge
Ruben J. Boado
IITLE OF INVENTION: Delivery Of Pharmaceutical Agents
Via The Human Insulin Receptor
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB 5; Length 118;
Pred. No. 0.038;
1; Mismatches 0; Indels
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COCATION: -19...1
COTHER INFORMATION: SCORE 9.7
COTHER INFORMATION: SEG ILFUVARATSAHS/QV
US-10-793-479-4122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: phage sequence US-09-926-323A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
    Harbeck, Nadia
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26 GYSFTSYDIN 35
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ORGANISM: Homo sapiens
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US-10-793-479-4122
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PCT-US03-36870-31
                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठ
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Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: William M. Pardridge
Ruben J. Boado
TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
Via The Human Insulin Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%; Score 48; DB 1; Length 10; 80.0%; Pred. No. 0.018;
STREET: Shapiro & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
STATE: CA Monica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSES: Shapiro & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
                                                                                                                             COMPUTER READBLE PORM:
COMPUTER READBLE PORM:
MEDIUM TYPE: RIOPPY Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 2000
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US03/36870
FILING DATE: 18-NOV-2003
CLASSIFICATION: CURRION:
NAME: OlderARION: CURRION:
NAME: OlderARION: CURRION:
TELEPHONE: (310) 319-5411
TELEPHONE: (310) 319-5411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REPRENCE/SDOKKT NUMBER: 0180.0038
TELECOMMINICATION INFORMATION:
TELEPHONE: (310) 319-5411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US03/36870
FILING DATE: 18-Nov-2003
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 2000
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: polypeptide
SEQUENCE DESCRIPTION: SEQ ID NO: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (310) 319-
INFORMATION FOR SEQ ID NO: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
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Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
PCT-US03-36870-5
; Sequence 5, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
                                                                                                                                                                                                                                                                                                                             85.7%; Score 48; DB 1; Length 113; 80.0%; Pred. No. 0.17; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSER: Shapiro & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US03/36870
FILING DATE: 18-Nov-2003
CLASSIFICATION: «Unknown»

ATTORNEY/AGENT INFORMATION:

RAME: Oldenkamp, David J.

REFERENCE/DOCKET NUMBER: 29,421

REFERENCE/DOCKET NUMBER: 29,421

REFERENCE/DOCKET NUMBER: 29,421

TELEPHONE: (310) 319-5411

TELEPHONE: (310) 319-5411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 2000 SOFTWARE: MS Word
                                                         LENGTH: 113 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3
PCT-US03-36870-3
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5
PCT-US03-36870-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
TELEFAX: (310) 319-5401 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYTFTSYDIN 10
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26 GYTFTNYDIH 35
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RESULT 7 PCT-US03-36870-7

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Pred. No. 0.17;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application PC/TUS0336870
GENERAL INFORMATION:
APPLICANT: William M. Pardridge
Ruben J. Boado
TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
Via The Human Insulin Receptor
                                                                  Ruben J. Boado
TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
Via The Human Insulin Receptor
                                                                                                                           NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shapiro & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Shapiro & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 2000
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US03/36870
FILING DATE: 18-NOW-2003
CLASSIFICATION: «UNKNOWN:»
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29-421
REFERENCE/DOCKET NUMBER: 10180.0038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US03/36870
FILING DATE: 18-Nov-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIF: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 2000
SOFTWARE: MS Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: PCT-US03-36870-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (110) 319-5411
TELEPHONE: (310) 319-5401
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
Sequence 7, Application PC/TUS0336870
GENERAL INFORMATION:
APPLICANT: William M. Pardridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.7%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GYTFTSYDIN 10
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                                                                                                                                                                                                                                                                     COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -US03-36870-8
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RESULT 10
PCT-US03-36870-10
; Sequence 10, Application PC/TUS0336870
; GENERAL INFORMATION:
; APPLICANT: William M. Pardridge
; APPLICANT: William M. Pardridge
; TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
... TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.7%; Score 48; DB 1; Length 113; 80.0%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
FCF-0303-56870-11
Sequence 11, Application PC/TUS0336870
GENERAL INFORMATION:
APPLICANT: William M. Pardridge
APPLICANT: William M. Pardridge
Ruben J. Boado
ITILE OF INVENTION: Delivery Of Pharmaceutical Agents
ITILE OF INVENTION: Via The Human Insulin Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: Shapiro & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: Shapiro & Dupont LLP
STREET: 233 Wilshire Boulevard, Suite 700
CITY: Santa Monica
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

CORRENT SYSTEM: Windows 2000

SOFTWARE: MS WORD

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US03/36870

FILING DATE: 18-Nov-2003

CLASSIFICATION INFORMATION:

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 29,421

REFERENCE/COKCET NUMBER: 29,421

REFERENCE/COKCET NUMBER: 29,421

REFERENCE/COKCET NUMBER: 29,421

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:

TELEFAX: (310) 319-5401

INFORMATION FOR SEQ ID NO: 10:

MENTICE CHARACTERISTICS:

ENGTH: 113 anino acids
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 10
PCT-US03-36870-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
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Best Local Similarity 80.0
Matches 8; Conservative
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          26 GYTFTNYDIH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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85.7%; Score 48; DB 1; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 85.7%; Score 48; DB 1; Length 113; Best Local Similarity 80.0%; Pred. No. 0.17; Matches 8; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application PC/TUS0336870
GENERAL INFORMATION:
APPLICANT: William M. Pardridge
Ruben J. Boado
TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
Via The Human Insulin Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: Shapiro & Dupont LLP
STREET: 213 Wilshire Boulevard, Suite 700
CITY: Santa Monica
ATTORNEY AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 0180.0038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 319-5411
TELEFRX: (310) 319-5401
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER LOA

COMPUTER RADABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 2000
SOFTWARE: MS WOLG
CURRENT APPLICATION DATA:
APPLICATION UNBER: PCT/US03/36870
FILING DATE: 18-Nov-2003
CLASSIFICATION: CUNRENCY
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 1960:0038
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8
PCT-US03-36870-8
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9
PCT-US03-36870-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (310) 319-5401
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||:|||:
26 GYTFINYDIH 35
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Gaps

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Sequence 7, Application US/10800197;
GENERAL INFORMATION:
APPLICANT: Morton, Philip A et al.
TITLE OF INVENTION: ANTIBODIES TO IGF-I RECEPTOR FOR THE TREATMENT OF CANCERS;
FILE REFERENCE: 01343/1
CURRENT APPLICATION NUMBER: US/10/800,197;
CURRENT FILING DATE: 2004-03-12;
PRIOR PAPLICATION NUMBER: 60/455,094
PRIOR FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 157
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
LENGTH: 245
                                                                                                                                                                                                                                                                             Score 47; DB 6; Length 226;
Pred. No. 0.48;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.9%; Score 47; DB 6; Length 245; Best Local Similarity 80.0%; Pred. No. 0.52; Matches 8; Conservative 1; Mismatches 1; Indels
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US-10-488-673-4

US-10-488-673-4

Sequence 4, Application US/10488673

GENERAL INFORMATION:

APPLICANT: KEIO UNIVERCITY

ITLE OF INVENTION: PEMPHIGUS MONOCLONAL ANTIBODIES

FILE REFERENCE: P10000238

CURRENT APPLICATION NUMBER: US/10/488,673

CURRENT FILING DATE: 2004-03-03

PRIOR APPLICATION NUMBER: JP P2001-267653

PRIOR FILING DATE: 2001-09-04

NUMBER: OF SEQ ID NOS: 55

SOFTWARE: Patentin Ver. 2.1

FROM TON 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
; OTHER INFORMATION: phage display generated antibody
US-10-800-197-7
CURRENT APPLICATION NUMBER: US/10/813,977
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ 1D NOS: 36
SEQ 1D NO 17
LENGTH: 226
                                                                                                                                                                                                             CTHER INFORMATION: SCFV-18-2 Antibody US-10-813-977-17
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYTFTSYDIN 10
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26 GYTFRNYDIN 35
                                                                                                                                                                                                                                                                                                                                                                         2 YTFTSYDIN 10
                                                                                                                                                                                                                                                                                                                                                                                                              27 YTPTTYDIN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CNGANISM: Homo sapiens
US-10-488-673-4
                                                                                                                                        TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-10-800-197-7
                                                                                                                                                                                         FEATURE:
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SEQUENCE INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODIES TO IGF-I RECEPTOR FOR THE TREATMENT OF CANCERS
TITLE OF INVENTION: ANTIBODIES TO 197
TITLE OF INVENTION: ANTIBODIES TO 197
CURRENT PELING DATE: 2004-03-12
PRIOR PELING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 157
SOFTWARE: PARENTIN VERSION 3.2
SEQ ID NO 120
LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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GENERAL INFORMATION:
APPLICANT: Dynan, William
APPLICANT: Takeda, Yoshiniko
APPLICANT: Li, Shuyi
TILE OF INVENTION: Compositions and Methods for Modulating DNA Repair
FILE REPERENCE: 791301-12010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.7%; Score 48; DB 1; Length 113;
80.0%; Pred. No. 0.17;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.9%; Score 47; DB 6; Length 116;
80.0%; Pred, No. 0.26;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: phage display generated VH or VL region US-10-800-197-120
                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US03/36870
FILLING DATE: 18-NOV-2003
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 0180.0038
TELECOMMUNICATION INFORMATION:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 2000
SOFTWARE: MS Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECTLE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 11
PCT-US03-36870-11
                                                                                                                                                                                                                                                                                                   TELEPHONE: (310) 319-5411
TELEFAR: (310) 319-5401
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 113 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 85.7
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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US-10-800-197-120
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Gaps

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1 GYTFISYDIN 10 |||||||||| 26 GYTFISYWIN 35

Search completed: April 21, 2004, 17:58:24 Job time : 8.10145 secs

seq1.open.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 21, 2004, 17:25:18 ; Search time 40 Seconds (without alignments) 70.637 Million cell updates/sec

Title: Perfect score:

1 gytftsydin 10 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters: 1586107 seqs, 282547505 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp1990s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

# SUMMARIES

		de				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	56	100.0	92	4	AAM20077	Aam20077 Peptide #
63	26	100.0	92	4	AAM33913	e
m	26	100.0	92	4	ABG55467	_
4	26	100.0	92	w	ABG43604	Human
ഹ	56	100.0	96	m	AAY50958	Human
9	26	100.0	86	Ŋ	ABG78170	_
7	26	100.0	96	w	ABG91861	Abg91861 Human ant
60	56	100.0	96	9	ABO27070	_
σ	56	100.0	116	7	AAR79241	. Heavy
10	56	100.0	117	N	AAR66302	
11	26	100.0	119	9	ABJ18572	Abj18572 Gangliosi
12	56	100.0	119	φ	ABJ18570	_
13	99	100.0	120	4	AAB62747	_
14	99	100.0	122	φ	ABR55829	Abr55829 Heavy cha
15	99	100.0	139	φ	ABG74245	2
16	. 26	100.0	146	ო	AAB53510	_
17	26	00	149	9	ABO04846	Abo04846 Human epi
18	56	•	199	7	AAY34302	02 IgM an
19	26	100.0	203	~	AAY34301	P. I.
50	56	ö	555	4	AAB19871	7,
21	26	•	565	4	AAB19873	Aab19873 Activatin
22	56		577	4	AAB19872	a
23	56	100.0	704	4	AAB19888	Aab19888 MLV envel
	54	96.4	120	9	ABR55815	Abr55815 Heavy cha
25	53	94.6	120	9	AA029544	Aao29544 Human 7.1

N D B H N IN H B # B N # K L IN K H IN	Aar44226 Chimeric Aay78328 Bispecifi
ABG71906 ABM78999 AABM78999 AABM78999 AAG0041 AAX64688 ABG0041 AAX64688 AAX50966 AAX50966 AAX50966 AAX17415 AAX17415 AAX17415 AAX17415	AAR44226 AAY78328
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120 243 243 243 113 113 113 122 122 122 122 123 123 111 111	268 532
	85.7
N N N N N N N N N N N N A 4 4 4 4 4 4 4	4, 4, 80 80
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# ALIGNMENTS

Peptide #6511 encoded by probe for measuring cervical gene expression. Probe; human; microarray; gene expression; cervical epithelial cell; AAM20077 standard; protein; 92 AA. (first entry) cervical cancer. 12-OCT-2001 AAM20077; RESULT 1 AAM20077

30-JAN-2001; 2001WO-US000670. WO200157278-A2. Homo sapiens. 09-AUG-2001. 

04-FEB-2000; 2000US-0180312P. 26-MX-2000; 2000US-020456P. 30-UJN-2000; 2000US-00608408. 03-AUG-2000; 2000US-00632366. 21-SEP-2000; 2000US-023468PP. 27-SEP-2000; 2000US-023468PP. 04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Rank DR; Chen W, Hanzel DK, Penn SG,

WPI; 2001-488901/53.

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.

Claim 27; SEQ ID NO 24903; 487pp; English.

The present invention relates to human single exon nucleic acid probes (SENP: see AA110068-AA120459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Heid cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                     Human, liver, cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
                                                                                                                                                            Human liver peptide, SEQ ID No 34115.
                        ABG55467 standard; peptide; 92 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0204456P.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00332366.
21-SEB-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                      WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                     ABG55467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
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  ABG55467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and diaplaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide #7950 encoded by probe for measuring placental gene expression.
                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 56; DB 4; Length 92; 100.0%; Pred. No. 0.06; tive 0; Mismatches 0; Indels
                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                              100.0%; Score 56; DB 4; Length 100.0%; Pred. No. 0.06;
                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 34182; 654pp; English.
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                                                                                                                                                                                                                                                                                                                                                             AAM33913 standard; protein; 92 AA.
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26-MAY-2000; 2000US-00207456P.
36-JUN-2000; 2000US-0060328408.
03-AUG-2000; 2000US-00633366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                                                                            10; Conservative
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                                                                                                                                                                                                                                                   GYTFTSYDIN 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488897/53
                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 92 AA;
                                                                   Sequence 92 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                           AAM33913;
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                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                             RESULT 2
AAM33913
AAM33913
AAM33913
AAM33913
AAM33913
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AAM391
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Rank DR;

Chen W,

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                                                                                   measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nuclectide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent dees not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                               The invention relates to a single exon nucleic acid probe (SENP) (1) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 56; DB 4; Length 92; 100.0%; Pred. No. 0.06; ive 0; Mismatches 0; Indels
Claim 27; SEQ ID NO 34115; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG43604 standard; peptide; 92 AA.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 92 AA;
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ABG43604
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1 GYTFTSYDIN 10

Matches

GYTFTSYDIN 26

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RESULT 3

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04-FEB-2000; 15-NOV-2001 

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Human peptide encoded by genome-derived single exon probe SEQ ID 33269
                                                                                                                                                                                                                                                                                            Hermansky-Pudlak syndrome; sarcoidosis, niemami-filo. dibedases pulmonary haemosiderosis; pulmonary histocytosis; pulmonary histocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocyetic pulmonary dysplasia; pulmonary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                      interstitial lung disease;
                                                                                                                                                      chronic obstructive pulmonary disease; interstitial lung dise
familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                  Human; single exon probe; asthma; lung cancer;
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Homo sapiens

WO200186003-A2

30-JAN-2001; 2001WO-US000665

2000US-0180312P 2000US-0207456P 2000US-00608408 26-MAY-2000; 30-JUN-2000;

2000US-00632366. 2000US-0234687P. 2000US-0236359P. 2000GB-00024263 03-AUG-2000; 21-SEP-2000; 27-SEP-2000; 04-OCT-2000;

(MOLE-) MOLECULAR DYNAMICS INC

Chen W, Rank DR; Penn SG, Hanzel DK,

WPI; 2002-114183/15

Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

Claim 27; SEQ ID NO 33269; 634pp; English

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from the man lung comprising single exon nucleic acid probes having one of 12614 mucleic acid sequences meating frames derived from the 12614 to proper sing frames derived from the 12614 mucleic acid sequences meating frames derived from the 12614 mucleic organization, or their complements or the 12387 open reading frames derived from the 12614 mucleic acid sequences which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample act derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a enkaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the existaryote; and (b) detecting specific hybridisation of detectably, labeled nucleic acids from euwaryote lung mRNA, to a single exon probe, having a framement identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, above and (b) measuring the expression of each of the exons in the transportation of a single gene, above and (b) measuring the expression of the exons should be assigned to a single gene; a petide comprising one of the exons should be assigned to a single gene; a petide comprising one of the exons should be assigned to a single gene; a petide comprising one of the exons should be assigned to a single gene; a petide comprising one comprise, mentioned in the specification, or encoded by the probes/open reading frames (ORP). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human analysis, and for the study of lung disease (ORP), interstitial lung disease (Lilbor maniforme, fishocopes/open reading frames (ORP). The p

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human factor VIII antibody A3-C1 specific scFv protein DP-15 which is used in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies.
present sequence is a peptide/protein encoded by a single exon probe the invention. Note: The sequence data for this patent did not form pot the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A;
ScFv; A3-C1.
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llarity 100.0%; Pred. No. 0.064;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Human FVIII antibody A3-C1 scFv heavy chain protein DP-15.
                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Turenhout BAM,
                                                                                                              100.0%; Score 56; DB 5; 100.0%; Pred. No. 0.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.
                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                          AAY50958 standard; protein; 98 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-NL000285.
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                                                                                                             Query Match
Best Local Similarity 100.
Matches 10; Conservative
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hes 10; Conserv
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                                                                                Sequence 92 AA;
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Matches
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Human antibody fragment #45.

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Human, Fv molecule, hypervariable region, single chain Fv; cytostatic, disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia, adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guy R, Lipschitz O, Szanton E, Levanon A;
                                                                                                                                                                                                                                                                                            Human Fv molecule hypervariable region related peptide #45.
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                                                                         ABG78170 standard; protein; 98 AA.
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                                                                                                                                                                                                                   (first entry)
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Plaksin D, Peretz T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WC200259264-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                  ABG78170;
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RESULT 6

RESULT 6

LD ABG738170

LD ABG738170

XX ABG738170

XX Huma ABG78

XX H
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The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scrv) or a disulfide Fv (dsrv). The peptide, optionally in association with or attached, coupled, combined, linked or fueed to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region related peptide of the invention

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Gaps
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100.0%; Score 56; DB 5; Length 98; 100.0%; Pred. No. 0.064; 1. Indels 1. O. Mismatches 0; Indels
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ABG91861 standard; protein; 98 AA. (first entry) 04-DEC-2002 ABG91861; RESULT 7
ABG91861
ID ABG9
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AC ABG9
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XX
DT 04-E

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The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigan-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful from inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restencisis, growth and/or replaced and/or rell-cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet platelet and/or cells in cease in number of tumour or leukaemia cells increasing the susceptibility of diseased cells to deareading the number of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to deareasing the number of tumour or leukaemia cells, for increasing the susceptibility cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for dispossing and treating diseases nuch as cancer, leukaemia, autoimmune diseases, inflammatory diseases and other diseases mediated by abnormal platelet function and diseases and other diseases mediated by abnormal platelet function and diseases and other diseases mediated by abnormal platelet function and diseases and other diseases mediated by abnormal platelet function and diseases and other diseases mediated by abnormal platelet function and diseases and other diseases mediated by abnormal platelet function and diseases and other diseases mediated by abnormal platelet function and diseases and other diseases mediated by abnormal platelet function and diseases and other diseases mediated by abnormal platelet function and diseases and other diseases mediated by abnormal platelet function and diseases and other diseases mediated by abnormal platelet function interesting and diseases and other diseases mediated by abnormal platelet function and diseases and other diseases mediated by abnormal platelet function interestin
                                                                            metastasis; hypervariable region; autoimmune disease; thrombosis; restencess; ludkaemia; inflammatory disease; acatdovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mar-Haim H;
Levanon A;
                                                       Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nimrod A,
Peretz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plaksin D, Vogel T,
Amit B, Kooperman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 246; Opp, English.
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29-DEC-2000; 2000US-0258948P.
                                                                                                                                                                                                                                                                                                                                                                                                      31-DEC-2001; 2001WO-US049442.
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Szanthon E, Richter T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-674776/72.
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                                                                                                                                                                                                                                Homo sapiens.
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Gaps .; 0 100.0%; Score 56; DB 5; Length 98; 100.0%; Pred. No. 0.064; iive 0; Mismatches 0; Indels 10; Conservative Query Match Best Local Similarity Matches

Sequence 98 AA;

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ABO27070 standard; protein; 98 AA. ABO27070; RESULT 8 ABO27070 HXXXH

(first entry) 10-SEP-2003

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The invention describes a method of making a humanised antibody, comprising making chimeric antibodies containing a complementarity comprising making chimeric antibodies containing a degramation of determining region (CDN) from a non-human antibody and appropriate framework sequences (I) of human antibodies. (I) is selected by using canonical CDR structure types of non-human antibodies as the basis of canonical CDR structure types of human antibodies as the basis for selection, for humanisation. The method is useful for making a to an interpret of any subject species to a less immunoganic form suitable for use in an object species. The method is reliable for identifying suitable human framework sequences to support non-human CDR regions and to provide humanis antibodies that retain this antigen binding with two immunogenicity in humans, without the need for determining critically important amino acid residues in the framework and without the need for multiple iteration and construction to obtain humanised antibodies with suitable therapeutic properties. The antibody has high affinity and low immunogenicity without need for comparing framework sequences between non-human and human antibodies. This sequence framework sequences between non-human and human antibodies. This sequence represents a human heavy chain variable region gene segment used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                            Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
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                                               Human; heavy chain variable region; VH; humanieed antibody;
chimeric antibody; complementarity determining region; CDR;
canonical CDR structure type.
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              Human germline heavy chain variable region gene segment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavy chain variable region for monoclonal antibody 4A10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3xample 1; Fig 1; 31pp; English.
                                                                                                                                                                                                                                                                                         12-JUL-2001; 2001US-0305111P.
                                                                                                                                                                                                                                                  12-JUL-2002; 2002US-00194975
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(first entry)
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Best Local Similarity 100.
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                                                                                                                                                                         US2003039649-A1.
                                                                                                                                                                                                                                                                                                                                 (FOOT/) FOOTE J
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                                                                                                                                    Homo sapiens
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21-DEC-1995
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rythiutuura aintivutes inave beein produced with Egypen Ceils of Embry compuse that had received multiple injections of mercuric ions reacted with compuse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate covalent compound which was covalently bound to keyhole limpet hemocyanin (KIAI). Eight hybridomas (CIFIO, 4AIO, 1CII, 5G4, 23F8, 2D5, 5B6 and 3EB) were producing Mabs that cover strongly positive against glutathone without mercuric ions. RNA was isolated from hybridoma cells with ganidine isothiocyanate. First strand cDNA synthesis was catalysed by Mulv reverse transcriptase. The primers used for conna synthesis were complementary to the 5' end of the CH1 domain of the cappa domain. Some of the brimers used for cDNA synthesis are shown in AAQ97511-Q97518. The primers used for cDNA synthesis of the CK kappa domain. Some of the brimers used for cDNA synthesis of the CK wariable region of a particular antibody polypeptide was also used for cPCR amplification of that variable region, in conjunction with an copropriate V-region primer. In addition, the VH primer AAQ97518 was used to amplified mucleotides were determined. These are given in AAQ97518 was used to amplified mucleotides were determined. These are given in AAQ97518 cand the deduced AA sequences in AAR79241-R79250 & AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are deferent from the descriptions in the sequence listings are used here. (Updated on 25-MAR-copy to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or neutralising heavy metals.
Monoclonal antibody; heavy metal; mercury; variable region; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies have been produced with the spleen cells of BALB/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Page 54; 106pp; English
                                                                                                                                                                                                                                                                                        Wagner F;
                                                                                                                                                                                                        94US-00187407.
                                                                                                                                                                 95WO-US001199.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                        Lopez O, Wylie DE,
                                                                                                                                                                                                                                                                                                                               WPI: 1995-275415/36
                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ97498
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                                                                                                                                                                                                          27-JAN-1994;
                                                                                                                                                                   27-JAN-1995;
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                                                                                                                         03-AUG-1995
                                           Synthetic.
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Thu Apr 22 05:59:06 2004

Homo sapiens

WO9426895-A1

06-APR-2001; 2001CU-00000084.

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The invention relates to a chimeric antibody, derived from a monoclonal antibody, which recognises N-glycosylated gangliosides and is produced by hybridoma ECACC 9413026. The chimeric antibody, and similar antibodies derived from the anti-idiotypic monoclonal 1E10 (recognising P3) are used for treatment, localisation and in vivo identification of breast cancer and melanoma, their metastases and relapses, tumours of lung, digestive and urogenital tracts, and sarcoma and tumours of neuroectodermal origin. This sequence represents a protein relating to the chimeric antibody of the invention
                                                                                                                                                                                                                                                                                                                                         diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                New chimeric antibodies, useful for treatment, prevention and di
of tumors that express gangliosides, are derived from monoclonal
antibodies P3 or 1E10.
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                                                                                                                                                                                                      Lombardero Valladares J;
                                             CENT IMMUNOLOGIA MOLECULAR. MATEO DE ACOSTA DEL RIO C M. LOMBARDERO VALLADARES J. ROQUE NAVARRO L T.
                                                                                                                                                                                                   il Rio CM, Lombar
Lopez Requena A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Fig 8; 31pp; Spanish.
                                                                                                                                                                                                      Mateo De Acosta Del Rio
Roque Navarro LT, Lopez
                                                                                                                               ROQUE NAVARRO L
LOPEZ REQUENA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GYTFTSYDIN 10
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                                                                                                                                                                                                                                                                                   WPI; 2003-046857/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 119 AA;
                                                                                                                            (NAVA/)
(REQU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein sequences (AAR66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (AAQ78939-97002) ware isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; Y5, Y24; 3-31; M64; M118 and M131, Dy DCR amplification using primers AAQ78917-38. The genes are subdivided into 5 families of Vh genes. The fragments over a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TaqI restriction enzyme. The fragments were peparated by gel electophoresis and 35-45 kb fractions were collected. The fragments were ligated with clar-digested cosmid vector DNBH. The fragments were ligated with clar-digested cosmid vector DNBH. The fragments were in vitro packed and infected into E.coll 499A. The fragments were buckloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human mammalian hosts. (Updated on 25-WAR-2003 to correct PN
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- for the

DNA fragment comprising human immunoglobulin Vh genes production of human immunoglobulin in mammalian hosts.

93WO-JP000603 93WO-JP000603

10-MAY-1993;

24-NOV-1994.

(NISB ) JAPAN TOBACCO INC

10-MAY-1993;

Honjo T, Matsuda F;

WPI; 1995-006791/01. N-PSDB; AAQ78946 Claim 17; Page 41-42; 130pp; Japanese.

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ABJ18570 standard; protein; 119 AA.

ABJ185

(first entry)

18-FEB-2003

ABJ18570;

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Gaps . 0

100.0%; Score 56; DB 2; Length 117; 100.0%; Pred. No. 0.076; tive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 10; Conservative

Sequence 117 AA;

1 GYTFTSYDIN 10

54

45 GYTFTSYDIN

g

Cytostatic, chimeric antibody, monoclonal antibody, ECACC 94113026, N-glycosylated ganglioside, anti-idiotypic monoclonal 1E10, metastatic, breast cancer, melanoma, tumour; lung; digestive, urogenital tract; sarcoma, neuroectodermal. Ganglioside-associated recombinant antibody related VH 1E10 protein. CENT IMMUNOLOGIA MOLECULAR.
MATEO DE ACOSTA DEL RIO C M.
LOMBARDERO VALLADARES J.
ROQUE NAVARRO L T.
LOPEZ REQUENA A. 08-APR-2002; 2002WO-CU000003 06-APR-2001; 2001CU-00000084 WO200281496-A2 Unidentified 17-OCT-2002. (IMMU-) (DRIO/) (VALL/) (NAVA/) (REQU/) 

Cytostatic; chimeric antibody; monoclonal antibody; ECACC 94113026; N-glycosylated ganglioside; anti-idiotypic monoclonal 1E10; metastatic; breast cancer; melanoma; tumour; lung; digestive; urogenital tract;

sarcoma; neuroectodermal

WO200281496-A2

17-OCT-2002.

Unidentified

Ganglioside-associated recombinant antibody related VHIB10 protein #2

ABJ18572 standard; protein; 119 AA.

18-PEB-2003 (first entry)

ABJ18572;

Lombardero Valladares J;

Mateo De Acosta Del Rio CM, Lombar Roque Navarro LT, Lopez Requena A;

08-APR-2002; 2002WO-CU000003

Sequence 120 AA;

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The invention relates to a chimeric antibody, derived from a monoclonal antibody, which recognises N-glycosylated gangliosides and is produced by hybridoma bcAcc 94113026. The chimeric antibody, and similar antibodies derived from the anti-idiotypic monoclonal 1810 (recognising P3) are used for treatment, localisation and in vivo identification of breast cancer and melanoma, their meteastases and relapses, tumours of lung, digestive and urogenital tracts, and sarcoma and tumours of neuroectodermal origin: This sequence represents a protein relating to the chimeric antibody of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gpl20. These can be used in diagnosis and therapy of HIV-1 infection
                                                        New chimeric antibodies, useful for treatment, prevention and diagnosis of tumors that express gangliosides, are derived from monoclonal antibodies P3 or 1810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gpl20, useful for detecting in biological sample and providing passive immunotherapy to HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus-1; HIV-1; human monoclonal antibody; envelope glycoprotein; gp120; diagnosis.
                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 56; DB 6; Length 119; 100.0%; Pred. No. 0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human HIV-1 monoclonal antibody SEQ ID NO: 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 51-52; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB62747 standard; protein; 120 AA
                                                                                                                          Example 6; Fig 6; 31pp; Spanish.
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Best Local Similarity 100.
Matches 10; Conservative
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N-PSDB; AAF29048.
              WPI; 2003-046857/04.
N-PSDB; ABT14040.
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                                                                                                                                                                                                                                                                                                                             Sequence 119 AA;
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                                                                                                                                                                                                                                                                                               the invention
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New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55769-830) or its fragment. The binding agents are antibodies that recognize and bind to angiopoietin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating or inhibiting the activity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease, inflammatory disease, inflammatory disease, or psoriasis) in a mammal. The present sequence represents a heavy chain variable region of an anti-Ang-2
                            ö
                                                                                                                                                                                                                                                                       Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic; gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer; angiogenesis; antibody.
                            Gaps
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                                                                                                                                                                                                                                                    Heavy chain variable region of anti-Ang-2 antibody IP-2C11 HC
100.0%; Score 56; DB 4; Length 120; 100.0%; Pred. No. 0.078;
                            0; Indels
                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                 ABR55829 standard; protein; 122 AA
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2002US-00269805.
                                                                                                                                                                                                                          (first entry)
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/note= "c
                              Conservative
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/note= "
                                                            1 GYTFTSYDIN 10
                                                                             GYTFISYDIN 36
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               Similarity
10; Conser
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10-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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   Query Match
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Gaps

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0; Indels

0; Mismatches

Length 122;

; 9 DB

Score 56;

100.08;

Sequence 122 AA;

Query Match

Search completed: April 21, 2004, 17:33:09 Job time : 42 Becs

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The invention relates to a chimaeric molecule comprising the GD3
(ganglioside antigen) binding domain of antibody MB3.6, with any of 3
variable gene sequences, or the PSMA (prostate-specific membrane antigen)
binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
sequences, the zeta signalling chain of the T cell receptor and an
indicate molecules expressed in which cysteine residues have been mutated.
The chimaeric molecules expressed in the T cells or NK cells or other
effector cells are useful in treating patients with cancers expressing
the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
and/or together with each other or with heterologous constructs to engage
additional stimulatory and functional properties of the effector cells to
enhance the antitumour therapeutic efficacy (claimed). They are
tumours and prostate and small cell lung cancer. The present sequence
tumours and prostate and small cell lung cancer. The present sequence
                                                                                                                                                                                                                                                                                                                                 T-cell receptor; cytostatic; dermatological; neuroprotective; immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4; all; procetate-specific membrane antigen; zeta signalling chain; CD81pha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer; heavy chain variable region; mouse.
                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimeric molecule useful in treating patients with disorders, such as melanoma, neuroendocrine disorders, prostate and small cell lung cancer comprises GD3 and/or PSMA binding domains of antibody.
                                  Gaps
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Pred. No. 0.079;
                                                                                                                                                                                                                                                                                                    Mouse antibody 4D4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 14-15; 35pp; English.
                                                                                                                                                                                                ABG74245 standard; protein; 139 AA.
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                 Best Local Similarity 100.0%;
Matches 10; Conservative 0
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Best Local Similarity 100.
Matches 10; Conservative
                                                                  1 GYTFISYDIN 10
                                                                                           26 GYTFTSYDIN 35
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N-PSDB; ABX16571.
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GYTFTSYDIN 10 GYTFTSYDIN 54

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Š		761-	JS-10-194-975-	JS-10-453-698-4	10-029-926B-4	US-10-041-860-289	US-10-041-860-29	US-10-041-860-29	US-10-041-860-296	US-10-041-860-342	US-10-041-860-	-860	US-10-041-860-350	JS-10-041-860-36	JS-10-041-860-36	-860	
SUMMARIES		864-	-194	-453	-029	-041	-041	-041	-041	-041	-041	-041	-041	-041	-041	-041	
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	* Query Match	100.0	100.0	0.00	0.001	0.00	100.0	100.0	100.0	0.001	0.00	0.00	0.00	0.00	0.00	0.00	
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Sequence 374, Apple Sequence 43, Apple Sequence 43, Apple Sequence 45, Apple Sequence 45, Apple Sequence 1, Apple Sequence 10, Apple Sequence 203, Apple Sequence 203, Apple Sequence 237, Apple Sequence 240, Apple Sequence 343,	equence 21 equence 10 equence 20 equence 28 equence 24 equence 24 equence 31 equence 31 equence 31
US-10-041-860-374 US-10-308-817-43 US-10-032-938-45 US-10-022-938-45 US-10-032-423A-45 US-10-041-860-1 US-10-041-860-237 US-10-041-860-238 US-10-041-860-240 US-10-041-860-343 US-10-041-860-343 US-10-041-860-343 US-10-041-860-343	US-10-041-86 US-10-041-86 US-10-041-86 US-10-041-86 US-10-041-86 US-10-041-86 US-10-041-86 US-10-041-86 US-10-041-86 US-10-041-86 US-10-041-86 US-10-041-86
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ALIGNMENTS

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| Designation of the process of the
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Sequence 45. Application US/10029926B
Publication No. US20040073011A1
GENERAL INFORMATION:
APPLICANT: HAGAY.
TITLE OF INVENTION:
FILE REFERENCE: 10793/50
CURRENT PELICATION NUMBER: US/10/029,926B
CURRENT PELING DATE: 201-12-31
PRIOR PILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 45
LENGTH: 98
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Sequence 2009, Application US/10041860

Publication No. US20030157109A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Peng, Xiao-Chi

APPLICANT: Peng, Xiao-Chi

APPLICANT: Peng, Xiao-Chi

APPLICANT: Reser, Francine

APPLICANT: Weber, Frichard

APPLICANT: Bezabch, Binyam

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: ABGENIX.051A

CURRENT APPLICANT: 051A

CURRENT APPLICANT: 2002-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 56; DB 12; Length 98; Best Local Similarity 100.0%; Pred. No. 0.03; Matches 10; Conservative 0; Mismatches 0; Indels
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100.0%; Score 56; DB 12;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 289
LENGTH: 98
     FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT PEDLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
SEQ ID NO 43
LENGTH: 98
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US-10-029-926B-45
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ORGANISM: homo sapiens
                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: human
US-10-453-698-43
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US-10-041-860-289
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US-10-029-926B-45
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
US-09-864-761-47202
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100.0%; Score 56; DB 9; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2001-01-30

PRIOR PLILING DATE: 2000-09-21

PRIOR PLILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR APPLICATION NUMBER: US 09/704,203

PRIOR PLILING DATE: 2000-06-30

PRIOR PLILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine Vers. 1.1

SEQ ID NO 47202
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US-10-194-975-3

US-10-194-975-3

Sequence 3, Application US/10194975

Publication No. US20030039649A1

GENERAL INFORMATION:

APPLICANT: FOOLE, Jefferson

TITLE REPRERENCE: 50121.01

CURRENT FILING DATE: 2002-10.19

PRIOR APPLICATION NUMBER: US/10/194,975

CURRENT FILING DATE: 2001-07

PRIOR PILING DATE: 2001-07

NUMBER OF SEQ ID NOS: 122

NUMBER OF SEQ ID NOS: 122

SOFTWARE: Patentin version 3.1
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Sequence 43, Application US/10453698
Publication No. US20040038308A1
APPLICANT: ROCHATION:
APPLICANT: ROCHAT.
TITLE OF INVENTION: HYBRID ANTIBODIES
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; ORGANISM: Homo sapiens
US-10-194-975-3
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Matches 10; Conser
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LENGTH: 96
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APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REPRENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
SOFTWARE: FactSEQ for Windows Version 4.0
SEQ ID NO 296
LENGTH: 98
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APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTHEODIES DIRECTED TO PDGFD AND USES;
TITLE OF INVENTION: THEREOF
FILE REFRENCE: ABGRNIX.051A
CURRENT APPLICATION
CURRENT APPLICATION
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PSESEE for Windows Version 4.0
SEQ ID NO 342
LENGTH: 98
Pred. No. 0.03;
; Mismatches 0; Indels
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o. US20030157109A1
   Best Local Similarity 100.0%; P
Matches 10; Conservative 0;
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Yang, Xiao-Dong
Chen, Francine
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Yang, Xiao-Dong
Chen, Francine
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                     1 GYTFTSYDIN 10
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CORGANISM: homo sapiens
US-10-041-860-296
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; ORGANISM: homo sapiens
US-10-041-860-342
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                                                                        100.0%; Score 56; DB 14; Length 98; 100.0%; Pred. No. 0.03;
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APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CORRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FREESEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels
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APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTHRODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: 105/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 295
LINGTH: 98
                                                                                                                                             0; Indels
                                                                                                                                                0; Mismatches
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APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 290, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
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Yang, Xiao-Dong
Chen, Francine
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Weber, Richard
                                                                            Query Match
Best Local Similarity 100.
Matches 10; Conservative
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; ORGANISM: homo sapiens
US-10-041-860-290
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          US-10-041-860-289
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Chen, Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES DIRECTED TO CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 31
LENGTH: 98
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                                                                                                                                              APPLICANT: Jia, Xiao-Chi
APPLICANT: Fang, Xiao-Chi
APPLICANT: Peng, Xiao-Chi
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APLICATION DOS: 377
NUMBER OF SEQ ID NOS: 377
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 350
LENGTH: 98
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hag 0; Indels
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| FEATURE:
| NAME/KEY: VARIANT
| LOCATION: 55
| OTHER INFORMATION: Xaa = Any Amino Acid
| FEATURE:
| NAME/KEY: VARIANT
| LOCATION: 55
| OTHER INFORMATION: Xaa = Any Amino Acid
| US-10-041-860-350
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Publication No. US20030157109A1
GENERAL INFORMATION:
                                                        Sequence 350, Application US/10041860
Publication No. US20030157109A1
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CORGANISM: homo sapiens
US-10-041-860-361
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                                                                                                                                                                                     APPLICANT: CORVALIAN, JOSE R.F.
APPLICANT: CORVALIAN, JOSE R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Peng, Xiao-Chong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Cazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ARGENIX: 051A
CURRENT APPLICANTION: THEREOF
FILE REFERENCE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTESEQ FOR WINGOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 98;
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100.0%; Score 56; DB 14; Length 9
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indel8
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TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGENIX:051A
CURRENT APPLICATION NUMBER: 13010/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 56; DE Best Local Similarity 100.0%; Pred. No. 0.( Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 348, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
                                                                                                                          Application US/10041860
5. US20030157109A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GYTFTSYDIN 10
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26 GYTFTSYDIN 35
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US-10-041-860-348
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US-10-041-860-344
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LENGTH: 98
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                                                                                                                                                                                                                                                                                               Sequence 362, Application US/10041860
; Sequence 362, Application US/10041860
; Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Gazir, Riao-
APPLICANT: Gazir, Riao-
APPLICANT: Bezabeh, Blanyam
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: APPLICANT: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ATPIBODIES
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100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels
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Publication No. US20030157109A1

GENERAL INPORMATION:

APPLICANT: Corvain, Jose R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Feng, Xiao-Chi

APPLICANT: Feng, Xiao-Dong

APPLICANT: Reng, Xiao-Dong

APPLICANT: Reng, Xiao-Dong

APPLICANT: Reng, Xiao-Dong

APPLICANT: Reng, Xiao-Dong

APPLICANT: Heng, Xiao-Dong

TATLE OF INVENTION: APPLICANT

TITLE OF INVENTION: THEREOF

FILE REFERENCE: AGGINIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOUTHARRE FASTSEQ FOR Windows Version 4.0
0; Indels
    0; Mismatches
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NAME/KEY: VARIANT
LOCATION: 57
OTHER INFORMATION: Xaa = Any Amino Acid
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . LOCATION: 57
. OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-362
    10; Conservative
                                                                         1 GYTFTSYDIN 10
                                                                                                                                       26 GYTFTSYDIN 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: homo sapiens
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US-10-041-860-373
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US-10-041-860-362
        Matches
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April 21, 2004, 17:25:48; Search time 7.6087 Seconds (without alignments) 102.653 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 inpnsgntdyagkfg 15 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P23083 homo sapien	homod	рошо	P01756 mus musculu	mus	30 mus	53 mus	mus	mns	mus	mus	mue	mus	BUM	mus	gnw	BUMB	enm	พนล ก	P01742 homo sapien	prichr	marc	mus	MUS		Q9sj09 arabidopsis	_			Q58205 methanococc		clos	P46935 mus musculu
	ID	HV1G HUMAN	HV1B HUMAN	HV1C_HUMAN	HV12 MOUSE	HV13 MOUSE	HV51_MOUSE	HV09_MOUSE	HV10 MOUSE	HV49 MOUSE	HV07 MOUSE	HV50_MOUSE	HV48 MOUSE	HV04 MOUSE	HV03_MOUSE	HV11_MOUSE	HV06_MOUSE	HV15_MOUSE	HV02_MOUSE	HV14 MOUSE	HV1A HUMAN	GSH1_BUCAP	YCF0 MARPO				WRS9_ARATH	FMT CANBF		AAAD HUMAN	Y795_METJA	PGMU_ECOLI	GUNG_CLOTM	NED4_MOUSE
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dФ	Query Match Length	86.6	75.6	•	69.5		٠	62.2	62.2	62.2	62.2	61.0	61.0	59.8	4.	54.9	•	ä				•		48.8		•	•	•	•	•	47.6	•	٠	47.6
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Q62940 rattus norv P46934 homo sapien Q8ulro pyrococcus P32004 homo sapien Q8kc1 streptococc Q99y0 streptococc Q99y0 streptococc Q99y0 streptococc Q99y1 catharanthu P5915 porphyromon Q01948 williopsis P12067 sus scrofa P58647 yersinia pe
NED4_RAT NED4_HUMAN YB45_PYRFU CAML_HUMAN YB49_STRP3 STS7_CATRO HGA1_PORGI HGA2_PORGI TOXK_WILSA IVC1_PIG ATPE_YERPE
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=88296408; PubMed=2841108; MEDIINE=88296408; PubMed=2841108; Medium = 8.0., Loa M., Zong S.Q., Ohno H., Fukuhara S., Honjo T.; Noispersed localization of D segments in the human immunoglobulin "Dispersed localization of D segments in the human immunoglobulin heavy.chain locus."; EMBO J. 7:1047-1051(1988).
                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 heary chain V-I region V35 precursor.
12 heary chains (Human).
13 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Cararrhini, Hominidae, Homo.
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86.7%; Pred. No. 3.2e-05;
iive 1; Mismatches 1; Indels
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                                                                117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X07448; -; NOT_ANNOTATED_CDS.

HSSP, P01772, 2FB4.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0008955; F:antigen binding; NAS.

GO; GO:0008955; P:immune response; NAS.

InterPro; IPR00710; Ig-like.

InterPro; IPR003596; Ig-like.
                                                         PRT;
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SMARI, SM00406; IGv. 1.
PROSITE; PS56835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                STANDARD;
RESULT 1
HVIG HUMAN
ID HVIG HUMAN
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Gould H.J.;
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                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration the the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ID HVIC HUMAN STANDARD; PRT; 147 AA.

AC PO1744;

DT 21-JUL-1986 (Rel. 01, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 19 heavy chain V-I region ND precursor (Fragments).

OS Homo sapiens (Human).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NOBI TAXID=9606;

RN | 11 | RP SEQUENCE FROM N.A.

REPLINE-83065234; PubMed=6815656;

RX Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE=83065234; FubMed=6815656;
Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
                                                                                                                                                                                        MEDINE-83144028; PubMed-6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;
                                                                                                                                                                                                                             (VH) gene subgroups.";
proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 heavy chain V-I region HG3 precursor.
HOmo sapiens (Human)
                                       117 AA.
                                                                                                                                                                                                                                                                                                                                                                         EMBL, J00240; AAA52988.1; -.
PIR; A02024; HYHUHG.
HSSP; POIT72; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig_v.
Ffam; PF00047; Ig; 1.
SMART; SM0406; IGv; 1.
PROSTIE; PSS0835; IG_LIKE; 1.
                                       PRT;
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                                         STANDARD;
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7117
                                                                                                                                                                              SEQUENCE FROM N.A.
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117
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                                         HV1B HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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P01756;
21-UTL-1986 (Rel. 01, Last sequence update)
21-UTL-1986 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 g heavy chain V region MOPC 104E.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
MEDLINE-83075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
"Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                       HISSP, PO1789; IMCP.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005953; P:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            th 75.6%; Score 62; DB 1; Length 147; I Similarity 73.3%; Pred. No. 0.0014; 11; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V-I REGION ND. IG-LIKE. PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 AA; 16491 MW; 948F9F72A5366C20 CRC64;
                                                                                                                                                                                                                                       PROTEIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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HSSP; P01789; 1MCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
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Pfam, PF00047; ig; 1.
SMART, SM00406; IGy, 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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51 INPNNGGTSYNQKFK 65
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Best Local Similarity 66.79
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NON TER
SEQUENCE
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HV51 MOUSE

TO 66330,

AC P06330,

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 01-JAN-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DT 15-JUL-1999 (Rel. 38, Last cannotation update)

SE 19 heavy chain V region AC38 205.12.

SE Mus musculus (Mouse).

CO Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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21-JJJL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region J558.
Ig heavy callas (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 113 TaxID=10090;
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                                                                            IG-LIKE.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (COMPLEX).
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                                                                                                                                                                                                                                                                                                      69.5%; Score 57; DB 1; Length 117; 66.7%; Pred. No. 0.0078; 11ve 2; Mismatches 3; Indels
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117 117
117 AA, 13024 MW, 292E2AF4BE447E41 CRC64;
                                                                                                    1 116 1G-LIKE.
22 96 BY SIMILARITY.
55 55 N-LINKED (GLCNAC. . .) (CC
117 117
117 AA; 12993 MW; 3CF8ACE4BE447E41 CRC64;
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BY SIMILARITY.
PROSITE, PSS0835; IG LIKE, 1.
Immunoglobulin V region; Glycoprotein.
DOMAIN
1 116 IG-LIKE.
DISULED 22 96 BY SIMILAR
CARBOHYD 55 55 N-LINKED IN TER 117 117
SEQÜENCE 117 AA; 12983 MM; 3CF8ACE4
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51 INPNNGGTSYNQKFK 65
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Best Local Similarity be...
Best Local 10, Conservative
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Best Local Similarity 66.7°
Matches 10; Conservative
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AC
DT 1-171-1986 |
DT 21-711-1986 |
DT 21-711-1986 |
DT 21-711-1986 |
DT 10-0CT-2003 |
DE 10 heavy chains of the second of the seco
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RA Bottwell A.L.M., resolution to the NPD family of
RT "Heavy chain variable region contribution to the NPD family of
RT "Heavy chain variable region contribution to the NPD family of
RT antibodies somatic mutation evident in a gamma 2a variable region.";
RL "HEAST SOME STATE COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR HSSP, PO1840; ZPBJ.
DR HSSP, PO1840; ZPBJ.
DR HSSP, PO1840; Jej.
DR PROSTITE; PS50835; IG_LIKE; 1.
DR RROSTITE; PS50835; IG_LIKE; 1.
FT CHAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 115 BY SIMILARITY.
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                                                                                                                               SEQUENCE.
MEDLINE=84182519; PubMed=6201362;
MEDLINE=84182519; PubMed=6201362;
MEDLINE=84182519; PubMed=6201362;
"A V region determinant (idiotope) expressed at high frequency in B lymphocytes are encoded by a large set of antibody structural genes."; PEMBO J. 3:517-523(1984).
PIR, A02040; MHMS38.
HSSP: PO1798; IMCP.
InterPro; IPR00710; Ig-like.
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SEQUENCE FROM N.A.
STAINACS-1812/6;
MEDILINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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99 104 D SEGMENT.

105 118 J SEGMENT.

2 96 BY SIMILARITY.

118 118 119 119 W, 94F7BEE4C762A018 CRC64;
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01-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
Mus musculus (Mouse)
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Matches

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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region B1-8/186-2 precursor.
Buks musculus (Mouse).
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                              01-JAN'1988 (Rel. 06, Created)
1-JAN'1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
17 heavy chain V region VH558 B4 precursor.
18 heavy chain (Mouse).
19 heavy chain (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE-85099340; PubMed-2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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PIR; A02035; MHMSB4.
HSSP; PO1810; 2FB-.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Ffam; PF00047; Ig; I.
SMART; SM00406; IGv; I.
FROSITE; PS50835; IG LIKE; I.
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MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unrearranged VH gene segments.";
Cell 40:271-281(1985).
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HV07 MOUSE
ID HV07 MOUSE
                                                       HV49 MOUSE
P06328;
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Matches
                             HV49_MOUSE
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
"Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
Cell 24:625-637(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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Pred. No. 0.083;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY - DETERMINING-2
                                                               62.2%; Score 51; DB 1; Length 117; 60.0%; Pred. No. 0.083; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION 145.
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12890 MW; 16191A088CB17F5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK-2.
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larity 60.0%;
Conservative
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70 IDPNSGGTKYNEKFK 84
                                                                                                                                                                                                            1 INPNSGNTDYAQKFQ 15
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70 IDPNSGGTKYNEKFK 84
                                                                                                                                         Conservative
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   117 AA;
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   SEQUENCE
                                                                  Query Match
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HV10\_MOUSE

HV10\_M

AC 101754, 10

DT 21-JUL-10

DT 21-JUL-10

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GN IGH-VJ

GN IGH-V

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Best Loc Matches

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Tucker P.W.;
"Illegitimate recombination generates a class switch from C mu to C delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
HISSP; P01810; 2FBJ.
InterPro; IPR00310; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=84248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION TEPC 1017.
FRAMEWORK-1.
COOPLEMEMPRITY-DETERMINING-1.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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Pred. No. 0.15;
4; Mismatches 3; Indels
                                                                                                                                       Score 50; DB 1; Length 120;
Pred. No. 0.13;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15576 MW; 748157E4C6907B8E CRC64;
                                                                                                              13311 MW; 914453F426F09834 CRC64;
                                                                                                                                                                                                                                                                                                                                   23-0CT-1986 (Rel. 02, Created)
23-0CT-1986 (Rel. 02, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
1G heavy chain V region TEPC 1017 precursor.
Mus musculus (Mouse).
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                                        V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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INPNDGRSNYNEKFK 84
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51 INPSNGGTNYNEKFK 65
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Best Local Similarity 53.34
Finance By Conservative
                                                                                                                                          Query Match
Best Local Similarity 53.3
Matches 8; Conservative
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138
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138 AA;
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106 1
22
120 1
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HV04_MOUSE
ID HV04_MOUSE
AC P01748;
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                                        DOMAIN
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DOMAIN
DISULFID
NON TER
SEQUENCE
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HV48 MOUSE
ID HV48 MOU!
AC P03980;
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                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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              Gaps
 Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region AC38 15.3.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V REGION B1-8/186-2.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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                                                                                                                                                                                                                                            EMBL, J00529; AAA38170.1; -.
PIR, A90809; MHMS18.
PDB; 1A6U; 27-NAY-98.
PDB; 1A6U; 27-NAY-98.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Ffam; PR0047; ig; 1.
SMAR; SM00406; IGy.
Immunoglobulin V region; Signal; 3D-structure.
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JH2 SEGMENT.
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Interpro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
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70 IDPNSGGTKYNEKFK 84
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Best Local Similarity 60.0
Matches 9; Conservative
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54
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139 AA;
                                                                                                   (NPB ANTIBODIES
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P06329;
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HV50 MOUSE
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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P01755;
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HV11_MOUSE
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SERVENCE FROM N.A.

Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,

Anarabak-Rotbatein A.;

Anarabak-Rotbatein A.;

The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";

Lau. J. Immunol. 12:1023.19821.

C. I. MISCELLANBOUS: FROM ANNLYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J. SEGHENT, JHZ.

C. SEGHENT, JHZ.

C. I. SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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I. Cell 24:625-637 (1981).

-I- MISCELLANEOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES FRAT COULD ENCODE V REGIONS OF NPB ANTIBODIES. RISP. PO1810; 2FPG..

RICHEPPO; IPRO0110; Ig-like.

R InterPro; IPRO0110; Ig-like.

R InterPro; IPRO0110; Ig-like.

R REATER FOROVAT; Igy. 1.

R RROSITE; PS50835; IG_LIKE; 1.

M Immunoglobulin V region; Signal.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 heavy chain V region 36-65.
Buka musculus (Mouse).
Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae; Mus. Muscul_TaxID=10090;
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB 1; Length 117; Pred. No. 0.18;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region 23 precursor.
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117 AA;
                                                                                                                                                      Mus musculus (Mouse)
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HV03 MOUSE
LD HV03 MOUSE
AC P01747;
DT 21-JUL-1986
DT 10-OCT-2003
DE IG heavy cha.
OC Bukaryota; M.
Mammalia; Eul
OC Bukaryota; M.
OC Mammalia; Eul
OC RN NCBI_TAXID=10
RN SEQUENCE FROM
RR MEDLINE=8313
RA Marshak-Rothi
RT idiotype resi
RL Gut. J. Immun
CC 1- MISCELLAB
CC CONCLUDE
CC SEGNENT;
CC SEGNENT;
CC SEGNENT;
CC SEGNENT;
CC -1- SIMILARI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Heavy chain, variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).
-!- MISCELLANGOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL (NPB ANTIBODIES).
                                                                                                                                                                                                                                                                                      Gaps
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MEDILTE=81214548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                               Query Match

54.9%; Score 45; DB 1; Length 120;

Best Local Similarity 53.3%; Pred. No. 0.91;

Matches 8; Conservative 3; Mismatches 4; Indels
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                                                                                                                            1 111 IG-LIKE.
120 120
120 AA; 13307 MW; FF04E4A167B654AF CRC64;
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D SEGMENT.
JH2 SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JTL-1986 (Rel. 01, Created)
21-JTL-1986 (Rel. 01, Last sequence upc
15-JTL-1999 (Rel. 38, Last annotation of the any chain V region S43 precursor.
Mus musculus (Mouse).
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 1.
PMCSTTE; SMO0406; 1Gv; 1.
PRCSTTE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Hybridoma.
DOMAIN 1 111 IG-LIKE.
NOW TER 120 120
SEQUENCE 120 AA; 13307 MW; FF04E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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PIR; A02038; GZMS43.
HSSP, POLIBIO; ZEPA.
InterPro; IPR007110; InterPro; IPR003596; Ig_v.
FRam; PR0047; igf; 1.
PR081TB; R00406; Igv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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AA,
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Query Match Best Local Similarity 53.3%; Pred. No. 1.1; Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps

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1 INPNSGNIDYAQKFQ 15 |:|||| | | : |: 70 IDPNSGGTIYNEHFR 84

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Search completed: April 21, 2004, 17:33:57 Job time : 8.6087 secs

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REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-9081
TELEPHONE: 612-332-9081
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 116 anino acids
TYPE: amino acids
TOPOLOGY: linear
8
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Sequence 96, Appl
atent No. 5189147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                          April 21, 2004, 17:28:28 ; Search time 12:029 Seconds (without alignments) 42.918 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 96,
Patent No. 51
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Sequence 6
Sequence 1
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1: /cgm2_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgm2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-545-809A-96
US-09-192-545-2
US-09-192-545-2
US-08-478-039-65
US-08-478-039-65
US-08-478-039-65
US-08-478-039-65
US-08-478-039-65
US-08-478-039-13
US-08-476-349A-13
US-08-476-349A-13
US-08-881-037-64
US-08-881-037-64
US-08-881-037-64
US-08-881-037-64
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US-08-881-037-65
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                      389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                      Scoring table: BLOSUM62 Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Sequence 124, App Sequence 126, App Sequence 126, App Sequence 126, App Sequence 28, App Sequence 28, App Sequence 66, App Sequence 67, App Sequence 29, App Sequence 88, App Sequence 28, App Sequence 28, App Sequence 29, App Sequence 67, App Sequence 67, App Sequence 67, App Sequence 124, App Sequence 124, App Sequence 124, App		and Nucleotides Coding Therefore
1 US-08-488-113B-124 1 US-08-47-484B-124 1 US-08-477-484B-124 1 US-08-107-669D-29 1 US-08-107-669D-29 1 US-08-107-669D-67 1 US-08-107-669D-67 1 US-08-107-669D-67 1 US-08-472-78BA-28 1 US-08-472-78BA-28 1 US-08-472-78BA-89 1 US-08-477-78BA-89 1 US-08-477-78BA-89 2 US-08-477-531B-29 2 US-08-477-531B-66 2 US-08-477-531B-66 2 US-08-477-531B-66 2 US-08-477-531B-66 2 US-08-477-531B-66 2 US-08-477-531B-66 2 US-08-477-531B-66	ALIGNMENTS	US/08888366 svaldo anane E. Fred W. Mercury Binding Polypeptides an 39 39 31 31 31 32 31 34 35 35 35 35 35 35 35 35 37 36 30 30 30 30 30 30 30 30 30 30 30 30 30
9 43 76.8 118 128 43 76.8 118 128 43 76.8 118 128 43 76.8 118 128 43 76.8 118 6 43 76.8 118 6 43 76.8 118 6 43 76.8 118 6 43 76.8 118 6 43 76.8 118 6 43 76.8 118 6 43 76.8 118 6 43 76.8 118 6 6 8 118 6 8 118		1 10. 5972656 10. Application 10. 5972656 10. 5972656 10. 5972656 10. 5972656 10. 5972656 10. 5972656 10. 5972656 10. 5972656 10. 5972656 10. 5972657 10. 5972657 10. 5972657 10. 5972657 10. 5972657 10. 5972657 10. 5972657 10. 5972657 10. 5972657 10. 5972657 10. 5972657 10. 5972657 10. 597267 10.
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, 1
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TITLE OF INVENTION:
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US-07-942-245-22
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APPLICANT: Honjo, Tasuku
APPLICANT: Mateuda, Fumihiko
IITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
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100.0%; Pred. No. 0.02;
tive 0; Mismatches 0; Indels
                                                                                                    DB 2; Length 116;
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;Patent No. 5189147
A APPLICANT: SAITO, HARUO;KRANZ, DAVID M.;ELSEN, HERMAN N.;
;TONEGAWA, SUSUMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TITLE OF INVENTION: METERODIMERIC T LYMPHOCYTE RECEPTOR; ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATION SYSTEM: Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 17-MAR-1996
FRICK APPLICATION NUMBER: US/08/545,809A
FILING DATE: 10-MAY-1933
ATTORNEY/AGENT INFORMATION:
FILING DATE: 10-MAY-1933
ATTORNEY/AGENT INFORMATION:
FILEPHONE: 617-542-5070
TELESHONE: 617-542-5070
TELESPAX: 617-542-8006
                                                                                                 Query Match
100.0%; Score 56; DB 2;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-08-245-809A-96
Sequence 96, Application US/08545809A
; Patent No. 6096878
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Best Local Similarity 100.
Matches 10; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 21
; MOLECULE TYPE: protein US-08-888-366-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYTFTSYDIN 10
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                                                                                                                                                                                                                                                                                             26 GYTFTSYDIN 35
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APPLICANT: Karasuyama, Hajime
APPLICANT: Karasuyama, Hiromichi
APPLICANT: Taya, Choji
APPLICANT: Taya, Choji
APPLICANT: Taya, Choji
APPLICANT: Matsuoka, Kunie
TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
TITLE REPERENCE: 799879570
CURRENT APPLICATION NUMBER: US/09/192,545
CURRENT APPLICATION NUMBER: US/09/192,545
CURRENT APPLICATION NUMBER: US/09/192,545
EARLIER PILING DATE: 1996-11-13
EARLIER PILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 561
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                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE: Description of Artificial Sequence: Designed heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 561;
                                                                                                                                                                                                                                                            Score 49; DB 6; Length 200; Pred. No. 0.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEDERSEN, Jan T.
SEARLE, Stephen M.J.
Anthony R.
ROGUSKA, Michael A.
GUILD, Braydon C.
GUILD, Braydon C.
WENTICN: SURFACE RESIDUE. VENEERING OF RODENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Sughrue, Mion, Zinn, Macpeak & Seas 2100 Pensylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49; DB 3;
Pred. No. 1.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                           0; Mismatches
APPLICATION NUMBER: US/07/271,216
FILING DATE: 14-NOV-1988
APPLICATION DATA:
APPLICATION NUMBER: 666,988
FILING DATE: 31-OCT-1984
APPLICATION NUMBER: 620,122
FILING DATE: 13-JUN-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SERIE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: QUILD, Braydon C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-192-545-2; Sequence 2, Application US/09192545; Patent No. 6118044; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.5%;
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Gaps

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PATCHEN NO. 575105

SARENEAL INFORMATION:
APPLICANT: Hanna, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Romald M.
APPLICANT: Raab, Romald M.
APPLICANT: Raab, Romald M.
TITLE OF INTEWARTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDERS: 13
ADDRESSEE: BURNS, DOANS, SWECKER & MATHIS
STREET: 699 Prince St.
COUNTY: ALexandria
STATE: VA
ALEXANDRESEE: BURNS, DOANS, SWECKER & MATHIS
STREET: 699 Prince St.
COUNTRY: BURNS DOANS, SWECKER & MATHIS
STREET: 699 Prince St.
COUNTRY: BURNS DOANS, ST.
APPLICATION NUMBER: US 07/912,292
FILING DATE: 25-JAN-1995
PRIOR APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION NUMBER: US 07/956,281
FILING DATE: 10-JUL-1992
PRIOR APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY APPLICATION NUMBER: 35,030
REBERNOREDOCKET NUMBER: 30,2012-161
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

83.9%; Score 47; DB 1; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 1; Indels
                      TELEPHONE: 703-836-6620

INPOTABLEAK: 703-836-6201

INPOTALION FOR SEQ ID NO: 65: SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids TYPE: amino acid STRANDEDNESS: not relevant FOCOLOGY: not relevant MOLECULE TYPE: peptide ORIGINAL SOURCE: ORGANISM: MONKEY POSITION IN GENOME: CHROMOSONE/SEGMENT: clone 1-14 US-08-478-039-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 65, Application US/08476349A Patent No. 5750105
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYTFISYDIN 10
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Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCE: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Paince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
Z113-1404
Z2313-1404
Z113-1405
Z2313-1406
ZUNDUTER: ELOPDY disk
COMPUTER: Datentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN BATA:
RESTENDENT NUMBER: US 07/35,064
FILING DATE: 23-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN BATA: ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%; Score 48; DB 1;
80.0%; Pred. No. 0.43;
tive 1; Mismatches
                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: TELECOMMUNICATION:
TELECHOME: (202) 293-7060
                                                                                                                                                                                                                                                                                                                                                TELEX: 6491103
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-942-245-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GYTFTSYDIN 10
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Gaps

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Indels

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Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches
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                                                                                                                                                                                                                   Sequence 27, Application US/08602725
Patent No. 5965710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 703-816-4091
TELEPAX: 703-816-4100
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||||| :|
26 GYTFTSYAMN 35
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                                                                 1 GYTFTSYDIN 10
                                                                                                          25 GYIFTSYDID 34
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US-08-602-725-27
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US-09-556-605-1

Sequence 1, Application US/09556605

Patent No. 6417324

GENERAL INFORMATION:
APPLICANT: Sallberg, Matti
APPLICANT: Lazdina, Una
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HEAPITITS B VIRUS CORE AND E ANTIGENS
FILE REPERENCE: TALEPE, 1020A
CURRENT PILING DATE: 2000-04-21

NUMBER OF SEQ ID NOS: 78

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 119

TYPE: PRT

CREATION: ATTIFICIAL Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8

US-09-556-605-6

j Sequence 6, Application US/09556605

patent No. 6417324

j GENERAL INFORMATION:
   APPLICANT: Sallberg Matti
   APPLICANT: Lazdina, Una
   TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
   TITLE OF INVENTION: SYNTHETIC B VIRUS CORE AND E ANTIGENS
   TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
   TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
   TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
   CURRENT PILING DATE: 2000-04-21
   NUMBER OF SEQ ID NOS: 78
   SOFTWARE: FastSEQ for Windows Version 4.0
   SEQ ID NO 6
   LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.4%; Score 45; DB 4; Length 119;
                                                                                                                                                                                                                        Query Match

83.9%; Score 47; DB 1; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.4%; Score 45; DB 4; Length 20; 80.0%; Pred. No. 0.22;
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; OTHER INFORMATION: Artificial Oligonucleotide
US-09-556-605-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Artificial Oligonucleotide US-09-556-605-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
TYPE: amino acid
STRANDENBESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORIGINAL NONESY
POSITION IN GENOME:
CHROMOSOME/SEGMENT: clone 1-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                1 GYTETSYDIN 10
                                                                                                                                                                                                                                                                                                                                                       26 GYTFTSYYIN 35
                                                                                                                                                                                  US-08-476-349A-65
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GENERAL INFORMATION:
APPLICANT: BODNER, WALTER F
APPLICANT: BOTHER, DAVID
APPLICANT: STARY, DAVID
APPLICANT: STARY, DAVID
APPLICANT: STARY, LORNA MD
APPLICANT: STEMART, LORNA MD
APPLICANT: YOUNG, SUSAN
APPLICANT: PATES, PAUL A
TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR COLORECTAL CANCER
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REALBLE FORD

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/602,725

FILING DATE: 0.2 FEB. 1996

CLASSIFICATION NUMBER: PCT/GB94/01816

PILING DATE: 19-AUG-1994

PRIOR APPLICATION NUMBER: GB 9317423

APPLICATION NUMBER: GB 9317423

APPLICATION NUMBER: 3663

REGISTRATION NUMBER: 3663

REGISTRATION NUMBER: 3663

REGISTRATION NUMBER: 3663

REGISTRATION NUMBER: 36603

REFERENCE/DOCKET NUMBER: 1090-8

TELEPHONE: 703-816-4091
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relefax: 703-836-6620
INFORMATION FOR SEQ ID NO: 102: SEQUENCE CHARACTERISTICS: LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not rel-
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US-08-478-039-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 GFTFSSYDWN 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Monkey
POSITION IN GENOME:
                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-08-476-349A-73
                                                                                                                                                                                           STATE: VI
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Sequence 73, Application US/08478039

Sequence 73, Application US/08478039

Patent No. 5681722

GENERAL INFORMATION:

APPLICANT: Newman, Roland A.

APPLICANT: Raab, Ronald W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 1.5;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                           CULTURE: V.A.
COUNTRY: USA
CONDITER: LOSA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN PC-DOS/MS-DOS
SOFTWARE: PATENTEN PC-DOS/MS-DOS
SOFTWARE: PATENTEN PC-DOS/MS-DOS
SOFTWARE: PATENTEN PATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-UN-1995
FILING DATE: 10-UL-1992
FILING DATE: 10-UL-1992
FILING DATE: 39-MAR-1992
FILING DATE: 39-MAR-1992
FILING DATE: 30-MAR-1992
FILING DATE: 10-UL-1991
FILING DATE: 13-MAR-1992
FILING DATE: 25-UL-1991
FILING DATE: 25-UL-1991
FILING DATE: 25-UL-1991
FILING DATE: 25-UL-1991
FILING DATE: 30-MAR-1992
FILING DATE: 12-MAR-1992
FILING DATE: 30-MAR-1992
FILING DATE: 30-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-478-039-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 102, Application US/08478039; Patent No. 5681722; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.4%;
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYTFTSYDIN 10
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26 GFTFSSYDMN 35
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US-08-478-039-102
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Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Nabil
APPLICANT: Raab, Roland W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 128
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                                                                                                                                                                                                                                                                                          COMPREX: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: BND Compatible

COMPUTER: BND COMPATA:

APPLICATION NUMBER: US/08/479,072

PRIOR APPLICATION NUMBER: US 08/379,072

PRIOR APPLICATION NUMBER: US 07/912,292

PRIOR APPLICATION NUMBER: US 07/735,064

PILING DATE: 23-MAR-1992

RECOMMUNICATION NUMBER: US 07/735,064

PILING DATE: 25-JUL-1991

ATTORNEY/AGENT INPORMATION:

NAME: TESKIM ESG., ROBIN L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-160

TELEBEHONE: 02.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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Pred. No. 1.5;
3; Mismatches
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Pred. No. 1.5;
3; Mismatches 0; Indels
                                                                                   SUPERATING SYSTEM: PC-DOS/NS-DOS
SUSTRANE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 07-JUN-1995
CLASSIPICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
FILING DATE: 25-JAN-1995
FILING DATE: 10-JUL-1992
FILING DATE: 10-JUL-1992
FILING DATE: 23-JAN-1992
FILING DATE: 23-JAN-1992
FRIOR APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-JAN-1992
FRIOR APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JAN-1992
FRIOR APPLICATION NUMBER: US 07/735,064
FILING DATE: 128 amino acid
SEGURNCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 102:
SEGURNCE CHARACTERISTICS:
SEGURN SEGURNCE CHARACTERISTICS:
SEGURNCE 
                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-476-349A-102
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                  COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-UUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAM-1995
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-UUL-1992
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/35,064
FILING DATE: 23-WAR-1992
RILING DATE: 23-WAR-1992
RILING DATE: 23-WAR-1992
FILING DATE: 25-UL-1991
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-UL-1991
APPLICATION NUMBER: US 07/735,064
FILING DATE: S-UL-1991
APPLICATION NUMBER: US 07/735,064
FILING DATE: S-UL-1991
REPERENCE/DOCKER NUMBER: 35,030
REFERENCE/DOCKER NUMBER: 35,030
REFERENCE/DOCKER NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH3 clone 3-40
US-08-476-349A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: not relevant MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 73: SEQUENCE CHARACTERISTICS: LENGTH: 128 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                  STREET: 699 Prince St.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GYTFISYDIN 10
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      ADDRESSEE:
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RESULT 15
US-08-881-037-64

Sequence 64, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OP SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
CONTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BM PC Compatible
COMPUTER: BM PC Compatible
COMPUTER: BM PC Compatible
COMPUTER: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
```

Sequence 102, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria

RESULT 14 US-08-476-349A-102 Y: USA 22313-1404

COUNTRY: ZIP: 223

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Gaps

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J Thu Apr 22 05:59:07 2004
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FILING DATE: 23-UJW-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAX-1995
CLASSIFICATION: 530
ATJORNEY/AGENT INPORMATION:
NAME: KONSKI, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 813-5600
TELEFAX: (650) 494-0792
TELEFX: (650) 494-0792
TELEX:
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISICS:
LENGTH: 98 amino acids
TYPE: amino acids
TOPOLOGY: linear
US-08-881-037-64
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Search completed: April 21, 2004, 17:40:03 Job time : 13.029 secs

1 GYTFISYDIN 10 ||||||||| 26 GYTFISYGIS 35

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

April 21, 2004, 17:27:33 ; Search time 13.6957 Seconds (without alignments) 105.353 Million cell updates/sec Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 inpnsgntdyagkfg 15 Title: Perfect score: Scoring table: Sequence:

283366 seqs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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PH1667 PH1666	MHMS4E MHMSJ5 MHMS38				S18553 S17230		S17614
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3.0	335	# 55 YO	8 H	39 40	4 4 2 2	4 4 4	45

## ALIGNMENTS

	世
	human
	1
	(DP-15)
	region
	>
	chain
81	eavy

RESULT 1
S26918
Ig heavy chain V region (DP-15) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999
C;Accession: S26918
R;Tomlinson, I.M.; Malter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V, A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26918
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A;Accession: S26918
A;Accession: S26918
A;Accession: S26918
A;Accession: S26918
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-98 < TOM>A;Residues: L98 < TOM>A;Residues: I-98 < TOMAA;Residues: I-9

Gaps ö 87 8%; Score 72; DB 2; Length 98; 86.7%; Pred. No. 4.5e-05; tive 1; Mismatches 1; Indels Query Match
Best Local Similarity 86.7
Matches 13; Conservative

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1 INPNSGNTDYACKFO 15 :||||||| ||||||||| 51 MNPNSGNTGYAQKFQ 65 g

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RESULT 2 S31596

Journal V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999
C;Accession: 831596
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: 831596
A;Accession: 831596
A;Accession: S31596
A;Accession: C31596
A;Accession: C31596
A;Residues: 1-132 <UII>A;Residues: 1-132 <UII
A;Residues: 1-1

A;Cross-references: EMBL:214166; NID:930996; PIDN:CAA78535.1; PID:930997 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heteroretramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>

Gaps ö Query Match 87.8%; Score 72; DB 2; Length 132; Best Local Similarity 86.7%; Pred. No. 6.2e-05; Matches 13; Conservative 1; Mismatches 1; Indels

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1 INPNSGNTDYAQKFQ 15

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A;Cross-references: EMBL:X07448; NID:g33104; PIDN:CAB56703.1; PID:g6002173
A;Note: the authors translated the codon AGT for residue 89 as Met
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Tille: Nucleotidic sequence analysis of the variable domains of four human monoclonal JA;Reference number: S34001; MUID:93209281; PMID:7681398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C;Accession: 800476; 834013
EMBO J: 7, 1047-1051, 1988
EMBO J: 7, 1047-1051, 1988
A;Atille: Dispersed localization of D segments in the human immunoglobulin heavy-chain loc A;Reference number: 800476; MUID:88296408; PMID:2841108
A;Accession: 800476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region (DP-8) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession. 226912
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
J; Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V.
A;Reference number: S26885; MUID:93021117; PMID:1404388
A, Residues: 1-98 <TOM>
A, Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970
A, Cross-references: EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID:g32970
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C, Superfamily: immunoglobulin v region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMEL:212310; NID:932979; PIDN:CAA78180.1; PID:932980 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;IS-98/Domain: immunoglobulin homology <INM>
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
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Pred. No. 6.7e-05;
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                                                                                                                                                                                                                                                                                                                                       Query Match

86.6%; Score 71; DB 2; I
Best Local Similarity 86.7%; Pred. No. 6.7e-05;
Matches 13; Conservative 1; Mismatches 1;
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86.7%; Pred. No. o...
1; Mismatches
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A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
A;Introns: 16/1
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51 INPNSGGTNYAQKFQ 65
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A;Residues: 1-117 <MATS>
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A;Molecule type: mRNA
A;Residues: 20-116 <MAR>
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
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526310
C)26310
C)52610
C)5261
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256938
Ig heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Jc.Nov.1993 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: 82693
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: 826885; MUID:93021117; PMID:1404388
A;Accession: 826938
A;Accession: 826938
A;Accession: 826938
A;Accession: 826938
A;Accession: School Richam 
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroretramer; immunoglobulin
F;IS-98/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 86.7%;
Matches 13; Conservative
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                                                              MNPNSGNTGYAOKFO 84
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A, Residues: 1-98 < TOM>
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Jugary chain V region - human
Cipacies: Homo sapiens (man)
Cipacies: Homo sapiens (man)
Cipacies: Homo sapiens (man)
Cipacies: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
Cipacies: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
Cipacies: 10-1.295 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
Cipacies: 246393
Aprile: In viro assembly of repertoires of antibody chains on the surface of phage by Aprile: In viro assembly of repertoires of antibody chains on the surface of phage by Aprecession: 846393
Aprecession: 846393
Aprecession: 846393
Aprile: Invalidation

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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36265
S;Giffeiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
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C;Species: Homo sapiens (man)
C;Date: 01-Peb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: S49530
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IS-98/Domain: immunoglobulin homology <IMM>
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                               Length 117;
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A;Status; prellminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GRI>
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illarity 86.7%; Pred. No. 8.1e-05;
Conservative 1; Mismatches 1;
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86.7%; Pred. No. 8.9e-05;
iive 1; Mismatches 1.
                      Score 71; DB 2; I
Pred. No. 8.1e-05;
1; Mismatches 1;
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R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
                               Query Match 86.6%;
Best Local Similarity 86.7%;
Matches 13; Conservative
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nes 13; Conservative
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Matches 13
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Gradular V radional V radi
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C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F:119/Pomain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-2) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-117 <OLE>
A;Cross-references: EMBL:X59704; NID:932552; PIDN:CAA42225.1; PID:932553
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (V35) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <!MM>
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A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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86.6%; Score 71; DB 2; Length 117;
Best Local Similarity 86.7%; Pred. No. 8.1e-05;
Matches 13; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                   86.6%; Score 71; DB 1; Length 117;
86.7%; Pred. No. 8.1e-05;
iive 1; Mismatches 1; Indels
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70 INPNSGGTNYAQKFQ 84
                                                                                                                                                                                                                                                         Best Local Similarity 86.7
Matches 13; Conservative
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Search completed: April 21, 2004, 17:38:27 Job time : 13.6957 secs
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A;Molecule type: mRNA
A;Residues: 1-123 «XIP»
S;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C; Accession: D33548
R; Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
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A;Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune response for mumber: $69896; MUID:93272805; PMID:8500520
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S49530
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C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
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F;15-98/Domain: immunoglobulin homology <IMM>
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86.7%; Pred. No. 0.00016;
tive 0; Mismatches 2;
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80.0%; Pred. No. 0.00027;
tive 2; Mismatches 1;
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Pred. No. 9.4e-05;
1; Mismatches 1;
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Best Local Similarity 80.0.
Best 12; Conservative
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Best Local Similarity 86.73
Matches 13; Conservative
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A;Molecule type: mRNA
A;Residues: 1-135 <MAH>
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
Cipate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
Cipates 23.623
Riolee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; (Mang, 17): R.; Sal-847, 1992
A; Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv
A; Reference number: S23623; MUID:92156804; PMID:1740665
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A;Modecule type: DNA
A;Modecule type: DNA
A;Residues: 1-171 < CoLE>
A;Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
P;34-117/Domain: immunoglobulin homology < IMM>
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Ig heavy chain V region precursor - human (fragment)
2/Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.3%; Score 65; DB Best Local Similarity 80.0%; Pred. No. 0.00 Matches 12; Conservative 0; Mismatches
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991195 homo sapien
991194 homo sapien
991192 homo sapien
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0921k1 mus musculu
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094x60 mus musculu
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                                                        April 21, 2004, 17:26:23 ; Search time 40 Seconds (without alignments) 118.319 Million cell updates/sec
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                                                                                                                                                               1017041
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
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sp_vorganelle:*
sp_vortebrate:*
                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                       SEQ2
82
1 inpnsgntdyaqkfg 15
                                                                                                                                                                                                                                        SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
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                                                                                                                                                 Searched:
                                                                                                                                                                                                                                          Database
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No.
                                                          Run on:
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ALIGNMENTS

099131 08K0F2 08VIJ1 091L85 08VAP1 080TB7 0921C4

916	PRELIMINARY;
	Ol-MAY-2000 (TrEMBLE). 13, Created) Ol-MAY-2000 (TrEMBLE). 13, Last sequence update) Ol-OCT-2003 (TrEMBLE). 25, Last annotation update) Myosin-reactive immunoglobulin heavy chain variable region
OS Homo OC Eukar OC Mamma OX NCBI	<pre>(Fragment). Homo sapiens (Human). Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.</pre>
-, -, -,	E FROM N.A. ==98277139; PubMed=9614934; ==08277139; Van der Merwe P.L., Kalis N.N., Berney ).Ci
	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."; Clin. Immunol. Immunopathol. 87:184-192(1998). EMBL; AP035019; AAD56255.1;
	INTERPRO IPRO07110; Ig-like. INTERPRO; IPRO03596; Ig_v. Pfam; PF00047; ig; 1. PROSITE; PS50835; Ig_LIKE; 1. PROSITE; PS50835; Ig_LIKE; 1. NON TER 125 125 SEQÜENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
Query Match Best Local Matches 1	Query Match 18.0%; Score 64; DB 4; Length 125; Best Local Similarity 80.0%; Pred. No. 0.0064; Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps.
Qy Db	1 INPNSGNIDYAQKFQ 15 

Gaps

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RESULT 2
OGUL94
ID OGUL94
OGUL97
OGUL

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LASTOCIAGE FROM N.A.

SEQUENCE FROM N.A.

Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;

Indentification and characterization of SNC66, a Ig-like gene which is indentification and characterization of SNC66, a Ig-like gene which is unarted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

L. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

R. EMBL, AF283666; ABJ6987.1;

R. InterPro; IPR003296; Ig-N.

R. InterPro; IPR003296; Ig-N.

R. SMART; SM00406; IG-N.

R. SMART; SM00406; IG-N.

R. PFAM; PF00047; IG-N.

R. PROSITE; PS508299; IG-NHC; I.

R. PROSITE; PS508299; IG-NHC; I.

R. PROSITE; PS002299; IG-NHC; I.

R. PROSITE; PS002299; IG-NHC; I.
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Strausberg R.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC009851; AAH09851.1; -.

PIR; 815590; 815590.

OO; GO:0005622; C:intracellular; IEA.

GO; GO:0005622; F:transcription factor activity; IEA.

GO; GO:0003750; F:transcription of transcription, DNA-dependent; IEA.

InterPro; IPR0000105; HTHARAG.

InterPro; IPR00110; IG_11ke.

InterPro; IPR003006; IG_1Ke.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                 Query Match 75.6%; Score 62; DB 4; Length 124; Best Local Similarity 73.3%; Pred. No. 0.014; Matches 11; Conservative 2; Mismatches 2; Indels
124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo seations (Human).
                                                                                                                                                                                                                                                                                                                                                                 08WY24;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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70 MNPQTGNTEFAQKFQ 84
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TISSUE=B-cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNC66 protein.
        SEQUENCE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                      (Fragment).

Momo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-98277139; PubMed-9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Myosin-reactive autoantibodies in rheumatic carditis and normal
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SEQUENCE FROM N.A.
WLX., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 16.8%; Score 63; DB 4; Length 119; Local Similarity 80.0%; Pred. No. 0.009; 2, Indels 12; Conservative 1; Mismatches 2; Indels
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119 AA; 13205 MW; 13E64F5345F4A16E CRC64;
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035022, AAD56258.1; -.
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig-v.
Pfan; PF00047; 4g; 1.
PR0SITE; PS50835; IG_LIKE; 1.
NON_TER 124 124
NON_TER 124 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF015020, AAD56256.1; -.
HSSP, PO1010; DFBJ.
INTERFO: JPR07110; Ig-like.
InterPro; IPR003596; Ig_v.
FROMORT; SMO466; IGv.
PROSTIE; PS50835; IG_LIKE; 1.
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                                                                                                              119 AA.
                                                                                                              PRT;
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                                                                                                                 PRELIMINARY;
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SEQUENCE
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Q9UL92;
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Q9UL94;
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Matches
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RESULT 3 Q9UL92

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FTT DE REP DE STANDE DE ST

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Gaps

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STRAIN=DBA/2;
MEDLINE=2048942; PubMed=10992488;
MAININE=20489942; PubMed=10992488;
MAIKIEL S., Lidao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.5%; Score 57; DB 11; Length 117; 66.7%; Pred. No. 0.088; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                    69.5%; Score 57; DB 11; Length 117; 66.7%; Pred. No. 0.088; 3; Indels ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clemens A., Radenaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
REMEL; AJC2111; CAB65236.1; -.
REMEL; AJC2111; CAB65236.1; -.
RESP; PO1789; IMCP.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR0047; ig; 1.
RAMARI; SM00406; IGv; 1.
ROSITE; PS50835; IG LIKE; 1.
RON TER 117 117
SEQÜENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON TER 1.7 1.7
SEQÜENCE 117 AA; 13000 NW; CDDE2AF84D499734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9QXF0;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Immunoglobulin heavy chain V-D-J region (Fragment).
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Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 10; Conservative
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Q9JL77
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Q9QXF0
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©1-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Immunoglobulin heavy chain V-D-J region (Fragment).

Mus musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                         72.0%; Score 59; DB 4; Length 614; 73.3%; Pred. No. 0.27; cive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ225174; CAB65237.1; -.
PIR; F33932; F33932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BCO12207; ARH12207.1;
InterPro; IPR007110; Ig-like.
InterPro; IRR03566; Ig-v.
Pfam; PF00647; Ig: 2.
SMRT; SM0406; IGv: 1.
PROSITE; PS500835; IG-IKE; 2.
Hypothetical protein.
SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AA
                                    PFGM, PFG0047; ig; S. SMART; SM0046; IGv; IGv; SM00405; IGv; IGv; PROSTIE; PSG0041; HTH ARAC FAMILY 1; 1. PROSTIE; PSG0835; IG LIKE; S. PROSTIE; PSG0299; IG MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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70 INPNSGGTNYNEKFK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 ITPFNGNTNYACKFO 84
InterPro; IPR003596; Ig_v
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les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 73.3
Matches 11; Conservative
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Best Local S
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2090XX
AC 090XX
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AC 090XX
DT 01-M
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0921K1
10 09211
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NCBI_TaxID=10090
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PH1125;
PH1126;
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PH1139;
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Q924R6
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                                                                                                                                                                                                                                                                                                                                                                       "Homo sapiens putative microfibrillar protein with Ig-like domain 3 mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";

submitted (UTN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY039025; AAK82649.1; ...

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

Pfam; PF00047; ig; 1.

SMART; SMO4046; Ig-v.

SMART; SMO4046; IG-v.

SEQUENCE 159 AA; I7497 MW; 5D29537E881FAP02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ol-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Byman muschus (Mouse).
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                     Homo sapiens (Human).

Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                           65.9%; Score 54; DB 11; Length 110; 60.0%; Pred. No. 0.26; ive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.4%; Score 52; DB 4; Length 159;
60.0%; Pred. No. 0.85;
ive 3; Mismatches 3; Indels
                                                                                       NON TER 1 10 110 110 SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;
                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative matrix cell adhesion molecule-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 470 AA.
                                                                                                                                                                                                                                           PRT; 159 AA
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STRAIN=CZECH II; TISSUE=Breast tumor;
MEDLINE=22388257; PubMed=12477932;
Infect. Immun. 68:5803-5808(2000)
      EMBL; AP206029; AAF69327.1; -. PIR; F33932; F33932. HSSP; P01810; 2FBJ. InterPro; IPR007110; IG-like. InterPro; IPR00710; IG-v. Pfam; PP00047; ig; 1. SWART; SM00406; IGv; 1. SWART; SW00406; IGV; 1. SWART; SW50835; IG_LIKE; 1.
                                                                                                                                                                      1 INPNSGNTDYACKFO 15
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43 IHPNSGHTNYNEKFK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0%
Matches 9; Conservative
                                                                                                                                        Best Local Similarity 60.0
Matches 9; Conservative
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Richarder R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bara N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broak S.A., McEwan P.J., McKernan K.J., Malak J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Raha Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rahakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Radiguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Radiguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Radiguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Radiguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Radiguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Galmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Galmwood J., Schmutz J., Marra M.A.;
Reneration and initial analysis of more than 15,000 full-length human
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Xozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. EMBL; EC055910; AAH55910.1; .. Hypothetical protein. SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seguence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
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STRAIN-CZECH II; TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB067783; BAB63268.1; -.
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F28833; F28833.
PH1105; PH1105.
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PH1125.
PH1126.
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PH1129.
PH1131.
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PERGUNCE FROM N.A.

STRAIN=C57BL/6;

Kozono Y., Kozono H., Azuma T.;

Kozono Y., Kozono H., Azuma T.;

Kozono Y., Kozono H., Azuma T.;

Minity Maturation of Relative Affinity by Flow Cytometry Reveals

Affinity Maturation of B Cell Antigen Receptors in Response to (4-

Minity Maturation of B Cell Antigen Receptors in Response to (4-

Kozono M. Subarited (Aug-2001) to the SMBL/GenBank/DDBJ databases.

BMBL; AB067788; BAB63273.1; -.

Subarited (Aug-2001) to the SMBL/GenBank/DDBJ databases.

BMBL; PH108; PH1108.

PR; PH1108; PH1108.

PR; PH1109; PH1129.

PR; PH1129; PH1129.

PR; PH1129; PH1129.

PR; PH1131; PH1131.

PR; PH1137; PH1131.

PR; PH1144; PH1144.

PR; PH1147; PH1144.

PR; PH1147; PH1144.

PR; PH1147; PH1147.

PR; PH1151; PH1151.

PR; PH1151; PH1151.
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Q924Q4;
Q924Q4;
Q924Q4;
Q924Q4;
Q925QQ1 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
WH186.2-D-J-C mu protein (Fragment).
Buls musculus (Mouse).
Buls ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscullaria; LaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6;
Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Acetyl (NP).";
                                             Mus musculus (Mouse)
Makaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCSI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.2%; Score 51; DB 11; Length 140; 60.0%; Pred. No. 1.1; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER 1 1
NON TER 140 140
SEQÜENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;
       VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 INPNSGNTDYAQKFQ 15
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Best Local Similarity 60.0%
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A Kozono Y., Kozono H., Azuma T.;

Kininty Maturation of Bolative Affinity by Flow Cytometry Reveals

RT Affinity Maturation of Bolat Receptors in Response to (4-

RT Affinity Maturation of Bolat MP).";

RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

BR Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

BR PH1137; PH1137.

BR PROSTIP: PRO03596; Ig.v.

BR SMART; SM00406; IGv: 1.

BR PROSTIE; PS50835; IG_LIKE: 1.
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DD 0924R5,
DD 10-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DCC-2003 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 19, Last sequence update)
DE VH186.2-D-J-C mu protein (Fragment).
DE VH186.2-D-J-C mu protein (Fragment).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musc. OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musc. OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musc. OC NOBI TAXID=10090;
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137 AA, 15171 MW; 5C38D966DC6A4124 CRC64;
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PIR; PH1142; PH1144.
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Search completed: April 21, 2004, 17:37:14 Job time : 41 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Abp45370 Human BLY
Abp45880 Human BLY
Abp45880 Human BLY
Am20077 Peptide #
Am33913 Peptide #
Abg35467 Human Iiv
Abg43604 Human pep
Aay50958 Human pep
Aay50958 Human pep
Abg91861 Human per
Abg91861 Human ger
Abg91861 Human ger
Abg4846 Human imm
Abu2576 Anti-adip
Aay34302 Igw antib
Aay44016 Human BLY
Abp44916 Human BLY Abp45897 Human BLy
Abp45880 Human BLy
Abg55467 Human liv
Abg5467 Human liv
Abg74604 Human pep
Abg78170 Human FV
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Abg78161 Human mn
Abo27070 Human ger
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Au02576 Anti-adip
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Abg48355 Anti-prog
Aae28548 GFV anti Description SUMMARIES ABP45370
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## ALIGNMENTS

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomulatory; antirheumatic; antiAIDS; vaccine, cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome. Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders. Ü Hilbert Vaughan T, Claim 1; Page 2051-2052; 3148pp; English. (HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY Human BLyS binding scFv SEQ ID 1381. ABP45370 standard; protein; 248 AA. Choi GH, 16-JUN-2000; 2000US-0212210P. 17-CCT-2000; 2000US-0240B1EP. 21-MAR-2001; 2001US-027624BP. 21-MAR-2001; 2001US-027379P. 25-MAY-2001; 2001US-0293499P. 15-JUN-2001; 2001WO-US019110. (first entry) Barash SC, WPI; 2002-114799/15. WO200202641-A1. Homo sapiens. 19-AUG-2002 10-JAN-2002. Ruben SM, ABP45370; ABP4537 

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

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antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantizate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, theumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABB43990-ABB47228 represent the antibodies and fragments of the antibodies described in the method of
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
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16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-027379P.
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inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and isseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
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Pred. No. 0.00014;
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25-MAY-2001; 2001US-0293499P.
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                                                                                                                                                                                                                                                                                                                                          1 INPNSGNTDYAOKFO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                           51 INPNSGNTGYAOKFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-114799/15.
                                                                                                                                                                                                                                Sequence 241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200202641-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                               the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
ABP45880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           888888888888888888
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Gaps

; 0

Length 92;

Score 72; DB 4; I Pred. No. 0.00016; 1; Mismatches 1;

87.8%; 86.7%;

1 INPNSGNTDYAOKFO 15

Conservative

13;

Matches

Local Similarity

Query Match

Sequence 92 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to human single exon nucleic acid probes (SENP: see AAIIO068-AAII28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human agene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical achieves. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l probes useful for analyzing cells.
         biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumarcid arthritis, ammunodeficiency (e.g. common variable immunodeficiency (cVID) and acquired immunodeficiency suddome (ALDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #6511 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; human; microarray; gene expression; cervical epithelial cell;
may be used to detect and quantitate the presence of BLyS in
                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                 Length 249;
                                                                                                                                                                                                                                   Score 75; DB 5; Length 249
Pred. No. 0.00015;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid
gene expression in human cervical epithelial c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 24903; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM20077 standard; protein; 92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0033468P.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US000670
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                             1 INPNSGNTDYAOKFO 15
                                                                                                                                                                                                                                                                                                                                                51 INPNSGNTHYAQKFQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488901/53
                                                                                                                                                                                                Sequence 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157278-A2
                                                                                                                                              the antibodies
the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM20077;
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT A
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                                                                                                                                                Peptide #7950 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 72; DB 4; Length 92;
Pred. No. 0.00016;
1; Mismatches 1; Indels
                                                                                                                                                                        microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 34182; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
ABG5S467
ID ABG5S467 standard; peptide; 92 AA.
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression in human placenta.
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                                                                                                                                                                                                                                                                                                                             26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0069408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
                                                                        AAM33913 standard, protein; 92
                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.8%;
                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000663.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488897/53.
                                                                                                                                                                                        genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 92 AA;
                                                                                                                                                                                                                                         WO200157272-A2.
                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
                                                                                                                         17-0CT-2001
                                                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                 AAM33913;
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                                                                                                                                                                            Probe;
                                                            AAM33913
                                              RESULT
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chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrone; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary displasia; pulmonary displasia; hyaline membrane disease.

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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained, in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                              Human, liver, cirrhosis, hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.8%; Score 72; DB 4; Length 92;
86.7%; Pred. No. 0.00016;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 34115; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                         Human liver peptide, SEQ ID No 34115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0207456P.
2000US-00608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34-FEB-2000; 2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US000664
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488898/53
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                                                                                                                                                                                                                                                                                                                                                                                                           WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000;
                                                                    25-FEB-2003
                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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ABG55467;
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Spatially-addressable set of single exon nucleic acid probes, used to

Chen W, Rank DR,

Penn SG, Hanzel DK, WPI; 2002-114183/15.

(MOLE-) MOLECULAR DYNAMICS INC

27-SEP-2000; 2000US-0236359P-04-OCT-2000; 2000GB-00024263

2000US-00608408. 2000US-00632366. 2000US-0234687P.

30-JAN-2001; 2001WO-US000665

04-FEB-2000; 30-JUN-2000; 1-SEP-2000; 26-MAY-2000;

WO200186003-A2 Homo sapiens.

15-NOV-2001.

measure gene expression in human lung samples.

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expession in a sample derived from human lung comprising single exon nucleic acid probes abaving one of from human lung comprising single exon nucleic acid probes having one of from human lung comprising frames derived from the 12614 probes shich hybridise at high stringency to a nucleic complements or the 12397 open reading frames derived from the 12614 probes which hybridise at high stringency to a nucleic derived from human lung, measuring gene expression in a sample collection of detectably labeled nucleic acids derived from human lung comprising (a) contracting the array with a carray; identifying exons in a eukaryotic genome, comprising (a) agorithmically predicting at least one exon from genomic sequences of agorithmically predicting at least one exon from genomic sequences of agorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) descerting specific by hybridisation of detectably. I abeled nucleic acids from eukaryote lung mRNA, to a single exon probe, in the above mentioned microarray; assigning exons to a single exon probe, in the above mentioned microarray; assigning exons to a single exon probe of nature and (b) measuring the expression of the exons in several comprising (a) identifying exons from genomic sequence by the method comprision of the exons in the tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene; a peptide comprising on analysis, and for identifying exons in a gene, particularly using human compression of the exons in a gene, particularly using human analysis, and for identifying exons in a gene, particularly using human control constructive pulmonary disease (ODP), interstitial lung cancer, chronic obstructive pulmonary disease (DDP), interstitial lung cancer, chronic obstructive pulmonary disease (DDP), interstitial lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 33269; 634pp; English.
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Gaps

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Human peptide encoded by genome-derived single exon probe SEQ ID 33269.

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ABG43604 standard; peptide; 92

RESULT 7 ABG43604 19-AUG-2002

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ABG43604;

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13; Conservative

Matches

Best Local Similarity

Human; single exon probe; asthma; lung cancer; COPD; ILD

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Query Match

8 g

SXS

AAY50958;

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The invention relates to a peptide or polypeptide comprising an FV molecule, a construct of a construct of a fragment with endecude, a construct or a construct of a fragment with binds to a target cell in favour of other cells, where binding is consint for the cells, where binding is a single chair by determined by a first hypervariable region and FV is a single chair FV (scFV) or a disulfide FV (dsFV). The peptide, optionally in a sociation with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, arcming, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human FV molecule hypervariable region related peptide of the invention
                                                                                                                                          Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levanon A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                     Human Fv molecule hypervariable region related peptide #45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Szanton E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.8%; Score 72; DB 5; Length 98;
86.7%; Pred. No. 0.00017;
iive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guy R, Lipschitz O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Page 168-169; 232pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                GEN CORP
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                                                                                                                                                                                                                                                                                                                                                                                                       9-DEC-2000; 2000US-00751181.
                                                                                                                                                                                                                                                                                                                                                              31-DEC-2001; 2001WO-US049440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human antibody fragment #45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 INPNSGNTDYACKFO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                             (first entry)
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13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lazarovits J,
, Peretz T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOT-) BIO-TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-619166/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 98 AA;
                                                                                                                                                                                                                                                                             WO200259264-A2
                                                                                                                                                                                                                                      Homo sapiens
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                                                               15-NOV-2002
                                                                                                                                                                                                                                                                                                                   01-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hagai Y, Lé
Plaksin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG91861;
                      4BG78170;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG91861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel polynucleotide (I) (and complements and hybridizable polynucleotides) comprising a contiguous nucleotide sequence coding for a human antibody with factor VIII specificity which has hemostatic activity. (I) is useful a primer or probe for detecting the presence of inhibitory antibodies directed against factor VIII. The polypeptides of the invention and the antibodies generated from them are useful in compositions for neutralizing factor VIII inhibiting antibodies in hemophilia A patients. This sequence represents the human factor VIII antibody A:-C1 specific scFv protein DP-15 which is used in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide, polypeptide and antibody useful for diagnosing the presence of neutralizing antibodies against factor VIII and for treatment of hemophilia A patients with these antibodies.
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia R_i scFv; A3-C1.
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directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human FVIII antibody A3-C1 scFv heavy chain protein DP-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 72; DB 3; Length 98; Pred. No. 0.00017; 1; Mismatches 1; Indels
                                                                                 Score 72; DB 5; Length 92; Pred. No. 0.00016; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Den Brink EN, Turenhout EAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SANQ-) STICHTING SANQUIN BLOEDVOORZIENING.
                                                                                                                                                                                                                                                                                                                 AAY50958 standard; protein; 98 AA.
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                                                                                 87.8%;
86.7%;
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                                                                                                                                                                                                              42 MNPNSGNTGYAQKFQ 56
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                     Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity
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                                        Sequence 92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Voorberg JJ,
                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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RESULT 8
AAYS 0958
ID AAYS 0958
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DT 23-M
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PN W099

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Matches

RESULT 9 ABG78170 ID ABG7

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The invention relates to an isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune classes, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increasing mortality of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer or anti-cleukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for disgnosing and treating diseases cardiovascular diseases such as myocardial infarction, diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-protein interactions. This sequence represents a human antibody fragment of the invention
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metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; laukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer.
                                                                                                                                                                                                                                                                                                                                       Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
Amit B, Kooperman L, Peretz T, Levanon A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 72; DB 5; Length 98;
Pred. No. 0.00017;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 246; Opp; English.
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                                                                                                                                                                                                                                                                                                   (BIOT-) BIO-TECHNOLOGY GEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO27070 standard; protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.8%;
                                                                                                                                                                                                                                           29-DEC-2000; 2000US-00751181.
29-DEC-2000; 2000US-0258948P.
                                                                                                                                                                                                         31-DEC-2001; 2001WO-US049442.
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les 13; Conservative
                                                                                                                                                                                                                                                                                                                                       Lazarovits J, Hagai Y,
Szanthon E, Richter T,
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-674776/72.
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                                                                                                                               MO200253700-A2.
                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-2003
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Matches
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The invention describes a method of making a humanised antibody, comprising making chimeric antibodies containing a complementarity determining region (CDR) from a non-human antibody and appropriate canonical CDR structure types of non-human antibody in comparison to germine canonical CDR structure types of human antibodies as the basis of numanised antibody or a converted antibody. The method is useful for making a humanisad antibody or a converted antibody. The method is applicable for converting a subject antibody sequence of any subject species to a less immunogenic form suitable for use in an object species. The method is reliable for identifying suitable human framework sequences to support non-human CDR regions and to provide humanised antibodies that retain high antigen binding with low immunogenicity in humans, without the need for direct comparison of framework sequences, without the need for determining critically important amino acid residues in the framework, and without the need for multiple iteration and construction to obtain humanised antibodies with suitable therapeutic properties. The antibody has high affinity and low immunogenicity without need for comparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   framework sequences between non-human and human antibodies. This sequence represents a human heavy chain variable region gene segment used in the creation of humanised antibodies
                                                                                                                                                                                                                                                                                                                                                                                            Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain; cosmid; placenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Human; heavy chain variable region; VH; humanised antibody; chimeric antibody; complementarity determining region; CDR; canonical CDR structure type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.8%; Score 72; DB 6; Length 98; 86.7%; Pred. No. 0.00017; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunoglobulin variable heavy chain #8.
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                                                                                                                                                                                                 12-JUL-2002; 2002US-00194975.
                                                                                                                                                                                                                                    12-JUL-2001; 2001US-0305111P
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                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-492151/46.
                                                                                                                                                                                                                                                                            (FOOT/) FOOTE J.
                                                                                                                      US2003039649-A1
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                                                                                 Homo sapiens
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                                                                                                                                                           27-FEB-2003.
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                                                                                                                                                                                                                                                                                                                   Foote J;
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Matches
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Vaughan TJ;

Edwards BM, Main SH,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain sequences encoded by novel isolated genes. The genes (AAQ78939-7002) were isolated and cloned from a series of cosmid constructs: Y202, 7103; Y21; Y6;Y24; 3-31; M84; M18 and M131, by FCR amplification using primers AAQ78917-38. The genes are subdivided into 5 families of Vh genes. The fragments cover a region of 800 kb. The DNA fragments were isolated from high molecular weight DNA from human placents. The DNA was partially digested with TaqI restriction enzyme. The fragments were separated by gel electrophoresis and 35-45 kb fractions were collected. The fragments were ligated with ClaI-digested cosmid vector pJB81. The fragments were ligated with ClaI-digested cosmid vector pJB81. The fragments were subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immammalian hosts. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein sequences (AAR66295-51) are novel human immunoglobulin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA fragment comprising human immunoglobulin Vh genes - for the production of human immunoglobulin in mammalian hosts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 41-42; 130pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU02576 standard; protein; 121 AA
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                                                                                                                                                                                  93WO-JP000603
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                                                                                                                                                                                                                                                                                                     (NISB ) JAPAN TOBACCO INC
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nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Honjo T, Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-006791/01.
N-PSDB; AAQ78946.
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Homo sapiens
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AAU02576
ID AAU02576
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese parient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to by complement mediated lysis. The antibodies may be labeled with a characterizable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                             Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic; gynaecological; antinflammatory; osteopathic; antipsoriatic; cancer; angiogenesis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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86.7%; Pred. No. 0.00021;
cive 1; Mismatches 1; Indels
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                                                                                                                                                    Claim 1; Page 140; 182pp; English.
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N-PSDB; AAS03476.
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Human, epidermal growth factor receptor; EGF-r; antibody; cytostatic; antiinflammatory; immunosuppressive; tyrosine phosphorylation; EGF-2; EGF-r degradation; vascular endothelial cell growth factor; VEGF; tumour; endothelial cell; threonine phosphorylation; autoimmune disease; colon; The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55769-830) or its fragment. The binding agents are antibodies that recognize and bind to angiopoietin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating or inhibiting to a cativity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocullar neovascular disease, obesity, haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease, inflammatory disease, inflammatory disease, or psoriasis) in a mammal. The present sequence represents a heavy chain variable region of an anti-Ang-2 New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis. Human epidermal growth factor receptor (EGF-r) antibody #19. ABO04846 standard, protein; 149 AA. Claim 1; Page 93; 161pp; English 1 INPNSGNTDYAQKFQ 15 inflammation; lung; cancer Query Match
Best Local Similarity 86.7
Matches 13; Conservative WPI; 2003-504963/47 (AMGE-) AMGEN INC. Sequence 122 AA; US2002173629-A1. Homo sapiens 05-NOV-1998; 05-MAY-1997; 29-SEP-1998; 12-AUG-2003 21-NOV-2002 Oliner JD; ABO04846; antibody RESULT 15 ABO04846 à а 

N-PSDB; ACD10930

Fully human monoclonal antibodies that bind to epidermal growth factor receptors, useful in cancer therapy.

Example 3; Fig 59; 100pp; English.

The invention relates to an antibody that binds to an epidermal growth factor receptor (FGF-r) and exhibits inhibition of tyrosine phosphorylation of EGF-r, the degradation of EGF-r, the EGF induced degradation of EGF-r, vascular endothelial cell growth factor (VEGF) production by tumour cells (by greater than 50%) and endothelial cells (by greater than 40%) and also protects threonine phosphorylation of EGF-r and a SIXD protein. The antibody may be used for treating tumours such as lung tumours and colon tumours and for treating inflammation and autoimmune diseases. Sequences ABO04854-ABO04859 represent human EGF-r receptor antibodies of the \*

Sequence 149 AA;

Gaps ö Query Match Best Local Similarity 86.7 Matches 13; Conservative

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1 INPNSGNTDYAQKFQ 15

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Gaps ö

Score 72; DB 6; Length 122; Pred. No. 0.00022; 1; Mismatches 1; Indels

87.8%; 86.7%;

65

(first entry)

Gallo M, Jia X;

Jakobovits A, Yang X,

WPI; 2003-328430/31.

(JAKO/) JAKOBOVITS A. (YANG/) YANG X. (GALL/) GALLO M.

(GALL/) GALLO (JIAX/) JIA X.

97US-00851362, 98US-00162280, 98US-00187693

Score 72; DB 6; Length 149; Pred. No. 0.00027; 1; Mismatches 1; Indels 87.8%; Scc... 86.7%; Pred

53 39 MNPNSGNTGYAQKFQ 원 ઠ

Search completed: April 21, 2004, 17:33:10 Job time : 61 secs

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

April 21, 2004, 17:28:28 ; Search time 18.0435 Seconds (without alignments) 42.918 Million cell updates/sec Run on:

SEQ2 82 Title: Perfect score: Sequence:

1 inpnsgntdyaqkfq 15

Scoring table:

389414 seqs, 51625971 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*

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5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

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BE F. Haley, Jr., Esq.  DOCKET NUMBER: 27,794  DOCKET NUMBER: 27,794  ATION INFORMATION: (212)596-9000  (212)596-9000  R. SEQ. ID NO: 22:  RACTERISTICS: 17 amino acids  SS: 11 amino acids  SS: 11 amino acids  SS: 12 acids  SS: 13 acids  SS: 14 acids  SS: 15 acids  SS: 16 acids  SS: 17 acids  SS: 17 acids  SS: 17 acids  SS: 18 acids  SS: 18 acids  SS: 10 acids  SS:	ATTORNEY/AC	ENT INFORMATION:	
DN NUMBER: 27,794 DOCKET NUMBER: MORPHO/5 ATION INFORMATION: (212)596-9000 R (212)596-9000 R SEQ ID NO: 22: RACTERISTICS: 17 amino acids SS: 11 no acid SS: 11 amino acids SS: 12 amino acids SS: 13 amino acids SS: 14 amino acids SS: 15 amino acids SS: 16 amino acids SS: 17 amino acids SS: 18 amino acids SS: 18 amino acids SS: 19 amino acids SS: 10 amino acids SS: 10 amino acids SS: 11 amino acids SS: 12 amino acids SS: 13 amino acids SS: 14 amino acids SS: 15 amino acids SS: 16 amino acids SS: 17 amino acids SS: 18 amino	NAME: Ja	:	
OCCKET NUMBER: WORPHO/5 ATION INFORMATION: (212)596-9000 (	REGISTRAT		
1212) 10 INFORMATION: (212) 596-9000 (212) 596-9000 (212) 596-9000 (212) 596-9000 (212) 596-9000 (213) 596-90000 (213) 596-90000 (213) 596-90000 (213) 596-90000 (213) 596-90000 (213) 596-90000 (213) 596-90000 (213) 596-90000 (213) 596-90000 (213) 596-90000 (213) 596-90000 (213) 596-90000 (213) 596-90000 (213) 596-900000 (213) 596-9000000 (213) 596-900000000000000000000000000000000000	REFERENCE	/DOCKET NUMBER: MORPHO/5	
(212)596-9000 (212)596-9000 (RECTENISTICS: 17 amino acids 17 amino acids SS: 1inear E: protein 93.9%; Score 77; DB 4; Length 117;	TELECOMMUNI	CATION INFORMATION:	
K SE2 596-9090 R SE2 10 NO: 22: RACTERISTICS: 17 amino acide no acid SS: 1 inear E: protein 93.9%; Score 77; DB 4; Length 117; larity 93.3%; Pred. No. 9.2e-06;	TELEPHONE	: (212) 596-9000	
RACTERACITCS: 17 amino acids no acid no acid SS: 1inear E: protein 193.9%; Score 77; DB 4; Length 117; larity 93.3%; Pred. No. 9.2e-06;	TELEFAX:		
RATERISTICS: 17 amino acids SS: 1inear E: protein 93.9%; Score 77; DB 4; Length 117; larity 93.3%; Pred. No. 9.2e-06;	INFORMATION		
17 amino acids 0S: 1inear E: protein 93.9%; Score 77; DB 4; Length 117; larity 93.3%; Pred. No. 9.2e-06;	SEQUENCE C	ARACTERISTICS:	
no acid SS: linear E: protein 93.9%; Score 77; DB 4; Length 117; larity 93.3%; Pred. No. 9.2e-06;		amino	
SS: linear E: protein 93.9%; Score 77; DB 4; Length 117; larity 93.3%; Pred. No. 9.2e-06;	TYPE: an	ino acid	
<pre>incar E: protein 93.9%; Score 77; DB 4; Length 117; larity 93.3%; Pred. No. 9.2e-06;</pre>	STRANDED		
<pre>E: procein  93.9%; Score 77; DB 4; Length 117; larity 93.3%; Pred. No. 9.2e-06;</pre>	TOPOLOGY	Ħ	
93.9%; Score 77; DB 4; Length 117; larity 93.3%; Pred. No. 9.2e-06;	MOLECULE T	 Ш	
93.9%; Score 77; DB 4; Length 117; Similarity 93.3%; Pred. No. 9.2e-06;	S-09-025-769B-2	2	
Similarity 93.3%; Pred. No. 9.2e-06;	Ouery Match	Score 77; DB 4;	
	Best Local Sin	93.3%; Pred. No. 9.2e-06	

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US-08-545-8094-90
US-08-545-8094-90
US-08-56-8094-90
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US-08-56-8094-90
US-08-56-8094-90
US-08-56-8094-90
US-08-56-80-80-80
UNUMER OF SOURNES:
UNUMER:
UNUME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 86.6%; Score 71; DB 3; 1
Best Local Similarity 86.7%; Pred. No. 9.5e-05;
Matches 13; Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.6%; Score 71; DB 4; 186.7%; Pred. No. 1.2e-05; tive 1; Mismatches 1.
                            PRIOR FILING DATE: 1998-02-28
PRIOR APPLICATION NUMBER: GB 9724850.4
PRIOR FILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 21
LENGTH: 17
APPLICATION NUMBER: GB 9804195.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 INPNSGNTDYAQKFQ 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 inphsegrnyaokro 16
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 86.73
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-545-809A-90
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-09-424-712-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-08-545-809A-90
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Sequence 21, Application US/09424712

Sequence 21, Application US/09424712

Sequence 21, Application US/09424712

Patent No. 6620587

GENERAL INCORMATION:
APPLICANT: TAUSSIG, Michael John
APPLICANT: HE Mingyue
TITLE OF INVENTION: REDOGNE COMPLEXES AS SELECTION PARTICLES FOR IN VITRO DISPLAY AN TITLE OF INVENTION: EVOLUTION OF PROTEINS
FILE REFERENCE: 37945-0017
CURRENT APPLICATION NUMBER: 1999-11-29
CURRENT FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/GB98/01564
                                                                                                                                                                                                                                                                                 USSOB-SEB-809A-98
US-08-545-809A-98
US-08-545-809A-98
US-08-62-809A-98
US-08-62-808A-98
USBURDATION: Tacuku
APPLICANT: HONJO: Tacuku
APPLICANT: Matsuda, Fuminiko
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CUNTRY: BOSTON
STATE: MA
COUNTRY: BOSTON:
MADDIUM TYPE: DISKETTE
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATION:
MARE: FEREMEN, ODEN WHERE: 29,066
REFERENCE DOCKET NUMBER: 06501/00401
TELEDRANG SOUTH NUMBER: 07-42-5006
TELEDRANG SOUTH TELEDRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 117;
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86.7%; Pred. No. 6.4e-05
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
TENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 INPNSGNTDYAQKFQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|||||| |||||
70 MNPNSGNTGYAQKFQ 84
                                                1 INPNSGNIDYAQKFQ 15
                                                                                        51 INPNSGNTNYAQKFQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 86.7
Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / MOLECULE TYPE: protein US-08-545-809A-96
                                                                                                                                                                                                                                     RESULT 2
US-08-545-809A-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
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TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS: LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 INPNSGNTDYAQKFQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
               CITY: New York STATE: New York COUNTRY: USA ZIP: 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-025-769B-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr.,
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59 Application US/09025769B

Patent No. 630064

GENERAL INFORMATION:
APPLICANT: Knappk, Achim
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Bluckhun, Andreas
APPLICANT: Plucckhun, Andreas
APPLICANT: Pluckhun, Andreas
APPLICANT: Pluckhun, 333
CORRESPONDENCE ADDRESS:
                                                                                                                        Sequence 36, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION
APPLICANT: Pack, Peter
APPLICANT: Ilaq, Vic
APPLICANT: Ilaq, Vic
APPLICANT: Moroney, Simon
APPLICANT: Plueckchun, Andreas
TITLE OF INVENTION
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 71; DB 4; I
Pred. No. 9.8e-05;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (212)566-9090
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERICTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 86.7%;
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70 INPNSGGTNYAQKFQ 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-09-025-769B-59
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                                                                                     RESULT 5
US-09-025-769B-36
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US-084-77-8778-94

US-084-77-8778-94

US-084-77-8778-94

Pacent No. 573097

Pacent No. 573097

PAPLICANT: Bazin, Herv

APPLICANT: Bazin, Herv

APPLICANT: Bazin, Herv

APPLICANT: Latine, Dominique

TITLE OF INVENTION: LO-CD24 Antibody and Uses Thereof for Inhibiting T-Cell Activa

TITLE OF INVENTION: 10-CD24 Antibody and Uses Thereof for Inhibiting T-Cell Activa

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS: 05

CORRESPONDENCE ADDRESS: Carella, Byrne, Bain, Gilfillan,

ADDRESSES: Cacchi, Stewart & Olstein

STREET: New Jersey

COMPTR: U.S.A.

COMPTR: New Jersey

COMPTR: New Jersey

COMPTR: U.S.A.

MEDIUM TYPE: 3.5 inch diskette

COMPTR: U.S.A.

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                                                                                                                                                                                                                                                                       CALF: LOUGL
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYETEM: PC -DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Halley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 120;
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ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 71; DB 4; I
Pred. No. 9.8e-05;
1; Mismatches 1.
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                                                                                                                                                                                                                  Length 123;
TOPOLOGY: linear
NOLECULE TYPE: polypeptide
FEATURE:
NAME/KEY: Human Amu 5-3 heavy chain variable region.
US-08-472-281A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Latinne, Dominique
APPLICANT: Latinne, Dominique
APPLICANT: Latinne, Dominique
APPLICANT: Latinne, Dominique
APPLICANT: Mite-Scharf, Mary
TITLE OF INVENTION: LO-CDDA Antibody and Uses
TITLE OF INVENTION: LO-CDDA Antibody and Uses
TITLE OF INVENTION: LO-CDDA Antibody and Uses
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Giffillan,
ADDRESSEE: Carella, Stewart & Olstein
STREET: Roseland
CITY: Roseland
STATE: Now Jersey
COUNTRY: Roseland
STATE: Now Jersey
COUNTRY: LIMP ES/2
CONPUTER READALE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM ES/2
COMPUTER: IBM ES/2
COMPUTER: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,989B
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/19,009
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Ellict M.
REGISTRACTION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 21,000
TELERANG: 201-004-17.4
                                                                                                                                                                                                         Query Match

Best Local Similarity 86.7%; Pred. No. 0.0001;

Matches 13; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: Human Amu 5-3 heavy chain variable; NAME/KEY: region.
US-08-477-989B-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 94, Application US/08477989B Patent No. 5951983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 94
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                           51 INPNSGGTNYAQKFQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Sequence 94, Application US/08472281A |
| Sequence 94, Application US/08472281A |
| Patent No. 58173131 |
| Patent No. 58173131 |
| APPLICANT: Latinne, Dominique |
| TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa |
| APPLICANT: Latinne, Dominique |
| TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa |
| CORRESSORES Cacclla, Stewart & Olstein |
| ANDRESSEE: Cacclla, Stewart & Olstein |
| STREET: Geechi, Stewart & Olstein |
| STREET: Geechi, Stewart & Olstein |
| STREET: Beneder Farm Road |
| STATE: New Jorsey |
| COMPTRY: NOWBER: New Jorsey |
| COMPTRY: NOWBER: New Jorsey |
| COMPTRY: NOWBER: 06/10/1008 |
| ATTORNEY AGENT INFORMATION: |
| RESIDENCE: COMPTRY: 201-994-1144 |
| NOWBER OFFICE |
| COMPTRY: CON-994-1144 |
| NOWBER OFFICE |
| COMPTRY: CON-994-1144 |
| NOWBER: OFFICE |
| COMPTRY: CON-994-1144 |
| NOWBER: OFFICE |
| COMPTRY: CON-994-1144 |
| NOWBER: OFFICE |
| COMPTRY: CON-994-1144 |
| CON-994-
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86.6%; Score 71; DB 1; Length 123;
Best Local Similarity 86.7%; Pred. No. 0.0001;
Matches 13; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: Human Amu 5-3 heavy chain variable region.
US-08-477-877B-94
                             FILING DATE: 05-MAR-1993

ATTORNEY AGENT INFORMATION:
NAME: 01stein, Elliot M.
REGISTRATION NUMBER: 24,025

REFERENCE/DOCKET NUMBER: 61750-146

TELEPHONE: 201-994-1700

TELEPHONE: 201-994-1704

INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 and no acids
TYPE: and acids
TYPE: and acids
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 INPNSGNTDYACKFO 15
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US-08-472-281A-94
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51 INPSNGNTGYAQKFQ 65
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                                                                                                                                                                                                               RESULT 10
US-08-478-039-65

; Sequence 65, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hannan, Nabil
; APPLICANT: Hannan, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS: 3
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
STATE: VA
                                                                       .
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80.0%; Pred. No. 0.00046;
Live 2; Mismatches 1; Indels
                          86.6%; Score 71; DB 2; Length 123; 86.7%; Pred. No. 0.0001;
                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:

STATE: VA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PALONIN Release #1.0, Version #1.30
SOFTWARE: PALONIN Release #1.0, Version #1.30
SOFTWARE: PALONIN DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-UN-1995
CLASSIFICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION NUMBER: US 07/912,292
PRIOR APPLICATION NUMBER: US 07/912,292
PRIOR APPLICATION NUMBER: US 07/912,292
PRIOR APPLICATION NUMBER: 10-UL-1991
PRIOR APPLICATION NUMBER: 23-UL-1991
PRIOR APPLICATION NUMBER: 35,030
PRIOR APPLICATION NUMBER: 35,030
PRIOR APPLICATION NUMBER: 35,030
PRIOR APPLICATION NUMBER: 35,030
REPERRORE/DOCKET NUMBER: 35,030
REPERRORE/DOCKET NUMBER: 35,030
REFERRORATION INFORMATION:
"MOMBER: 703-836-6620
""TS:
TOS NUMBER: 703-836-6620
""TS:
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POSITION IN GENOME:

CHROMOSOME/SEGMENT: clone 1-14

US-08-478-039-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                  1 INPNSGNTDYAQKFQ 15
                                                                                                                                                          51 INPNSGGTNYAQKFQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.03
Matches 12; Conservative
                                        Best Local Similarity
Matches 13; Conserv
                            Query Match
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Gaps
RESULT 11
US-08-476-349A-65
; Sequence 65, Application US/08476349A
; Patent No. 5750105
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Alexan...
STREE. VA
COUNTRY: USA

ZIF: 12313-1404

ZIF: 22313-1404

ZIF: Z2313-1404

MEDIUM TYPE: Floppy disk
COMPUTER: ERDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ERDABLE FORM:
SOFTWARE: PatentIn Release #1.0, Version #1.30

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NAME: US /08/476,349A

FILING DATE: 07-UN-1995

RIOR APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-UU-1992

PRIOR APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-UU-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281

FILING DATE: 13-MA-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064

FILING DATE: 23-MA-1992

RIOR APPLICATION NUMBER: US 07/735,064

FILING DATE: 23-UM-1991

ATTORNEY AGENT INFORMATION:
MANE: TERENICE/DOCKET NUMBER: 012712-161

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 67; DB 1; I
Pred. No. 0.00046;
2; Mismatches 1,
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CHROMOSOME/SEGMENT: clone 1-14
US-08-476-349A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.7%;
80.0%;
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Best Local Similarity 80.0
Matches 12; Conservative
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US-08-290-592E-16
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1 INPNSGNTDYAQKFQ 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2 INCH DISKETTE
COMPUTER: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09448
FILING DATE:
CLASSIFICATION NUMBER: 08/290,592
FILING DATE: AUGUST 15, 1994
APPLICATION NUMBER: 07/413,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: HERROW, CHARLES J.
RESISTRATION NUMBER: 28,019
RESISTRATION NUMBER: 28,019
RESISTRATION NUMBER: 28,019
RESISTRATION NUMBER: 469201-257
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMA
                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
PRIOR APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATPOINTY/ABENT INFORMATION:
NAME: FERRARC, GREGORY D.
REGISTRATION NUMBER: 36,134
REGISTRATION NUMBER: 469201-
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 AMINO ACIDS
STRANDEDNESS:
TOPPLICATION INFORMATION:
STRANDEDNESS:
TOPPLICATION OF STRANDEDNESS:
TOPPLICATION INFORMATION:
STRANDEDNESS:
TOPPLICATION INFORMATION:
THE STRANDEDNESS:
TOPPLICATION INFORMATION:
THE STRANDEDNESS:
THE STRA
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Concurrently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 INPSGGSTSYAQKFQ 65
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Best Local Similarity 73.33
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN
PCT-US95-10053-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US96-09448-16
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TITLE OF INVENTION:

HUMBER OF SEQUENCES:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CACGII, STEWART & OLSTEIN
STREET: GECKII, STEWART & OLSTEIN
STREET: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OOMPUTER: IBM PS/2
OOMPUTER: TOSELCATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10053
                                                                              GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
TITLE OF INVENTION: Respiratory Syncytical Virus
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
ADDRESSEE: OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 62; DB 2; Length 97;
Pred. No. 0.0026;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY CONTROL OF COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18M PS/2
CURRENT APPLICATION DATA: 1994
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGBNT INFORMATION:
NAME: Olstein, Ellict M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 469201-257
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
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GENERAL INFORMATION:
        Sequence 16, Application US/08290592E
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 AMINO ACIDS
TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.6%;
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Best Local Similarity 73.3'
....hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: PROTEIN US-08-290-592E-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
PCT-US95-10053-13
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### SCHEMENBURSES:
### SCHEMENBURSES:
### SCHEMENBURSES:
### PROPLICATION
### SCHEMENBURSES:
### SCHEMENBURS
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Search completed: April 21, 2004, 17:40:03 Job time : 18.0435 secs

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Sequence 289, App Sequence 296, App Sequence 296, App Sequence 342, App Sequence 344, App Sequence 341, App Sequence 361, App Sequence 45, Appl Sequence 45, Appl Sequence 61, Appl Sequence 21, Appl Sequence 238, App Sequence 238, App Sequence 246, App Sequence 246, App Sequence 21, Appl Sequence 236, Appl

Run

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APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gait, Gadi
APPLICANT: Beaabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051.A
CURRENT APPLICATION NUMBER: US.10/041,860
CURRENT APPLICATION NUMBER: US.2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 377
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 82; DB 14;
100.0%; Pred. No. 3.4e-06;
Live 0; Mismatches 0;
US-10-029-926B-45
US-10-041-860-289
US-10-041-860-290
US-10-041-860-290
US-10-041-860-296
US-10-041-860-296
US-10-041-860-344
US-10-041-860-344
US-10-041-860-344
US-10-041-860-361
US-10-041-860-361
US-10-041-860-398
US-10-041-860-398
US-10-041-860-398
US-10-041-860-398
US-10-041-860-398
US-10-041-860-209
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US-10-041-860-200
; Sequence 200, Application US/10041860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 48, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 INPNSGNTDYAQKFQ 15
          15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: homo sapiens
US-10-041-860-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                          US-10-041-860-48
          Матсрев
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Sequence 230, App
Sequence 372, App
Sequence 373, App
Sequence 1381, Ap
Sequence 1381, Ap
Sequence 1948, Ap
Sequence 1948, Ap
Sequence 1891, Ap
Sequence 1891, Ap
Sequence 1891, Ap
Sequence 47202, Appl
Sequence 47202, Appl
Sequence 47202, Appl
Sequence 47202, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                       April 21, 2004, 17:37:29 ; Search time 45.2174 Seconds (without alignments) 91.715 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12. (cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2. (cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
3. (cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4. (cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5. (cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
6. (cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
7. (cgn2_6/ptodata/2/pubpaa/NEONB.PUB.pep:*
8. (cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
9. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
12. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
14. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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11. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
12. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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14. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18. (cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-041-860-200
US-10-041-860-237
US-10-041-860-373
US-10-041-860-373
US-09-880-748-1381
US-10-293-418-1381
US-10-293-418-1948
US-10-293-418-1891
US-10-293-418-1891
US-10-293-418-1891
US-10-193-418-1891
US-10-193-418-1891
US-10-194-975-3
US-09-664-761-47202
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                       Sequence:
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1 INPNSGNIDYAQKFQ 15
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                         Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
                                                                                               Gazit, Gadi
Weber, Richard
  Jia, Xiao-Chi
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                                                                                                                                                                                                                                                                                                                                                                         ) TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-372
                                                                 Chen,
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US-09-880-748-1381
                                                                   APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 82; DB 14; Length 125; 100.0%; Pred. No. 3.4e-06; tive 0; Mismatches 0; Indels (
                                                                           APPLICANT: Peng, Nimo
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES
FILE REFREENCE: ABGANTX.051A
CURRENT APPLICANTON NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FESTEEQ for Windows Version 4.0
SEQ ID NO 200
LENGTH: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 237, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gen, Francine
APPLICANT: Gen, Francine
APPLICANT: Gazir, Gadi
APPLICANT: Heaber, Richard
APPLICANT: Heaber, Richard
APPLICANT: APPLICANT: ABLINAM
TITLE OF INVENTION: THEREOF
FILE REREMENCE: ABGANX.031A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 372, Application US/10041860; Publication No. US/30030157109A1
GENERAL INFORMATION: APPLICANT: CORVAIAN, JOSE R.F.
Publication No. US2030157109A1
GENERAL INFORMATION:
PEPITCANT: COPYALAN, JOSE R.F.
APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 INPNSGNIDYAOKFO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: homo sapiens
US-10-041-860-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: homo sapiens
US-10-041-860-237
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Gaps
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Publication No. US2030059937A1

GRNERAL INFORMATION:
APPLICANT: Ruben et al.
APPLICANTON: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF53
CURRENT APPLICATION NUMBER: US/09/880,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 82; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-041 Sequence 373.

Sequence 373. Application US/10041860

Sequence 373. Application US/10041860

Sequence 373. Application US/2003015710941

GENERAL INPORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Yang, Xiao-Chi

APPLICANT: Yang, Xiao-Chi

APPLICANT: Yang, Xiao-Chi

APPLICANT: Mebar, Riao-Chi

APPLICANT: Mebar, Riao-Chi

APPLICANT: Mebar, Richard

APPLICANT: Mebar, Richard

APPLICANT: Mebar, Richard

APPLICANT: Mebar, Richard

APPLICANT: Mebar, Sinyam

TITLE OF INVENTION: THERROP

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TITLE OF INVENTION: THERROP

TITLE OF INVENTION INMERR: 2002-01-07

NUMBER OF SEQ ID NOS: 377

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SOFTHARE: PRESERE OF Windows Version 4.0

SEQ ID NO 373

LENGTH: 98
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APPLICANT: Bezabeh, Binyam TITLE OF INVENTION: ANTIDODIES DIRECTED TO PDGFD AND USES TITLE OF INVENTION: THEREOF PILE REFERENCE: ABGENIX.051A CURRENT APPLICATION NUMBER: US/10/041,860 CURRENT FILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377 SOFTWARE FASES FOR Windows Version 4.0 SEQ ID NO 372 LENGTH: 125
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1 INPNSGNIDYAQKFQ 15
Publication No. US20030157109A1
                     GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
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CRGANISM: Homo sapiens
US-09-880-748-1948
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: homo sapiens
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US-10-293-418-1381
i Sequence 1381, Application US/10293418
i Publication No. US2003022396A1
i GENERAL INFORMATION:
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/31,469
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-2
PRIOR PLING DATE: 2001-03-2
PRIOR PLING DATE: 2001-03-16
PRIOR PRIOR DATE: 2001-03-16
PRIOR PLING DATE: 2000-01-17
PRIOR PLING DATE: 2000-01-16
PRIOR PLING DATE: 2000-01-16
PRIOR PLING DATE: 2000-01-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1381
LENGTH: 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 77; DB 10; Length 248;
Pred. No. 5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
    CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 1381
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US-10-041-860-374
; Sequence 374, Application US/10041860
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Best Local Similarity 93.3%; Pr
Matches 14; Conservative 1;
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Best Local Similarity 93.3
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-10-293-418-1381
                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1381
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APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazir, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE REFERENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 374
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

91.5%; Score 75; DB 14; Length 98;
Best Local Similarity 93.3%; Pred. No. 4.1e-05;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: VARIANT
COTHER INFORMATION: Xaa = Any Amino Acid
FEATURE:
NAME/KEY: VARIANT
LOCATION: 59, 73, 97
COTHER INFORMATION: Xaa = Any Amino Acid
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-374
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1 INPNSGNTDYAQKFQ 15

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Gaps
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Pred. No. 0.00011;
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Best Local Similarity 93.3%;
Matches 14; Conservative
51 INPNSGNTGYAQKFQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 INPNSGNIDYAOKFO 15
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; ORGANISM: Homo sapiens
US-09-880-748-1891
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CRGANISM: Homo sapiens
US-10-293-418-1948
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| Page | March | Page |
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seq2.open.rapb
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Gaps

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; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62

; OTHER INFORMATION: SWISSPROT HIT: P23083, EVALUE 2.00e-39

; OTHER INFORMATION: EST_HUMAN HIT: AW405627.1, EVALUE 8.00e-48

US-09-864-761-47202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 87.8%; Score 72; DB 14; Length 96; Best Local Similarity 86.7%; Pred. No. 0.00013; Matches 13; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10194975;
Publication No. US20030039649A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson;
TITLE OF INVENTION: Super Humanized Antibodies;
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US 10/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR FILING DATE: 2002-10-10
PRIOR FILING DATE: 2001-07-12
; ROFTWARE: Patentin version 3.1
; SOFTWARE: Patentin version 3.1
                                                                                                                                                  Score 72; DB 9; 1
Pred. No. 0.00012;
1; Mismatches 1;
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                                                                                                                                                         Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                     1 INPNSGNTDYACKFO 15
                                                                                                                                                                                                                                                                                    1 INPNSGNTDYAQKFQ 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT CAGANISM: Homo sapiens US-10-194-975-3
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-10-194-975-3
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                                                                                           87.8%; Score 72; DB 14; Length 17;
86.7%; Pred. No. 2e-05;
live 1; Mismatches 1; Indels
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ORGANIEM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
OTHER INFORMATION:
                                                                                                                                                                                                                                                                 2 MNPNSGNTGYAQKFQ 16
                                                                                                                                                                                                                             1 INPNSGNTDYAOKFO 15
                                                                                                                               Best Local Similarity 86.7
Matches 13; Conservative
      ; ORGANISM: Homo sapiens
US-10-148-844-40
                                                                                                    Query Match
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Gaps

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

model protein search, using sw OM protein April 21, 2004, 17:25:18 ; Search time 64 Seconds (without alignments) 70.637 Million cell updates/sec Run on:

score: Title: Perfect :

1 gfgysynydyyygmdv 16 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 Total number of hits satisfying chosen parameters: 1586107 seqs, 282547505 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A\_Geneseq\_29Jan04:\*
1: geneseqp1980s:\*
3: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003s:\*
7: geneseqp2003bs:\*
8: geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	203 Human	172	Human	Human			Human	Human	57	8	Human	ū		6 Human	Mouse		Abg77142 Anti-IGF-	Aam51170 Human rec	Aam51171 Human rec	8 Нишап		Abg77158 Germline	Human	Human	Abp45447 Human BLy
ID	03	AAM51172	ABR41574	ABP46758	ABP45542	ABG77138	AAM79672	AAM24101	ABG77157	AAM78688	ABG31313	ADA89202	ABP57367	AB004856	AAU70375	ABP46976	ABG77142	AAM51170	AAM51171	AAM51168	ABP45614	ABG77158	ABP46915	AAE37205	ABP45447
DB	!							4																	
Length	143	146	112	21	257	124	170	384	470	590	44	128	145	157	18	19	125	146	146	146	254	470	24	145	260
% Query Match	! _:	:	~	_:	58.2		57.7	57.7	57.7	57.7	56.7	56.7	10	55.7	10	54.6	54.6	54.6	54.6	54.6	54.6	54.6	54.1	54.1	54.1
Score	62.5	59	57	9	56.5	26	26	26	26	26	55	55	55	54	53.5	ഗ	53	53	53	53	53	23	ď	•	'n
		73	m	4	ιO	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	.23	24	25

Human 1	Abp46724 Human BLy	Human	Human	Human	Human	Human	Abp45260 Human BLy	Human	Aaw36052 Human occ	Aaw34638 Human occ	Human	Human	• •		Abp46756 Human BLy	Aay37253 Protein w	Huma	Aaw03964 VDJ joint	Aaw41127 VH251 DXP	
ABP46825	ABP46724	AAW34640	AAM51169	ABP45404	ABP45248	ABP45273	ABP45260	ABP45272	AAW36052	AAW34638	AAB35731	ABJ37076	ADD46545	ADA34312	ABP46756	AAY37253	ABP45290	AAW03964	AAW41127	
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17	19	24	146	252	254	255	255	257	522	522	522	522	522	733	~	101	256	36	ň	
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25	52	22	20	25	125	52	25	52	52	52	52	25	52	52	٦,					
26	27	00	0 0	30	31	3.5	33	34	5	36	3.7	. e	6	40	4	4 2	6. 4	4	4.5	

#### **ALIGNMENTS**

RESULT 1

AAE37203 standard; protein; 143 AA 

AAE37203;

(first entry) 07-AUG-2003

Human AB-PG1-XG1-026 PSWA antibody heavy chain variable region (VH).

Human; Prostate specific membrane antigen; carcinoma; sarcoma; cancer; PSMA; melanoma; therapy; N-acetylated alpha-linked acidic dipeptidase; folate hydrolase; dipeptidyl dipeptidase IV; gamma-glutamyl hydrolase; NAALADase; antibody; heavy chain variable region; VH.

Homo sapiens.

WO2003034903-A2.

01-MAY-2003.

23-OCT-2002; 2002WO-US033944.

23-OCT-2001; 2001US-0335215P. 07-MAR-2002; 2002US-0362747P. 20-SEP-2002; 2002US-0412618P.

(PSMA-) PSMA DEV CO LLC.

Maddon PJ, Donovan GP, Olson WC,

ä ď

Gardner J,

Schuelke N,

WPI; 2003-403281/38. N-PSDB; AAD56218.

Novel isolated antibody which binds to epitope on prostate specific membrane antigen, and competitively inhibits binding of second antibody to its target epitope on the antigen, useful for treating prostate cancer.

Claim 26; Page 229-230; 238pp; English.

The invention relates to an antibody or its antigen-binding fragment which specifically binds to epitope on prostate specific membrane antigen (PSMA), and competitively inhibits the specific binding of a second antibody to its target epitope on PSMA. The invention is useful for diagnosing, treating or preventing PSMA-mediated disease such as prostate cancer or non-prostate cancer bladder chosen from cancer including transitional cell carcinoma, pancreatic cancer including pancreatic duct

Novel isolated mammalian anti-tumor necrosis factor antibody, useful for treating sickle cell anemia, diabetes, atherosclerosis, restenosis, angina pectoris, myocardial infarction, leprosy.

Shealy D;

Heavner G, Scallon B,

Giles-Komar J, Knight DM,

WPI; 2002-217194/27.

(CENZ ) CENTOCOR INC.

07-AUG-2000; 2000US-0223360P. 29-SEP-2000; 2000US-0236826P. 01-AUG-2001; 2001US-00920137. 07-AUG-2001; 2001WO-US024785.

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carcinoma, lung cancer including non-small cell lung carcinoma, kidney cancer including conventional renal cell carcinoma, sarcoma including soft tissue sarcoma, breast cancer including breast carcinoma, brain cancer including glioblastoma multiforme, neuroendocrine carcinoma, colon cancer including colonic carcinoma, testicular cancer including colonic carcinoma, testicular cancer including testicular embryonal carcinoma, or melanoma including malignant melanoma. The invention is useful also for inhibiting or enhancing folate hydrolase activity of a cloate hydrolase polypeptide, Nacetylated alpha-linked acidic dipeptiday dipeptidase (NALADase) activity of a NALADase polypeptide, polypeptide, gamma-glutamyl hydrolase activity of a gamma-glutamyl hydrolase activity of a gamma-glutamyl hydrolase activity of a gamma-glutamyl chain variable region (VH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour necrosis factor alpha, TNF; antibody; heavy chain; CDR; complementarity determining region; antirheumatic; antiarthritic; antiducer; antiarthmatic; antialergic; antidifammatory; antisickling; antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic; antidanginal; cardiant; antibacterial; virucide; fungicide; antileprotic; protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic; human; diagnosis; therapy; TNV196; monoclonal antibody; mAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-7 are PCR primer-encoded and may
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                       64.4%; Score 62.5; DB 6; Length 143; 73.3%; Pred. No. 0.23; cive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human recombinant mAb TNV196 heavy chain variable region.
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differ from the native sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l. .19
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20. .146
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "encoded by A"
136. .146
/label= J6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM51172 standard; protein; 146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69. .85
/label= CDR2
86. .117
/label= FR3
118. .135
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50. .54
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55. .68
/label= FR2
                                                                                                                                                                                                                                                                                                                                           118 GYNWNYEYHYYGMDV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31. .49
/label= FR1
                                                                                                                                                                                                                                                                                                                        3 GYSYNYDY-YYGMDV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 73.3
Matches 11; Conservative
                                                                                                                                                                                                                              Sequence 143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200212502-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM51172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
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14-FEB-2002

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The present sequence is that of the heavy chain variable region of anticumour necrosis factor (TMF) human mabs produced from a GenTWV fusion using raviable moells from a hybrid mouse containing human variable and constant region antibody transgenes that was immunised with high avidity and had a contain and to the human germline D-46 heavy chain sequence (see AAMS1167). The and to the human germline D-46 heavy chain sequence (see AAMS1167). The invention provides isolated human, primate, rodent, mammalian, chimmeric, humanised and/or complementarity determining region (CDR) -grafted anti-cry and variants, as well as anti-TWF antibody compositions, chimmeric, compositions, formulations, devices, transgenic animals, transgenic compositions, formulations, devices, transgenic animals, transgenic compositions, formulations, devices, transgenic animals, transgenic compositions, formulations of making and using them. The antibody complement and/or light chain variable regions given in the present sequence and in AAMS1165, or either all of the CDRs of the heavy chain and/or light chain variable regions given in the present (sequence and in AAMS1165, or either all of the CDRs of the heavy chain (see AAMS1185-60) or all of the CDRs of the heavy chain (see AAMS1185-60) or all of the CDRs of the heavy chain (see AAMS1185-60) or all of the CDRs of the heavy chain (see AAMS1185-60) or all of the CDRs of the heavy chain and arthritis, gastric ulcer, asthma, allergio rhinitis, Crohn's inhibit TMF induced cell andhesion or animal (claimed) such as rhematoid arthritis, gastric ulcer, asthma, allergio rhinitis, Crohn's pathology, sickle cell anaemia, diabetes, acardiovascular disease such as meteriosclerosis, atherosclerosis, restenosis, angina pectoria or angina pectoria or angina malignant disease such as Burkaemia, chronic myclocytic leukaemia, Burkitt's disease and configuence or a leukaemia, chronic wylelocytic leukaemia, Burkitt's andignant or sulvaemia, chronic myclocytic disease such as militared configuence or an annual e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sclerosis, Parkinson's disease, spinal ataxīa, Alzheimer's disease and
Creutzfeldt-Jakob disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DITHP antigen recognition protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR41574 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 4; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GFGYSYNYDYYYGMDV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GIGAGGNYYYYYGMDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 68.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 146 AA;
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ABR41574
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seq3.open.rag

Sequence 112 AA;

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Page

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cancer; cell proliferative disorder; autoimmune disorder; inflammancy disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; antetion, hormonal disorder; transport disorder; connective tissue disorder; drug screening; proteome analysis; ene therapy; antisense therapy; genotyping; transgenic animal; knock in; disease model; toxicological testing; transcript imaging; antigen recognition.
Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
                                                                                                                                    28-MAR-2001; 2001US-0279619P.
29-MAR-2001; 2001US-0280067P.
29-MAY-2001; 2001US-0291080F.
17-MAY-2001; 2001US-029129P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
20-JUN-2001; 2001US-0299776P.
                                                                                                                      27-MAR-2002; 2002WO-US010056
                                                                                        WO200297031-A2.
                                                                        Homo sapiens.
                                                                                                       05-DEC-2002
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(INCY-) INCYTE GENOMICS INC.

EH; Jones AL, Tran AB, Dahl CR, dietzen D, Chinn J;
, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Geretin B,
Javid MH, Lewis SA, Chen AJ, Panzer SR, Harrig B;
Marwaha R, Lo A, Lan RY, Urashka ME; Daffo A, Jones AL, Trai Dufour GE, Hillman JL, Daughtery SC, Dam TC, Peralta CH, David MH, Flores V, Marwaha R, L

WPI; 2053-129518/12. N-PSDB; ACC46512.

Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.

Claim 27; SEQ ID NO 1109; 591pp; English

The invention relates to novel human diagnostic and therapeutic

polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded

proteins (DITHP; ABRA1812). The invention also relates to

polynucleotide sequences at least 90% identical to the dithp cDNA

sequences of the invention; recombinant vectors, host cells and

cransgenic organisms comprising althp nucleic acid sequence; the

recombinant production of DITHP proteins; antibodies specific for DITHP

crecombinant production of DITHP proteins; antibodies specific for DITHP

crecombinant production of DITHP proteins; antibodies of sereening

crecombinant production of DITHP proteins; and methods of

assessing the toxicity of test compounds using a dithp hybridiaation

crecombinant uncleic acid sequences and DITHP protein; and methods of

assessing the toxicity of test compounds using a dithp hybridiaation

crecombinant production of later compounds using a dithp hybridiaation

crecombinant production of test compounds using a dithp hybridiaation

crecombinant production of sequences and DITHP proteins may be used in the

crecompounds which specifically bind a DITHP proteins and conferences and conferences; and conferences and conferences and conferences. They may also be used to disorders; neurological disorders; partointestinal disorders; transport

crecompined above, as source of artisens sequences, as source of additionally useful in somatic or germline gene therapy of the disorders

crecompicated above, as source of antiense sequences, as a source of the generation of transgenic or mentioned above, as a source of mathiems and primers, in toxicological testing, and in transcript imaging.

The present sequence represents a DITHP protein which has antied or thumanised animals, in toxicological testing of the primers of the primed specification, but was obtained in electronic form part of the primed specification, but was obtained in electronic computation activity. Note: The sequence date for this part of the primers and primers are sequence. The

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TWS) super family and induces B cell tumour necrosis factor (TWS) super family and induces B cell proliferation and differentiation. The antibodies of the invention have proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antithermatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant supersection of BLyS. They may also be ancievity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (cyll) and activity and activity and as cancer, immune, and autoimmatoid arthritis, immunodeficiency (cyll) and activity and activity and as cancer, immune (AlDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                      BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulator; antirheumatic; antiAIDS; vaccine; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
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Length 112
                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi GH, Vaughan T, Hilbert D;
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9
Score 57; DB 6;
Pred. No. 1.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Human BLyS binding scFv VH CDR3 SEQ ID 2769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 3048; 3148pp; English.
                                                                                                                                                                                                                              ABP46758 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUN-2000; 2000US-0212210F.
17-OCT-2000; 2000US-0240B16F.
16-MAR-2001; 2001US-0276248F.
21-MAR-2001; 2001US-027379F.
25-MAY-2001; 2001US-0293499F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2001; 2001WO-US019110.
  Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                  GYSYNYDYYYGMDV 16
                                                                                                                     GYDGDYYYYYGMDV 58
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-114799/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200202641-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                            19-AUG-2002
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ABP46758
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1;

Gaps

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Indels

1; . 2 B

Score 56.5; DB Pred. No. 3.2; 1; Mismatches

Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative

Length 257;

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell correction and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, ammunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunosuppressive; immunostimulant; immunosi, antirheumatic; surtiAIDS; vaccine; cancer; immune alsorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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                                                                                                                                 Gaps
                                                                                                                                     ٦;
                                                              Length 21;
                                                       Score 56.5; DB 5; Length 2
Pred. No. 0.21;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 2256-2257; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human BlyS binding scFv SEQ ID 1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP45542 standard; protein; 257 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-2000; 2000US-0212210P.
17-OCT-2000; 2000US-0240B16P.
16-MAR-2001; 2001US-0276248P.
12-MAR-2001; 2001US-0293499P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2001; 2001WO-US019110
                                                       S8.2%;
Local Similarity 78.6%;
les 11; Conservative
                                                                                                                                                                                                    3 GYSYNYDYYYGMDV 16
                                                                                                                                                                                                                                                9 GY-YLWDYYYGMDV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-114799/15.
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Sequence 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP45542;
                                                                      Query Match
                                                                                                                                 Matches
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ABP45542

ABP4564

ABP4664

ABP46644

ABP466444

ABP466444

ABP466444

ABP466444

ABP466444

ABP466444

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ABP466444

ABP466444

ABP
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This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to insulin-like growth factor I receptor (IGF-IR). The antibodies of the invention can act as an inhibitor of binding of IGF-IR tyrosine.

IR and can inhibit in vivo tumour growth and IGF-IR tyrosine phosphorylation. The antibodies of the invention are useful for diagnosing the presence or location of an IGF-IR-expressing tumour in a subject. The antibody or its antigen-binding portion is also useful for reating cancer in a human. The method for this further involves an antipodistic, anti-tumour, anti-anglogenic or chemotherapeutic agent. The antibodies may also be useful for Increasing IGF-IR activity and thus articles and inducing apoptosis. An antibody of the invention is also useful for inducing apoptosis of specific cells in a patient, and to treat non-cancercous states or disease, e.g. acromegaly, gigantism, or the immunogenic and allergic responses intrinsic to mouse or mouse entitied and allergic responses intrinsic to mouse or mouse and activity in a condition of the interess the efficacy and activity is a shiping an anti-local and allergic responses intrinsic to mouse or mouse carriers and antibodies and thus interess the efficacy and activity in the antibodies and thus interess the efficacy and activity in the antibodies and thus interess the efficacy and activity in the antibodies and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel humanized, chimeric monoclonal antibody that specifically binds to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
                                                                                                                                                                                                                                                                                                                                                                                                       Insulin-like growth factor I receptor; antibody; human; cytostatic; osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis; acromegaly; gigantism; psoriasis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and safety of the administered antibodies. The present sequence
represents an anti-insulin-like growth factor I receptor antibody of the
                                                                                                                                                                                                                                                                                                                                                     Anti-IGF-IR antibody (2.13.2) variable region heavy chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corvalan JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moyer JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 127; 172pp; English
                                                                                                                                                                                          ABG77138 standard; protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-2001; 2001WO-US051113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-2001; 2001US-0259927P.
                                   107 GY-YLWDYYYGMDV 119
3 GYSYNYDYYYGMDV 16
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-575410/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beebe J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABS62700.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200253596-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                    24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cohen BD,
                                                                                                                                                                                                                                                  ABG77138;
                                                                                                                                         RESULT 6
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Gaps

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1;

Mismatches

.. (1)

Conservative

.. 80

seq3.open.rag

|:|:|||||| 16 YNYGEDYYYGM 4 YSYNYDYYYGM

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AAM24101 standard, protein; 384 AA.
 Matches
                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, nematopoissis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                 Gaps
                                   6
 Length 124;
                                   2; Indels
 Score 56; DB 5;
Pred. No. 1.7;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 306; 6221pp; English.
                                                                                                                                                                                      AAM79672 standard; protein; 170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00532S.
01-SEP-2000; 2000US-0054936.
15-SEP-2000; 200US-0065351.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00693325.
                                                                                                                                                                                                                                                                                      Human protein SEQ ID NO 3318.
ch 57.7%;
1 Similarity 71.4%;
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-FEB-2001; 2001WO-US004098
                                                                                      100 GWSDSYYYYYGMDV 113
                                                                     3 GYSYNYDYYYGMDV 16
                                                                                                                                                                                                                                                      06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-476283/51.
N-PSDB; AAK52805.
Query.Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001.
                                                                                                                                                                                                                    AAM79672;
                                                                                                                                                    g
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Length 170

Score 56; DB 4; Pred. No. 2.4;

57.78;

Query Match Best Local Similarity

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ö
                                                                                                                                      Human, sheep, pig, cow, fruit fly, yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; BST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, form the organism of interest. They can be used in diagnostics, formsics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen R, Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.7%; Score 56; DB 4; Length 384; 76.9%; Pred. No. 5.9; 2; Indels :ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou P, Qian XB, Wang Z, A, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 1102-1103; 1275pp; English
                                                                                                         Human EST encoded protein SEQ ID NO: 1626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG77157 standard; protein; 470 AA.
                                                                                                                                                                                                                                                                                                                                               25-JAN-2000; 2000US-00491404.
17-JUL-2000; 2000US-0061746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-00663870.
                                                                                                                                                                                                                                                                                                                  25-JAN-2001; 2001WO-US002687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||:|||||||
129 YSSHYYYYYGMDV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 YSYNYDYYYGMDV 16
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 76.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein of the invention
                                                                                                                                                                                           gene therapy; nutrition
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Liu C, Zh
Cao Y, Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-476164/51.
N-PSDB; AAH98760.
                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 384 AA;
                                                                                                                                                                                                                                                      WO200154477-A2.
                                                                                                                                                                                                                         Homo sapiens
                                                                             12-OCT-2001
                                                                                                                                                                                                                                                                                    02-AUG-2001.
                                              AAM24101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG77157
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ABG77157
ID ABG7
XX
AC ABG7
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Human protein SEQ ID NO 1350.

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This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to insulin-like growth factor I receptor (IGF-IR). The antibodies of the invention can act as an inhibitor of binding of IGF-IR tyrosine phosphorylation. The antibodies of the invention are useful for its and can inhibit in vivo tumour growth and IGF-IR tyrosine phosphorylation. The antibodies of the invention are useful for diagnosing the presence or location of an IGF-IR tyrosine treating cancer in a human. The method for this further involves an antipoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The antibodies may also be useful for increasing IGF-IR activity and thus restoring IGF-IR activity and thus restoring IGF-IR activity and thus are sold in a nondition characterised by low IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the invention is also useful for inducing apoptosis of specific cells in a patient, and to treat non-cancerous states or disease, e.g. acromegaly, gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies or mouse-derivatised monoclonal antibodies and thus increase the efficacy and safety of the administered antibodies. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel humanized, chimeric monoclonal antibody that specifically binds to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
                                                                                        Insulin-like growth factor I receptor; antibody; human; cytostatic; osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-anglogenic; neuropathy; osteoporosis; acromegaly; gigantism; psoriasis; atherosclerosis.
                                                         Amino acid sequence of anti-IGF-1R antibody 2.13.2 Vh domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corvalan JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moyer JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Fig 19B; 172pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller PE,
                                                                                                                                                                                                                                                                                                                                                                         05-JAN-2001; 2001US-0259927P.
                                                                                                                                                                                                                                                                                                                                 20-DEC-2001; 2001WO-US051113
                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-575410/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beebe J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 470 AA;
                                                                                                                                                                                                                                                  WO200253596-A2.
                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                       11-JUL-2002.
                      24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cohen BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Invention
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Gaps ö Query Match 57.7%; Score 56; DB 5; Length 470; Best Local Similarity 71.4%; Pred. No. 7.4; Matches 10; Conservative 2; Mismatches 2; Indels δ

AAM78688 standard; protein; 590 AA. (first entry) 06-NOV-2001 AAM78688; RESULT 10 AAM78688

Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor, immunomodulatory, cancer, leukaemia, nervous system disorder, arthritis, inflammation. 2000US-00560875. 2000US-00598075. 2000US-00620325. 05-FEB-2001; 2001WO-US004098. 01-SEP-2000; 2000US-00654936 15-SEP-2000; 2000US-00663561 20-OCT-2000; 2000US-00693325. WO200157190-A2 Homo sapiens. 27-APR-2000; 20-JUN-2000; 19-JUL-2000; 03-FEB-2000; 09-AUG-2001. 

Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy. Asundi V, Zhou P, Xu C, Cao Y; J, Zhang J, Ren F, Chen R, Wang ZW; Goodrich R; Drmanac RT, Wang D, Wang Wejhrman T, WPI; 2001-476283/51. Tang YT, Liu C, Ma Y, Zhao QA, 1 Xue AJ, Yang Y, N-PSDB; AAK51821

(HYSE-) HYSEQ INC.

Gallo M;

Claim 20; Page 3595-3596; 6221pp; English.

The invention relates to polynuclectides (AAK514156-AAK534135) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity uses useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK5281), 2111 (AAK5282) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication

Gaps ö Score 56; DB 4; Length 590; Pred. No. 9.5; 2; Mismatches 1; Indels ; 57.78; Query Match
Best Local Similarity 72.7
Matches 8; Conservative

Sequence 590 AA;

4 YSYNYDYYYGM 14

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ABG31313 standard; protein; 44 AA. |:| :|||||| 155 YNYGFDYYYGM 165 RESULT 11 XXXEXE BXEXXX 셤

Human heavy chain CDR3 variable region from patient #1.

(first entry)

21-OCT-2002

ABG31313;

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Use of DNA sequences coding for hypervariable region (VH- complementarity determining region 3 (CDR3)) of idiotypic immunoglobulin expressed on B-cells of chronic B- lymphoproliferative disorders, as therapeutic
      Human, immune response, chronic B-lymphoproliferative disorder; CDR: complementarity determining region 3; hypervariable region; B-cell; immunoglobulin heavy chain; VH-CDR3; idiotypic immunoglobulin; cytostatic; hairy cell leukaemia.
                                                                                                                                                                                                                                                                                           Disclosure, Fig 2; 30pp; English.
                                                                                                                                       15-JAN-2001; 2001WO-IT000014.
                                                                                                                   L5-JAN-2001; 2001WO-IT000014.
                                                                                                                                                                                        Fazio VM, Saglio G;
                                                                                                                                                                                                             WPI; 2002-583654/62
                                                                                                                                                          (FAZI/) FAZIO V M.
(SAGL/) SAGLIO G.
                                                                                                                                                                                                                      N-PSDB; ABK90003
                                                                               WO200255559-A1.
                                                          Homo sapiens
                                                                                                 18-JUL-2002.
                                                                                                                                                                                                                                                                       vaccine
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The present invention relates to a method for inducing an immune response against B-lymphoproliferative disorders. The method comprises DNA sequences encoding for the complementarity determining region 3 (CDR3) spervariable region of immunoglobulin heavy chain (VH-CDR3) alone or in combination with at least another immunomodulating sequence. The DNA sequences are useful as therapeutic vaccines for thronic B-combinant plasmid expression vector containing a DNA sequence of a recombinant plasmid expression vector containing a DNA sequence of the invention is useful as a therapeutic vaccine or for the manufacture of invention is useful as a therapeutic vaccine or for the manufacture of a vaccine effective against chronic B-lymphoproliferative disorders expressing the surface idiotypic immunoglobulin on B-cells in mammals, preferably humans. An efficient, safe and easily reproducible DNA-based immune response against B-lymphoproliferative pathologies can be achieved. The present sequence representing human CDR3 variable region is isolated from a hairy cell leukaemia patient ö Gaps .; 0 Score 55; DB 5; Length 44; Pred. No. 0.76; 0; Mismatches 3; Indels 56.7%; Query Match Best Local Similarity 76.9 Matches 10; Conservative Sequence 44 AA;

4 YSYNYDYYYGMDV 16 à

21 YISNYYYYGMDV 33

ADA89202 standard; protein; 128 AA. ADA89202; ADA89202 

Human antibody 2F1 heavy chain amino acid sequence SEQ ID NO:46.

(first entry)

20-NOV-2003

immunoglobulin; Ig; heavy chain variable domain; light chain variable domain; major histocompatibility complex; MHC; gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder; cancer.

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The present invention describes a protein comprising an immunoglobulin CC [19] heavy chain variable (VH) domain and an IG 11ght chain variable (VL) domain. The protein binds a complex comprising a major histocompatibility complex (MHC) and a peptide, does not substantially bind the MHC in the absence of the bound peptide, and does not substantially bind the peptide in the absence of the MHC. The peptide is a peptide fragment of gp100, MUC1, TAX or MTERT. Also described: (1) a pharmaceutical composition comprising one or more nucleic acids for expressing the IG that binds a comprising one or more nucleic acids for expressing the IG that binds a comprising one or more nucleic acids for expressing the IG that binds a comprising a first segment that encodes the IG that bind the CC comprising a first segment that encodes the IG sequences that encodes the CC comprising a first segment that encodes the IG variable domain; (4) a comprising a first segment that encodes the IG variable domain; (5) a transgenic animal whose genome includes heterologous curleic acid sequences that encode the protein; (6) identifying the protein that specifically binds the MHC-peptide complex; (7) expressing an antigen-binding protein; (8) ablating or killing a target cell that complex in a sample. A protein of the invention has cytostatic actual accorded in gene therapy. The protein is useful for preparing a composition for treating or preventing a cancerous disorder in a subject; and (10) detecting an MHC-peptide composition for treating or preventing a cancerous disorder the peptide composition has experted to an MHC-peptide complex where the peptide component in as peptide complex of many component in a septide component of an antibode component of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New protein comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, useful for preparing a composition for treating or preventing a cancerous disorder.
                                                                                                                                                                                                                                                                                  (DYAX-) DYAX CORP.
(TECR ) TECHNION RES & DEV FOUND LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 10B; 224pp; English
                                                                                                                                                                                20-FEB-2003; 2003WO-US005128.
                                                                                                                                                                                                                                    0-FEB-2002; 2002US-0358994P
                                                                                                                                                                                                                                                                                                                                                                    Hoogenboom HRJM, Reiter Y;
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-663847/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADA89201
                                                                          WO2003070752-A2
                         Homo sapiens.
                                                                                                                                28-AUG-2003
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Gaps ö Anti-TRAIL-R antibody related clone 0304 protein SEQ ID NO:29. Score 55, DB 6, Length 128; Pred. No. 2.5; 0; Mismatches 2; Indels ABP57367 standard; protein; 145 AA. Match 56.7%; Local Similarity 83.3%; Los 10; Conservative ( 22-APR-2003 (first entry) 106 SYPYYYYGMDV 117 5 SYNYDYYYGMDV 16 ABP57367; Query Match Best Loc Matches RESULT 13 ABP57367 ઠ a

antibody therapy

Homo sapiens. Synthetic.

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The invention relates to an antibody that binds to an epidermal growth factor receptor (FGF-r) and exhibits inhibition of tyrosine phosphorylation of EGF-r, the degradation of EGF-r, the EGF induced degradation of EGF-r, vascular endothelial cell growth factor (VEGF) production by tumour cells (by greater than 50%) and endothelial cells (by greater than 40%) and also protects threonine phosphorylation of EGF-r and a 63M protein. The antibody is internalised with EGF-r. The antibody may be used for treating tumours such as lung tumours and colon tumours and for treating inflammation and autoimmune diseases. Sequences ABO04859 represent human EGF-r receptor antibodies of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin; antibody; light chain; heavy chain; CDR; FR; complementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA; IgD; IgB; IgY; IgM; kappa; lambda; CHBP.
                                                                                                                                                                                                                                                                                      Fully human monoclonal antibodies that bind to epidermal growth factor receptors, useful in cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54; DB 6
Pred. No. 4.3;
2; Mismatches
                                                                                                                                                                                            Jia X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU70375 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 69; 100pp; English.
                                                                                                                                                                                              Gallo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2000; 2000US-00563222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2001; 2001WO-US014349.
98US-00187693.
                                     97US-00851362.
98US-00162280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 GQKWSYYYYGMDV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GYSYNYDYYYGMDV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse heavy chain I CDR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIC-) EPICYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 64.3
                                                                                                                                                                                              Jakobovits A, Yang X,
                                                                                              (JAXO/) JAKOBOVITS A.
(YANG/) YANG X.
(GALL/) GALLO M.
(JIAX/) JIA X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-055482/07
                                                                                                                                                                                                                                  WPI; 2003-328430/31.
N-PSDB; ACD10940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hiatt AC, Hein MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200183806-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
05-NOV-1998;
                                       05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-2001
                                                          29-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU70375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes antibodies or their functional fragments that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies have cytostatic and apoptotic activities, and can be used in antibody therapy. The antibodies can be applied as remedies and preventives of diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful in the therapy of malignant tumours. Remedies produced with the antibodies are highly safe, and avoid hepatotoxicity. The present sequence represents an anti-TRAIL-R antibody amino acid sequence from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer cells and without exerting an effect on normal cells expressing TRAIL-Rs nor inducing injury to hepatocytes, for use in therapy of malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, epidermal growth factor receptor; EGF-r; antibody; cytostatic; antiinflammatory; immunosuppressive; tyrosine phosphorylation; EGF-2; EGF-r degradation; vascular endothelial cell growth factor; VEGF; tumour; endothelial cell; threonine phosphorylation; autoimmune disease; colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
    Human, TRAIL-R1, TRAIL-R2, antibody, cytostatic, apoptotic, tumcur,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 6; Length 145;
Pred. No. 2.8;
0; Mismatches 2; Indels
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Claim 54; Page 62; 92pp; Japanese.

Cumor.

18-MAY-2001; 2001JP-00150213. 09-AUG-2001; 2001JP-00243040. 11-OCT-2001; 2001JP-00314489.

(KIRI ) KIRIN BEER KK

Kataoka S;

Mori E,

WPI; 2003-120790/11. N-PSDB; ABZ59698.

17-MAY-2002; 2002WO-JP004816

WO200294880-A1.

28-NOV-2002

ABO04856 standard; protein; 157 AA

RESULT 14

ò 셤 (first entry)

12-AUG-2003

ABO04856;

inflammation; lung; cancer.

US2002173629-A1

21-NOV-2002

Homo sapiens

56.78;

83.3%;

Query Match
Best Local Similarity 83.3
Matches 10; Conservative

present invention Sequence 145 AA;

ö

Gaps

Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for preparing array. Disclosure; Page 15; 129pp; English

Sequence 18 AA;

Gaps Ä Query Match
Best Local Similarity 62.5%; Pred. No. 0.47;
Matches 10; Conservative 1; Mismatches 4; Indels

ठ g Search completed: April 21, 2004, 17:33:12 Job time : 66 secs

Sequence 1553, sp. Sequence 46, Appl

Sequence 67, Appl Sequence 2987, Appl Sequence 2987, Appl Sequence 1625, Appl Sequence 1625, Appl Sequence 2926, Appl Sequence 2926, Appl Sequence 2926, Appl Sequence 1458, Appl Sequence 2836, Appl Sequence 2836, Appl Sequence 2735, Appl Sequence 1735, Appl Sequence 1415, Appl Sequence 1259, Appl Sequence 1251, Appl

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Score 97; DB 14;
Pred. No. 3.3e-06;
; Mismatches 0;
2 US-10-289-418-1553

2 US-10-239-418-1553

US-10-29-187-693-67

US-09-187-693-67

US-09-187-693-67

US-09-187-693-67

US-09-187-693-67

US-09-880-748-1625

US-10-293-418-2987

US-10-293-418-2926

US-10-293-418-2926

US-10-293-418-2926

US-10-293-418-2926

US-10-293-418-2926

US-10-293-418-2926

US-10-293-418-1458

US-10-293-418-1458

US-10-293-418-1259

US-10-293-418-1259

US-09-880-748-1273

US-09-880-748-1273

US-09-880-748-1259

US-09-880-748-1259

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US-09-880-748-1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5-10-041-860-200
Sequence 200, Application US/10041860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFGYSYNYDYYYGMDV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GFGYSYNYDYYYGMDV 16
     CRGANISM: homo sapiens US-10-041-860-48
         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 200,
Sequence 237,
Sequence 38, A.
Sequence 203,
Sequence 240,
Sequence 19, A.
Sequence 19, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                  April 21, 2004, 17:37:29 ; Search time 48.2319 Seconds (without alignments) 91.715 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2
Sequence 2
Sequence 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: /cgm_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgm26/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
4: /cgm26/ptodata/2/pubpaa/US06_NBW_PUB_pep:*
4: /cgm26/ptodata/2/pubpaa/US06_NBW_PUB_pep:*
5: /cgm26/ptodata/2/pubpaa/US07_NBW_PUB_pep:*
6: /cgm26/ptodata/2/pubpaa/US07_NBW_PUB_pep:*
7/cgm26/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
8: /cgm26/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
9: /cgm26/ptodata/2/pubpaa/US08_PUBCOMB_pep:*
10: /cgm26/ptodata/2/pubpaa/US09B_PUBCOMB_pep:*
11: /cgm26/ptodata/2/pubpaa/US09B_PUBCOMB_pep:*
12: /cgm26/ptodata/2/pubpaa/US09B_PUBCOMB_pep:*
13: /cgm26/ptodata/2/pubpaa/US10B_PUBCOMB_pep:*
14: /cgm26/ptodata/2/pubpaa/US10B_PUBCOMB_pep:*
15: /cgm26/ptodata/2/pubpaa/US10B_PUBCOMB_pep:*
16: /cgm26/ptodata/2/pubpaa/US10B_PUBCOMB_pep:*
17: /cgm26/ptodata/2/pubpaa/US10B_PUBCOMB_pep:*
18: /cgm26/ptodata/2/pubpaa/US10B_PUBCOMB_pep:*
18: /cgm26/ptodata/2/pubpaa/US10B_PUBCOMB_pep:*
18: /cgm26/ptodata/2/pubpaa/US10B_PUBCOMB_pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-041-860-200

US-10-041-860-237

US-10-041-860-337

US-10-041-860-38

US-10-041-860-203

US-10-041-860-240

US-10-041-860-240

US-10-041-860-240

US-10-041-860-240

US-10-041-860-240

US-10-041-860-25

US-10-041-860-20

US-10-041-860-20
                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                 1133595 seqs, 276475211 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                            SEQ3
97
1 gfgysynydyyygmdv 16
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Maximum DB seq length: 2000000000
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Perfect score:
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Gaps

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Indels

Length 125;

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Gaps
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US-LU-GHISBOLS

Sequence 38, Application US/10041860

Publication No. US20030157109A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Feng, Xiao-Chi

APPLICANT: Feng, Xiao-Chi

APPLICANT: Feng, Xiao-Chi

APPLICANT: Feng, Xiao-Chi

APPLICANT: Reng, Xiao-Chi

APPLICANT: Reng, Xiao-Chi

APPLICANT: Reng, Xiao-Chi

APPLICANT: Bezabeh, Binyam

ITILE OF INVENTION: THEREOF

ITILE OF INVENTION: THEREOF

FILE REFERENCE: ABGENIX.051A

CURRENT PILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 38

LENGTH: 125

ITILE OF USANISH: CONSERVED

SEQ ID NO 38

US-10-041-860-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 125;
                                       APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadit
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ATTIEBDED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 377
LENGTH: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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85.6%; Score 83; DB 14;
Best Local Similarity 87.5%; Pred. No. 0.00029;
Matches 14; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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; Sequence 203, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
, APPLICANT: Yang, Xiao-Dong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 GSGYSYGYDYYYGMDV 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 16; Conservative
                          Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-372
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Best Local Similarity 100.0%; Score 97; DB 14; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 237, Application US/10041860
Sequence 237, Application US/10041860
Sublication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Reng, Xiao-Chi
APPLICANT: Rencine
APPLICANT: Reng, Xiao-Chi
APPLICANT: Mebar, Richard
APPLICANT: Mebar, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 237
LENGTH: 125
                                                                       APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Chen, Xiao
APPLICANT: Chen, Xiao
APPLICANT: Chen, Yangi Xiao
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: THEREOF
FILE REPRENCE: ABGRNIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ IN NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 200
LEBUTH 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0;
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Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 GFGYSYNYDYYYGMDV 114
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                       PUDLICAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
             No. US20030157109A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: homo sapiens
US-10-041-860-237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: homo sapiens
US-10-041-860-200
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US-10-041-860-237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INCORATION:

APPLICANT: MADDON, Paul J.
APPLICANT: DISON, William C.
APPLICANT: OLSON, William C.
APPLICANT: SCHELKE, No. US20040033229Albert
APPLICANT: SCHELKE, No. US20040033229Albert
APPLICANT: GRADNER, Jason
APPLICANT: MA, Dangshe
APPLICANT: MA, Dangshe
FILE REFERENCE: P00741-70005, US
FILE REPERENCE: P00741-70005, US
CURRENT APPLICATION NUMBER: US/10/395,894
CURRENT PILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 60/33944
PRIOR FILING DATE: 2002-10-23
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: US 60/362,747
PRIOR APPLICATION NUMBER: US 60.912,618
PRIOR PRING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 33
LUMPER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
APPLICANT: Bezabeh, Binyam TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES TITLE OF INVENTION: ATTEREOF FILE REFERENCE: ABGENIX.051A CURRENT APPLICATION NUMBER: US/10/041,860 CURRENT FILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377 SOFTWARE FastSEQ for Windows Version 4.0 SEQ ID NO 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 87.5%; Pred. No. 0.00029;
Matches 14; Conservative 0; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-041-860-25; Application US/10041860; Publication No. US20030157109A1; GENERAL INFORMATION: APPLICANT: Corvalan, Jose R.F.; APPLICANT: Feng, Xiao-Chi; APPLICANT: Yang, Xiao-Chi; APPLICANT: Yang, Xiao-Dong; APPLICANT: Chen, Francine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-395-894-19; Sequence 19, Application US/10395894; Publication No. US/0040033229A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 GSGYSYGYDYYYGMDV 114
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Best Local Similarity 73.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||::||:| |||||
118 GYNWNYEYHYYGMDV 132
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US-10-395-894-19
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: homo sapiens
US-10-041-860-343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Use R.F.
APPLICANT: Use Xiao-Chi
APPLICANT: Use Xiao-Chi
APPLICANT: Sensy Xiao-Chi
APPLICANT: Pensy Xiao-Chi
APPLICANT: Vang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Bezabeh, Binyam
APPLICANT: Sezabeh, Binyam
APPLICANT: Sezabeh, Binyam
APPLICANT: Sezabeh, Binyam
APPLICANT: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 240
SEQ ID NO 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

85.6%; Score 83; DB 14; Length 125;
Best Local Similarity 87.5%; Pred. No. 0.00029;
Matches 14; Conservative 0; Mismatches 2; Indels
                                             APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
ITILE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
ITILE OF INVENTION: THEREOF
FILE REPERENCE: ABGENIX.031A
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 203
LENGTH: 125
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US-10-041-860-343
Sequence 343, Application US/10041860
Sequence 343, Application US/10041860
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yang, Xiao
APPLICANT: Yang, Xiao
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Repair APPLICANT: Repair APPLICANT: Repair APPLICANT: Repair APPLICANT: Repair APPLICANT: Repair APPLICANT: Reper APPLICANT: Repe
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US-10-041-860-240
US-10-041-860-240
Sequence 240, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 GSGYSYGYDYYYGMDV 114
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CRGANISM: homo sapiens
US-10-041-860-240
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CORGANISM: homo sapiens
US-10-041-860-203
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Gaps
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Query March 61.3%; Score 59.5; DB 14; Length 126; Best Local Similarity 80.0%; Pred. No. 0.54; Matches 12; Conservative 0; Mismatches 2; Indels 1

101 GYSYGYVYYDYGMDV 115

3 GYSYNYDYY-YGMDV 16

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; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES; TITLE OF INVENTION: THEREOF; PILE REFERENCE: ABGENTX.051A; CURRENT APPLICATION NUMBER: US/10/041,860; CURRENT FILING DATE: 2002-01-07; NUMBER OF SEQ ID NOS: 377; SOFTMARE: PRESESQ for Windows Version 4.0; SEQ ID NO 246; LENGTH: 126; TYPE: PRT

1 CARGANISM: homo mapiens
1 CARGANISM: homo mapiens
1 CAS-10-041-860-246
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61.3%; Score 59.5; DB 14; Length 126;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 12; Conservative 0; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-10-041-860-210
US-10-041-860-210
Sequence 210, Application US/10041860
FUBLication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Gracine
APPLICANT: Pang, Xiao-Chi
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Reber, Richard
APPLICANT: Bezabeh, Binyam
TILLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 210
LENGTH: 126
              APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Blnyam
ITILE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
ITILE OF INVENTION: THEREOF
ITILE OF INVENTION: THEREOF
ITILE OF INVENTION WHERE: US/10/041,860
CURRENT APPLICATION WHERE: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER: OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 126
ITILE OF MANAGER IN ANTIBODIES
ITILE OF US ARGANISM: homo sapiens
US-10-041-860-25
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| Publication No. US20030157109A1
| Publication No. US20030157109A1
| APPLICANT: Corvalan, Jose R.F.
| APPLICANT: Tola, Xiao-Chi
| APPLICANT: Yang, Xiao-Dong
| APPLICANT: Pang, Xiao-Dong
| APPLICANT: Read: Reading APPLICANT: Reading APPLICANT: Reading APPLICANT: Reading APPLICANT: Reading APPLICANT: Bezabeh, Binyam
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CRGANISM: homo sapiens
US-10-041-860-210
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US-10-041-860-246
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RESULT 14
US-09-808-0769, Application US/0980748
; Sequence 2769, Application US/0980748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REPREENCE: FPS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT PILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 61.3%; Score 59.5; DB 14; Length 126; Best Local Similarity 80.0%; Pred. No. 0.54; Matches 12; Conservative 0; Mismatches 2; Indels 1;
                                                                                                                                          GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: React, Gadi
APPLICANT: Rebach, Binyam
TITLE OF INVENTION: ANTHEODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTHEODIES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ANTHEODIES
TITLE OF INVENTION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SEQ ID NOS: 377

SEQ ID NOS: 377

SEQ ID NOS: 377

TOWNERS: FastSEQ for Windows Version 4.0
                                                ; Sequence 306, Application US/10041860; Publication No. US20030157109A1; GENERAL INFORMATION:
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TYPE: PRT
CRGANISM: homo sapiens
US-10-041-860-306
RESULT 13
US-10-041-860-306
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US-10-293-418-2769
i Sequence 2769, Application US/10293418
i Sequence 2769, Application US/10293418
i Publication No. US2003022396A1
i GENERAL INFORMATION:
i APPLICANT: Ruben et al.
i TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
i TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
i CURRENT PRILICATION NUMBER: US/10/293,418
i CURRENT PRILICATION NUMBER: 60/331,469
i PRIOR APPLICATION NUMBER: 60/331,469
i PRIOR APPLICATION NUMBER: 60/40,817
i PRIOR FILING DATE: 2001-12-19
i PRIOR FILING DATE: 2001-62-15
i PRIOR FILING DATE: 2001-63-15
i PRIOR APPLICATION NUMBER: 60/276,248
i PRIOR FILING DATE: 2001-03-16
i PRIOR FILING DATE: 2000-06-16
i RUMBER OF SEQ ID NOS: 3247
i LENGTH: 21
i TATE OF THE APPLICATION NUMBER: 60/212,210
i LENGTH: 21
i TATE OF THE APPLICATION NUMBER: 60/212,210
i TAVER: DATE OF THE APPLICATION NUMBER: 60/212,210
i PRIOR FILING DATE: 2000-06-16
i LENGTH: 21
i LENGTH: 21
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S8.2%; Score 56.5; DB 10; Length 21;
Best Local Similarity 78.6%; Pred. No. 0.23;
Matches 11; Conservative 1; Mismatches 1; Indels 1
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S8.2%; Score 56.5; DB 12; Length 21;
Best Local Similarity 78.6%; Pred. No. 0.23;
Matches 11; Conservative 1; Mismatches 1; Indels 1
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2769
LENGTH: 21
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CORGANISM: Homo sapiens
US-10-293-418-2769
                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2769
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Search completed: April 21, 2004, 18:02:06 Job time : 49.2319 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 21, 2004, 17:25:48; Search time 8.11594 Seconds
(without alignments)
102.653 Million cell updates/sec

Title: Perfect score: 97 Sequence: 1 gfgysynydyyygmdv 16

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	homo sapie	Q16625 homo sapien	acine	Q17127 blaberus di	limu	homo sa	mus	028269 canis famil			-					Q56110 salmonella			P37489 bacillus su				_	4		7507 homo sapien			P11997 drosophila		erwinia a		0349 methanococc
	Deg	P547	S	022	덩	P8.	P0	90	8	8	23	8	P3	0	છ	8	Š	P7	8	Ξ,	8	8	28	18	04	E E	8	ô	8	2	P	Q.	23	ő
SUMMARIES	Α	ARSF HUMAN	OCLN HUMAN	PTK ACIJO	HEXA BLADI	CU7B_LIMPO	HV2I_HUMAN		OCLN CANFA			YC81 METJA	YKD0 YEAST	ROR HUMAN	NA95 HUMAN	VG74_HSVSA	OMS1_SALTI	YEDS ECOLI	DPOL_PYRSD	YYBO BACSU	YC06 KLEPN	BCC2_ACEXY	CU7A LIMPO	CU7C_LIMPO	HV1C_HUMAN	DERM BOVIN	DERM HUMAN	ADAS_DROME	NA95 MOUSE	LP1G_DROME			ייי	X034_METJA
					Н																													
	Length	!			733																	•												316
d		57.7	53.6	53.6	51.5	50.5	49.5	49.5	49.5	48.5	48.5	48.5	47.4	47.4	47.4	46.4	46.4	46.4	46.4	45.9	45.9	45.9	45.4	45.4	45.4	45.4	45.4	45.4	45.4	45.4	45.4	44.8	44.8	44.3
	Score	56	52	52	20	49	48	48	48	47	47	47	46	46	46	45	45	45	45	44.5	4.	•	44	44	44	44	44	44	44	44	44	43.5	m	
	Result No.	-	8	m	4	Ŋ	φ	7	80	0	10	11	12	13	14	15	16	17	8	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P32802 saccharomyc C958541 methanococc Q988541 methanococc Q90km9 homo sapien Q56828 xenorhabdus P10901 dictyosteli Q63014 ratuus norv P02640 gallus gall Q9kce0 bacillus ha P35183 saccharomyc Q9wx63 acetobacter P44112 heemophlus P83354 limulus pol
EM70 YEAST YB41_METJA METJA HUMAN OMPE_XENNE FUCO_DICDI FUCO_DICDI VILI_CHICK SLEB BACHD ASTI_YEAST ASTI_YEAST YA99 HAEIN C144_LIMPO
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664 306 306 306 886 826 1325 1325 130
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### ALIGNMENTS

RESULT 1 ARSF HUMAN ARSF HUMAN DID ARSF DT 10-0C DT 15-JUU DE ARSF OS OS ARSF OS O
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"Generation and initial analysis of more than 15,000 full-length human
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SEQUENCE FROM N.A.

TISSUB-Brain, and Lung;

MEDLINE-21388257; PubMed=12477932;

RIGHER-21388257; Runge G.B., Runge G.B., Hopkins R.P., Malek J.A., Gabavant T.L., Rulyk S.J., Rownerein M.J., Modin T.B., Peters G.J., Abramson R.D., Mullahy S.J., Boak S.A., McEwan P.N., McErnan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Amiting M., Madan A., Young A.C., Shevchenko Y., Bourfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Allakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Allakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Glimbord J., Schmutz J., Mers R.M., Gay L., Shailus D.E., Allatterfield Y.S.N., Kizywinski M.I., Skalska U., Smailus D.E., Allatterfield Y.S.N., Kizywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB=201on carcinoma;
MISSUB=201on carcinoma;
Ando-Akateuka Y., Satuchan, Hirase T., Kishi M., Sakakibara A.,
Itoh M., Yonemura S., Furuse M., Tsukita S.;
Interspecies diversity of the occludin sequence: cDNA cloning of human, mouse, dog, and rat-kangaroo homologues.";
J. Cell Biol. 133:43-47(1996).
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                      140 BY SIMILARITY.

51 N-LINKED (GLCNAC. ..) (POTENTIAL)

118 N-LINKED (GLCNAC. ..) (POTENTIAL)

3337 N-LINKED (GLCNAC. ..) (POTENTIAL)

66003 MW, 65B4B9BF3803A771 CRC64;
                                                                                                                                                                                   ;
0
                                             2-AMINO-3-OXOPROPIONIC ACID (BY SIMILARITY).
                                                                                                                                                      57.7%; Score 56; DB 1; Length 591; 72.7%; Pred. No. 0.85; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukasawa M., Toyota T., Yoshitsugu K., Yoshikawa T.;
"Genomic structure of occludin gene.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Liver;
van Itallie C.M., Fanning A.S., Anderson J.M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                               RESULT 2
OCLAN HUMAN STANDARD; PRT; 522 AA.
AC 016625; Q8N6K1;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-PRC-1998 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
                                   ARYLSULFATASE F.
                       POTENTIAL
        Glycoprotein; Signal
                                                                                                                                                                      Local Similarity 72.
                                                                                                                                                                                                                              |:| :||||||
156 YNYGFDYYYGM 166
                                                                                                                                                                                                              4 YSYNYDYYYGM 14
                       19
591
79
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                               591 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
        Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                Occludin.
                                                                         ACT_SITE
CARBOHYD
CARBOHYD
                                                                                                                  CARBOHYD
SEQUENCE
                                                                                                                                                            Query Match
                                              MOD RES
                                    CHAIN
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and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

- PUNCTION: May play a role in the formation and regulation of the tight junction (TJ) paracellular permeability barrier.

- SUBGINIT: Interacts with TJP1/ZO1 and with VAPA.

- SUBGINIT: Interacts with TJP1/ZO1 and with VAPA.

- TSUBINIT: Localized at tight junctions of both epithelial and endothelial cells. Highly expressed in kidney.

Not detected in testis.

- DOMAIN: The C-terminal is cytoplasmic and is important for interaction with ZO-1. Sufficient for the tight junction of the permeability barrier function of the tight junction (By similarity).

- PTM: Phosphorylated (By similarity).

- SIMILARITY: Belongs to the ELL / occludin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | InterPro; IPKUU425... | Pean, PRO1284; MRNUEL; I. | Pean, PRO1284; MRNUEL; I. | PRO1284; MRNUEL; I. | PRO1285; OCCUUDIN. | PROMAIN | 1 66 | CYTOPLAMIC (POTENTIAL). | PUMAIN | 90 | 135 | EXTRACELLULAR (POTENTIAL). | PT PRANSKEM | 136 | 160 | POTENTIAL). | PT PRANSKEM | 136 | 160 | POTENTIAL. | PT PRANSKEM | 137 | PT PRANSKEM | 137 | PT PRANSKEM | 137 | PT PRANSKEM | 138 | EXTRACELLULAR (POTENTIAL). | PT PRANSKEM | 171 | 195 | EXTRACELLULAR (POTENTIAL). | PT PRANSKEM | 136 | 243 | EXTRACELLULAR (POTENTIAL). | POMAIN | 196 | 243 | EXTRACELLULAR (POTENTIAL). | POMAIN | 196 | 243 | EXTRACELLULAR (POTENTIAL). | POMAIN | 196 | 243 | EXTRACELLULAR (POTENTIAL). | POMAIN | 196 | 243 | EXTRACELLULAR (POTENTIAL). | POMAIN | 196 | 243 | EXTRACELLULAR (POTENTIAL). | POMAIN | 265 | PT PANSKEM | PT PA
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Pred. No. 2.8;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> S (IN REF. 4).
A0CF9574BCF6E974 CRC64;
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COILED COIL (POTENTIAL).
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EMBL; AF400624; AAL47094.1; JOINED.
EMBL; AF400625; AAL47094.1; JOINED.
EMBL; AF400626; AAL47094.1; JOINED.
EMBL; AF400627; AAL47094.1; JOINED.
EMBL; AF400628; AAL47094.1; JOINED.
EMBL; AF400628; AAL47094.1; JOINED.
EMBL; BF400628; AAL47094.1; JOINED.
EMBL; AF400628; AAL47094.1; JOINED.
EMBL; BC02986; AAL47094.1; JOINED.
EMBL; AF400628; AAL47094.1; JOINED.
EMBL; AF400628; AAL47094.1; JOINED.
EMBL; AF400628; AAL47094.1; JOINED.
EMBL; GC2986; AAL47094.1; JOINED.
EMBL; GC2986; AAL47094.1; JOINED.
EMBL; GC2986; AAL47094.1; JOINED.
GO; GO; 0006461; P: Protein complex assembly; TAS.
InterPro; IPR002958; Occludin.
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EMBL; U53823; AAB00195.1; -.
EMBL; AF400630; AAL47094.1; -
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Best Local Similarity 61.5%;
Matches 8; Conservative
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522 AA;
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PTK ACIJO
ID PTK ACIJO
AC 052788;
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733 AA.

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                                                                                                                                                                                                                                                                                                                             TISSUEFEE FROM N.A.

TISSUEFEE body;

TISSUEFEE body;

TISSUEFEE body;

Submirz R.C., Beintema J.J., Stam W.T., Bradfield J.Y.;

Submirted (AUG-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Larval storage protein (LSP) which may serve as a st. of amino acids for synthesis of adult proteins (By similarity).

-!- SUBUNIT: Homohexamer (Potential).

-!- SUBCELLULAR LOCATION: Extracellular (By similarity).

-!- SUMILARITY; TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
                                                                                                                                                                       Hexamerin precursor.
Blaberus discoidalis (Tropical cockroach).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nicerpro; IPR008922; D1-copper_centre.
InterPro; IPR008926; Hemcyanin.
InterPro; IPR008033; hemcyanin.C.
InterPro; IPR005204; hemcyanin.C.
InterPro; IPR005204; hemcyanin.C.
InterPro; IPR007110; IG-11ke.
Pfan; PF03722; hemcyanin.C; 1.
Pfan; PF03722; hemcyanin.C; 1.
Pfan; PF03722; hemccyanin.C; 1.
PRNNTS; PR00187; HAEMCYANIN.1; PALSE NEG.
PROSITE; PS00210; HEMCCYANIN.1; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; Storage protein; Glycoprotein. SIGNAL 17 POTENTIAL.
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                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 199 N-
234 234 N-
431 431 N-
733 AA; 87813 MW;
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                                                            STANDARD;
                                                                                                                                                                                                                                                                      Blaberidae; Blaberus.
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                                                                                                                                                                                                                                                                                         NCBI TaxID=6981;
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ID HEXA BLADI
AC Q17127;
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P83360;
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CUTB LIMPO
AC P83360,
DT 28-FEB-
DT 10-OCT-
DE CULICIE
OC EURALYO
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Doublet P., Vincent C., Grangeasse C., Cozzone A.J., Duclos B.;
Doublet P., Vincent C., Grangeasse C., Cozzone A.J., Duclos B.;
Doublet P., Vincent C., Grangeasse C., Cozzone A.J., Duclos B.;
Doublet P., Vincent C., Grangeasse C., Cozzone A.J., Duclos B.;
Doublet P., Vincent C., Grangeasse C., Cozzone A.J., Duclos B.;
FEBS Lett. 445:137-143(1999).
-!- FUNCTION: May be involved in the production and the transport of exopolysaccharides in the production and the transport of tyrosine phosphate.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
-!- PATHWAY: Exopolysaccharide biosynchesis.
-!- PATHWAY: Exopolysaccharide biosynchesis.
-!- FATHWAY: Autophosphorylated on several Tyr residues. Dephosphorylated
                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDINE=9804241; PubMed=9434192;
Grangesse C., Doublet P., Vaganay E., Vincent C., Deleage G.,
Duclos B., Cozzone A.J.;
"Characterization of a bacterial gene encoding an autophosphorylating
protein tyrosine kinase.";
Gene 204:259-265(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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ATP (POTENTIAL).
K->M: NO LOSS OF AUTOPHOSPHORYLATION.
K->M: LOSS OF AUTOPHOSPHORYLATION.
S->C: LOSS OF AUTOPHOSPHORYLATION.
D->N: LOSS OF AUTOPHOSPHORYLATION.
                                                                                                                    Bacteria; Protéobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaces; Acinetobacter.
NCBI_TaxID=40214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.J.;
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Exopolysaccharide synthesis; Transmembrane; Inner membrane;
ATP-binding; Magnesium; Manganese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.6%; Score 52; DB 1; Length 733; 66.7%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96266486; PubMed=8683591;
Duclos B., Grangeasse C., Vaganay E., Riberty M., Cozzone Pautophosphorylation of a bacterial protein at tyrosine.";
J. Mol. Biol. 259:891-895(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82362 MW; EF3148A2AFF7B954 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGENESIS OF LYS-436; LYS-549; SER-550 AND ASP-651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by ptp.
SIMILARITY: BELONGS TO THE ETK/WZC FAMILY.
                   28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Tyrosine-protein kinase ptk (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PhosSite; 052788; -.
Interpro; IPR003856; LPS_Wzz_MPA.
(Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y15162; CAA75431.1; -.
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Matches 8; Conservative
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                                                                                                        Acinetobacter johnsonii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02706; wzz; 1.
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542
436
549
550
550
733 AA;
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28-FEB-2003
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TRANSMEM
NP BIND
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SEQUENCE
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Cuticle protein 7 lsoform b (LDCP7b).
Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota, Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                  ô
                                                                                                                                      51.5%; Score 50; DB 1; Length 733; 53.3%; Pred. No. 7.6; 4; Indels iive 3; Mismatches 4; Indels
                                                                                   083DF739DD665729 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 AA
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715 GYĞYĞYNYAYAY 726

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Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rakawa T., Hara A., Phukunishi Y., Komo H., Adachi J., Fukuda S., Ra Azawa T., Hara A., Phukunishi Y., Komo H., Adachi J., Fukuda S., Ra Aizawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Ra Kadota K., Matsuda H., Radio B., Kochiwa H., Rabell P., Lawis S., Matsuo Y., Nikaido I., Reole G., Quackenbush J., Rabell P., Lawis S., Matsuo Y., Nikaido I., Wagner I., Washio T., Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G., Rasai M., J., Bult C., Pletcher C., Pujita M., Gariboldi M., A Brownstein M.J., Bult C., Pletcher C., Pujita M., Gariboldi M., A Guetincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Reya T., Sakamoto N., A Wasaki H., Sato K., Schoebbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Havashi Zaki V.
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X MEDLINE=238857; Pubmed=12477932;

REDLINE=238857; Pubmed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Teingold E.A., Grouse L.H., Derge J.G.,

A Altechul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Blat N.K.,

A Altechul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Eammer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Casavant T.L., Scheetz T.E.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzardne P.H.,

A Richards S., Morley K.C., Hale S., Garcial A.M., Gabbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                     RALY MOUSE STANDARD; PRT; 312 AA.
064012; 099K76; 09CXH8; 09QXX6;
28-FEB-2003 (Rel. 41, Created)
10-CCT-2003 (Rel. 42, Last annotation update)
110-CCT-2003 (Rel. 41, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
MEDLINE=93307655; PubMed=8319910;
Michaud E.J., Bultman S.J., Stubbs L.J., Woychik R.P.;
Michaud E.J., Bultman S.J., Stubbs L.J., Woychik R.P.;
"The embryonic lethality of homozygous lethal yellow mice (Ay/Ay) is associated with the disruption of a novel RNA-binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94326666; PubMed=805375;
Duhl D.M., Stevens M.E., Vrieling H., Saxon P.J., Miller M.W.,
Epstein C.J., Barsh G.S.;
"Pleiotropic effects of the mouse lethal yellow (Ay) mutation
explained by deletion of a maternally expressed gene and the
simultaneous production of a gouti fusion RNAs.";
Development 120:1695-1708(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=CS7BL/6J; TISSUE=Embryonic head;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes Dev. 7:1203-1213(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                           MEDLINE=2215710; PubMed=12628379;
MEDLINE=2215710; PubMed=12628379;
Ditzel N., Andersen S.O., Hoejrup P.;
Ditzel N., Andersen S.O., Hoejrup P.;
Cuticular proteins from the horseshoe crab, Limulus polyphemus.";
Comp. Biochem. Physiol. 1348:489-497(2003).
-!- RASS SPECTROMETRY: MW=6970; METHOD=MALDI.
-!- SIMLIARITY: Contains 1 cuticle consensus domain.
InterPro; IPR006618; Insect cuticle.
PROSITE; PS00233; CUTICLE; FALSE NEG.
BCTUCTURI protein; Cuticle; PARSONIOSE Carboxylic acid.
MOD RES 1
SECTION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN'1988 (Rel. 06, Created)
01-JAN'1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 38, Last amonotation update)
16-JUL-1999 (Rel. 38, Last amonotation update)
17 homo sapiens (Human).
18 heavy cha, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V-II REGION ARH-77. V SEGMENT. D SEGMENT. J SEGMENT. BY SIMILARITY.
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                                                                                                                      SEQUENCE, MASS SPECTROMETRY, AND PYRROLIDONE CARBOXYLIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.5%; Score 49; DB 1; Length 59;
llarity 61.5%; Pred. No. 0.86;
Conservative 1; Mismatches 4; Indels
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SMART; SM0406; IGV; 1. PR051TE; PS50835; IG LIKE; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GFGYSYNYDYYYG 13
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146 1
146 AA;
Limulidae, Limulus.
NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                   rissue=carapace
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ID HV2I HUMAN
AC P06331;
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SEQUENCE
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RESULT 6

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Query Match

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DOMAIN SIGNAL

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                                                                                                                                                                                                                                                                                                                                                                Name=1;
Incled=064012-2; Sequence=VSP 005805;
-: TISSUE SPECIFICITY: Widely expressed in liver.

Jung, spleen and kidney. Weakly expressed in liver.

-: DEVELOPMENTAL STAGE: Expressed in the unfertilized egg, in the blastocyst, as well as in the developing embryo and fetus.

Expressed in developing skin.

-: DISBASE: Defects in RALY are the cause of lethal yellow mutation homoxygous, and pleiotropic effects when heteroxygous, including yellow pelage, obesity, non-insulin dependent diabetes and increased tumor susceptibility. A(y) is due to a 170 kb deletion that removes all but the promoter and non-coding first exon of RALY and links them to the ASIP/Agouti gene.

-: SIMILARITY: Contains 1 RNA recognition motif (RRW) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50102; RRM, 1.
PROSITE; PS00030; RRM_RNP 1; 1.
Ribonucleoprotein; RNA-binding; Nuclear protein; Alternative splicing.
                                                                                                                                    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schlein J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA-BINDING (RRM).
Missing (in isoform 1).
/FTIG=YSP 005805.
G -> S (IN REF 1).
T -> I (IN REF 1).
W, BF6BE0E8876BFCS0 CRC64;
                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                       Name=2;
IsoId=Q64012-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S72641; AAC60688.1; -.
EMBL; L17076; -; NOT ANNOTATED_CDS.
EMBL; AK014256; BAL29294.1; -.
EMBL; BC016587; AAH04851.1; -.
EMBL; BC16587; AAH16587.1; -.
EMBL; AF148458; AAF04488.1; -.
INTERPO; IFR000564; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
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281 21
312 AA;
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VARSPLIC
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97327764; PubMed=9182670; Sakakibara A., Furuse M., Saitou M., Ando-Akatsuka Y., Tsukita S.,; Sakakibara A., Furuse M., Saitou M., Ando-Akatsuka Y., Tsukita S.,; Sakakibara A., Furuse M., Saitou M., Ando-Akatsuka Y., Tsukita S.,; J. Call Biol. 137:1393-1401(1997).

-!- FUNCTION: May play a role in the formation and regulation of the tight junction (TU) paracellular permeability barrier. Interacts with Zo-1.

-!- SUBUNIT: Interacts with VAPA (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBCELLUIAR LOCATION: Integral membrane protein.
-:- SUBCELLUIAR LOCATION: Integral membrane protein.
-:- TISSUE SPECIFICTIY: Localized at tight junctions of both epithelial and emochelial cells.
-:- DOMAIN: The C-terminal is cytoplasmic and is important for interaction with ZO-1. Necessary for the tight junction localization. Involved in the regulation of the permeability barrier function of the tight junction (By similarity).
-:- PTM: PHOSPHORYLAYED. LESS PHOSPHORYLATED FORMS ARE FOUND IN BASCHATERAL MEMBRANE, CYTOSOL AND TIGHT UNCTION. MORE HEAVILY PHOSPHORYLATED FORMS ARE CONCENTRATED EXCLUSIVELY IN TIGHT
                                                                                                                                                                                                                                                                    TISSUE=Kidney;
MINDLIMES-65181088; PubMed=8601611;
Ando-Akateuka Y., Saltou M., Hirase T., Kishi M., Sakakibara A.,
Itoh M., Yonemura S., Furuse M., Tsukita S.;
"Interspecies diversity of the occludin sequence: cDNA cloning of human, mouse, dog, and rat-kangaroo homologues:";
J. Cell Biol. 133:43-47(1996).
                                                                                                                                                           Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               junction; Transmembrane; Coiled coil; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                              LS-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                 521 AA.
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InterPro; IPRO08253; Marvel..
InterPro; IPRO08258; Occludin.
Pfam; PF01284; MARVEL; 1.
PRINTS; PR01258; OCCLUDIN.
                                 STANDARD;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                  NCBI_TaxID=9615;
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                   OCLIN CANFA
ID OCLIN CANFA
AC Q28269;
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Score 48; DB 1; Length 312; Pred. No. 6.3; 2; Mismatches 0; Indels

49.5%;

Query Match Best Local S

Matches

Similarity 77.8 7; Conservative

GYSYNYDYY 11 |||::|||| GYSPDYDYY 119

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CYTOPLASMIC (POTENTIAL)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i-SUBCELLULAR LOCATION: Integral membrane protein.
-i-SUBCELLULAR LOCATION: Integral membrane protein.
-i-TISSUB SPECIFICITY: Localized at tight junctions of both epithelial and endothelial cells. Highly expressed in lung and liver. Expressed at a lower level in brain.
-i-DOMAIN: The C-terminal is cytoplasmic and is important for interaction with ZO-1. Necessary for the tight junction interaction with ZO-1. Necessary for the tight junction of calization. Involved in the regulation of the permeability barrier function of the tight junction. The second extracellular domain may also be implicated in the permeability barrier function of the tight junction.
-i-PTM: Phosphorylated (By similarity).
-i-SIMILARITY: Belongs to the ELL / occludin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSCOEEmbryonic brain,
MEDINIE-94103332; PubMed-8276896;
Furuse M., Hirase T., Itoh M., Nagafuchi A., Yonemura S., Tsukita S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      junctions.";
J. Cell Biol. 123:1777-1788(1993).
-!- FUNCTION: May play a role in the formation and regulation of the tight junction (TJ) paracellular permeability barrier. Interacts with ZO-1.
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Occludin: a novel integral membrane protein localizing at tight
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CYTOPLASMIC (POTENTIAL).

TRANSMEM 58 80 POTENTIAL.
                                       Score 48; DB 1; Length 521;
Pred. No. 10;
                                                                                        4; Indels
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EXTRACELLULAR (POTENTIAL)
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POTENTIAL.
  521 AA; 59275 MW; 2875E59F8F0A1FFA CRC64;
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CYTOPLASMIC (POTENTIAL)
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15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                       504 AA.
                                                                                      2; Mismatches
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InterPro; IPR00825; Marvel.
InterPro; IPR002958; Occludin.
Pfam; PF01284; MAKVEL; 1.
PRINTS; PR01258; OCCLUDIN.
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                                              53.8%;
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                           1 GFGYSYNYDYYYG 13
                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                       CHICK
      SQ SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
(Ferric reductase transmembrane component 4 precursor (EC 1.16.1.7)
FRE4 OR YNROGOW OR N3518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                 Score 47; DB 1; Length 504;
pred. No. 14;
0; Mismatches 5; Indels
                                                                  COILED COIL (POTENTIAL).
AD0352A45A0231FF CRC64;
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               YR/GLY-RICH.
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                                                 POLY-ARG
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55863 MW;
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                                                                                                                                                           8; Conservative
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127
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119
351
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Best Local Similarity
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363
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504 AA;
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P53746;
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-!- FUNCTION: Component of ribonucleosomes, which are complexes of at least 20 other different heterogenious nuclear ribonucleoproteins (hnRWP). hnRNP play an important role in processing of precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94262309; PubMed=8203146; Purnelle B., Skala J., van Dyck L., Goffeau A.; Purnelle B., Skala J., van Dyck L., Goffeau A.; Annalysis of an 11.7 kb DNA fragment of chromosome XI reveals a new "Annalysis of an 11.7 kb DNA fragment of chromosome XI reveals a new LRNA gene and four new open reading frames including a leucine zipper protein and a homologue to the yeast mitochondrial regulator ABF2.";
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Eukaryota; Metazoma: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NUV-1995 (Rel. 32, Last annotation update)
Hypothetical 23.0 kDa protein in IXRI-TFAl intergenic region.
YKLOSOW OR YKL243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 1; Length 201;
Pred. No. 7.8;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                    Rieger M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
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201 Aa; 22956 MW; AF7B9798DFA88459 CRC64;
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16-0CT-2001 (Rel. 40, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
Heterogeneous nuclear ribonucleoprotein R (hnRNP R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    633 AA.
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PIR, S37847; S37847
Germonline; 139786; -.
SGD; S0001513; YKL030W.
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ilarity 72.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-180 FROM N.A.
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tes 8; Conserv
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043390;
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STRAIN=JAL-1 / DSW 2661 / ATCC 43067;
STRAIN=JAL-1 / DSW 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8680897, Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gorare J.D.,
Scrlwage A.R., Dougherty B.A., Tomb U.F., Medms M.D., Reich C.I.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 29;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                              Score 47; DB 1; Length 719;
Pred. No. 20;
3; Mismatches 1; Indels
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DOMAIN 598 601 POLY-GLU.

SEQUENCE 1048 AA; 121014 MW; 14138CFDCE6A8A76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                              9CA91F1F890AF1F9 CRC64;
                                                                      (GLCNAC. (GLCNAC. (GLCNAC.
                                                                                                                                                                                    (GLCNAC
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                                            N-LINKED
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                                                                                                                               671 671 N-
675 675 N-
696 696 N-
719 AA; 82015 MW;
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10-0CT-2003 (Rel. 42, Last seq
10-0CT-2003 (Rel. 42, Last ann
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147 YGYYYNHDIPYYFG 160
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YKDO_YEAST
ID _YKDO_YEAST
AC _P36099;
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Q58677;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=2238827; PubMed=12477932;
MEDLINE=2238827; PubMed=12477932;
A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
Altachul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
Altachul S.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M.S., Garmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshhyuki S., Carninoi P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.M.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Rohalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A pilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Bakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Redriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,
B Huterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Henry L., Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anchoring protein 95 (AKAP95) on chromosome 19p13.11-p13.12 region."; J. Hum. Genet. 45:31-37(2000).
                                                                                                                                                                                                                                                                                                                                         TISSUE Placents, and T-cell lymphoma;
MEDLINE=20347256; PubMed=10748171;
Westberg C., Yang J.-P., Tang H., Reddy T.R., Wong-Staal F.;
Westberg C., Yang J.-P., Tang H., Reddy T.R., Wong-Staal F.;
"A novel shuttle protein binds to RNA helicase A and activates the retroviral constitutive transport element.";
J. Biol. Chem. 275:21396-21401(2000).
                                                                       SECUENCE FROM N.A.
MEDLINE=2022332; PubMed=10761695;
Orstavik S., Eide T., Collas P., Han I.O., Tasken K., Kieff E.,
Orstavik S., Eide T., Collas P., Han I.O., Tasken K., Kieff E.,
Jahnsen T., Skalhegg B.S.;
"Identification, cloning and characterization of a novel nuclear
protein, HASS, homologous to A-kinase anchoring protein 95.";
Biol. Cell 92:27-37(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB025905; BAA85003.1; -.
EMBL; AJ243467; CAB65092.1; -.
EMBL; AF19444; AAF86648.1; -.
EMBL; BC000713.3 AAH00713.1; -.
EMBL; AB015332; BAA34791.1; ALT_INIT.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0017151; F:DEAD/H-box RNA helicase binding; TAS.
InterPro; IPR007071; AKAR95.
InterPro; IPR007071; ZAI_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-358 FROM N.A., AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Placenta;
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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TISSUE=Fetal brain;
TISSUE=Fetal brain;
MEDLINE=20163068; Pubmed=10697960;
Seki N., Ueki N., Yano K., Saito T., Masuho Y., Muramatsu M.-A.;
"CDNA cloning of a novel human gene NAKAP95, neighbor of A-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo appiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 607201; -. 607201; -. 607201; -. 607201; -. 607201; -. 607.00056436; Fiheterogeneous nuclear ribonucleoprotein; TAS. GO; GO:0008436; F:RNA binding; TAS. GO; GO:0005723; F:RNA binding; TAS. InterPro; IPR006535; H:RNA processing; TAS. InterPro; IPR006504; H:RNA_rec_mot. From 3. From; 3. 
                     mRNA in the nucleus.
-!- SUBCELLULAR LOCATION: Nuclear; nucleoplasm.
-!- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.4%; Score 46; DB 1; Length 633; llarity 57.1%; Pred. No. 25; Conservative 1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                               EMBL; AP000364; AAC39540.1; -. PIR; T02673; T02673. HSSP; PO9651; 1HA1. Genew; POGC5047; HNRPR. GK; 043390; -. MIM; 667201; -.
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Best Local Similarity
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S -> N (IN REF. 3).

ALTODEN -> EFSWGAMC (IN REF. 4).

ALTODEN -> EFSWGAMC (IN REF. 4).

EEKEQEEAEGGALDEGAGGBAAGISEGAEGVPAQPPVPPE
PA -> RRRASRRALDAVPWIRGRRAKRQGFRRAGRAGRES
LDCDGQP (IN REF. 3).

EEEEGAVPLLGGALQAQIRGIPGIDVEDDEE -> GGGGGR
RGPCWEGRCNARSAAGRASTWRITRKK (IN REF. 3).

MW; CBCZ65BFZ5996BAZ CRC64;
                                         NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: MAY BE HIGHLY RELEVANT TO THE PROCESS OF CELLULAR TRANSFORMATION AND RAPID T-CELL PROLIFERATION EFFECTED BY HVS DURING LATERT INFECTIONS OF T-CELLS IN SUSCEPTIBLE HOSTS.
-!- SUBGELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=92333689; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=92230.225; PubMed=1314457;
MEDLINE=92230.225; PubMed=1314457;
Micholas J., Cameron K.R., Coleman H., Newman C., Honees R.W.;
"Analysis of nucleotide sequence of the rightmost 43 kbp of
"herpesvirus saminti (HVS) L-DNN: general conservation of genetic
organization between HVS and Epstein-Barr virus.";
Virology 188:296-310(1992).
                                                                                                                                                                                                                                                                                                                                                     9
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Nicholas J., Cameron K.R., Honess R.W.;
"Herpesvirus saimiri encodes homologues of G protein-coupled
                                                                                                                                                                                                                                                                                                                   Query Match

47.4%; Score 46; DB 1; Length 646;
Best Local Similarity 45.0%; Pred. No. 25;
Matches 9; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
NCBI_TaxID=10383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
04-protein coupled receptor homolog ECRF3.
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                                                                                                 TYR/GLY-RICH.
PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                             44 GYGYGYGYGDDNTTNYGYGM 63
                                                                                                                                                                                                                                                                                       71640 MW;
             SMART; SM00355; ZnF_C2H2; 1.
Nuclear protein; Zinc-finger.
Pfam; PF04988; AKAP95; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptors and cyclins.";
Nature 355:362-365(1992)
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507
100
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188
358
596
596
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489
1484
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VG74_HSVSA
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).

N.LINKED (GLCNAC...) (POTENTIAL)

N.LINKED (GLCNAC...) (POTENTIAL)

N-LINKED (GLCNAC...) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.4%; Score 45; DB 1; Length 321; 75.0%; Pred. No. 17; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                               InterProj irknow.c., ...
Pfam, PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN RECEP F1 1; FALSE_NEG.
PROSITE; PS00262; G_PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
34 EXTRACELLUMR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LINKED (GLCNAC. . .) (PC 9C4F4C760B962003 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          r (FOIENTIAL);
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC
                                                                                                                                                                                                                                                                                                       MBL; M86409; AAA46150.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37132 MW;
                                                                                                                                                                                                                                       EMBL; S76368; AAB21117.1; -. EMBL; X64346; CAA45697.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 YSYNY--DYYYG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 YSYNYSGDIYYG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
117
321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                              EMBL; M86409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
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Search completed: April 21, 2004, 17:33:58 Job time : 9.11594 Becs

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April 21, 2004, 17:26:23; Search time 42.6667 Seconds (without alignments) 118.319 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                      1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                           1017041 segs, 315518202 residues
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                      1 gfgysynydyyygmdv 16
                                                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                 Scoring table:
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sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\*
sp\_ntanelle:\*
sp\_phage:\*
sp\_plant:\*
sp\_plant:\*
sp\_plant:\* sp\_unclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\* vertebrate:\* SPTREMBL 25:\* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_archeap:\*

SUMMARIES

	Description	Q9a419 caulobacter	Q8tcc5 homo sapien	Q07834 saccharomyc	Q86el6 schistosoma	Q8abp9 bacteroides	Q8ie65 plasmodium	Q9rmd9 acinetobact	Q8s1t9 oryza sativ	Q8i1q8 plasmodium	Q8u3d2 pyrococcus	Q8ree7 fusobacteri	Q8sct5 pseudomonas	Q97gn9 clostridium	Q8ilk7 plasmodium	Q8cgb8 mus musculu	Q9n0w3 canis famil
OCE PROPERTY OF	ID	Q9A419	Q8TCC5	Q07834	Q86EL6	Q8ABP9	QBIE65	Q9RMD9	Q8S1T9	Q811Q8	Q8U3D2	Q8REE7	QBSCTS	6N9160	Q81LK7	Q8CGB8	CONOM3
	DB	16	4	ო	Ŋ	16	ഹ	~	2	Ŋ	17	16	თ	16	'n	11	9
	Query Match Length DB	205	590	825	152	779	3519	726	386	753	770	1089	171	1044	1781	360	260
o)e	Query Match	59.8	57.7	56.7	53.6	53.6	53.6	52.6	51.5	51.5	51.5	51.5	51.0	50.5	50.5	49.5	49.5
	Score	80.50	26	22	25	52	52	51	50	50	20	20	49.5	4,	4.	48	48
	Result No.	-	7	٣	4	ហ	y	7	σ	σ'n	10	11	12	13	14	15	16

Q802x5 brachydanio Q8cby3 mus musculu Q96pv6 homo sapien Q81z27 homo sapien Q8as51 bacteroides Q81in6 plasmodium	Q8iei2 plasmodium Q9p154 chlamydia m Q9kcw8 bacillus ha Q8c3p0 mus musculu Q9vc22 drosomila	Q67663 garlic late 097275 plasmodium Q8tp77 methanosarc Q822e5 chlamydophi O8xwf5 raletonia s		taenia cia taenia sol taenia sol taenia sol taenia sol taenia sol
Q802X5 Q8CBY3 Q96PV6 Q8IZ27 Q8AA51	Q81E12 Q9PL54 Q9KCW8 Q8C3P0	067663 097275 087277 0822E5	QBYAZO Q9AAZO Q7Z334 Q8BL32 Q9BOU1	Q955826 Q955826 Q95582 Q95582 Q95582 Q95582
e 4	2 2 2 2 2 2	0 100	45 000	
785 785 795 800 812	105 105 105 126	1 8 1 8 1 8 1 8 1 8 1 8 1 8 1 8 1 8 1 8	132 243 307 483	
4 4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		444444 088777 00044	44444	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
4 4 4 4 4 4 4 6 8 8 8 8 8 8 8 8	24.74 74.75 74.74	4 4 4 4 7 7 7 8 8 8 8	. 4 4 4 4 4. 0 0 0 0 0 0 0	4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6
11 19 20 21 21	7 7 7 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	, u u u u u u i u u u u u u	₩ ₩ � � � � � � � � B & O H Z W � Z

## ALIGNMENTS

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Gaps
                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                  / Match
Local Similarity 58.8%; Pred. No. 1.3;
les 10; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                             Hypothetical protein; Complete proteome.
SEQUENCE 205 AA; 22665 MW; C03B0E4FC08908E8 CRC64;
                             0.1-UN-2001 (TrEMBLrel. 17, Created)
01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CC3024.
CC3024.
Callobacter crescentus.
                205 A.A.
                PRT;
                PRELIMINARY;
                                                                                                                                                                                                                                                                      Query Match
                Q9A419
                                                                                                                                                                                                                                                                               Best Loc
Matches
RESULT 1
        09A419
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|:|| |:||| |||| 165 GYGYGYDYDYAPRPYYG 181 1 GFGYSYNYDY----YYG 13

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1 GFGYSYNYDYYY 12

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149; Lipoprotein_6; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 YSYNYDYYYGMDV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD001
Kinase; Compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8ABP9
Q8ABP9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
Q8ABP9
                                                                                                    RESULT 4

Q8 6EL6

R6 6

D1 01-0

D1 01-0

D1 01-0

D2 01-0

D2 01-0

D3 02-0

D4 02-0

D5 02-0

D6 02-0

D7 01-0

D7 01-0

D7 01-0

D8 02-0

D8 02
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Duesterhoeft A., Floeth M., Heuss-Neitzel D., Hilbert H., Moestl D.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56; DB 4; Length 590;
Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 KH DOMAIN.
EMBL; 27313; CAA97481.1; -.
SCH 781, 264783; CAA97483.
SCD; SO003955; YLL032C.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR004087; KH dom.
Pfam; PF00013; KH; 1.
SWART; SM00222; KH; 1.
SWART; SM00222; KH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Straubberg N.;
Straubberg N.;
Straubberg N.;
Straubberg N.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, 3919, AAH22389.1;
GO; GO:0003152; P:metabolism; IEA.
GO; GO:0003152; P:metabolism; IEA.
InterPro; IPR000917; Sulfatase.
PROSITE; PS00164; Sulfatase.
PROSITE; PS00164; Sulfatase.
PROSITE; PS00164; Sulfatase.
BYCOTHE; PS00164; Sulfatase.
SPROSITE; PS00164; Sulfatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      007834;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chromosome XII reading frame ORF YLL032C.
                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   825 AA.
                                                                                   590 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.7°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| :||||||
155 YNYGFDYYYGM 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                       Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Kidney;
RESULT 2
08TCC5
AC 08TCC5;
DT 01-JUN-2
DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            007834
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EMBL; AE016926; C.external outer membrane (sensu Gram-negativ. . .; IEA. GO; GO:000379; C.external outer membrane (sensu Gram-negativ. . .; IEA. GO; GO:000379; F:defense/immunity protein activity; IEA. GO; GO:0016952; P:defense response; IEA. GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA. InterPro; IPR001800; Lipoprotein_6.

InterPro; IPR001800; Lipoprotein_6.

InterPro; IPR001805; LPS_Wzz_MPA.
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STRAILS-PIT-5482 / ATCC 29148;
MEDLINE-2255088: PubMed-12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
Agnomic view of the human-Bacteroides thetalotaomicron symbiosis.";
Science 299:2074-2026(2003).
Q86EL6 PRELIMINARY; PRT; 152 AA.
Q86EL6;
Q86EL6;
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Clone ZZD208 mRNA sequence.
Schistosoma japonicum (Blood fluke).
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Liu F., Hu W., Yan Q., Xu X., Zhu Z., Zhang X., Wang J., Sun J.,

Ku X., Wang Z., Zeng L., Rong Y., Wu X., Qu J., Xu Z., Huang J.,

Ma Y., Wang S., Wang Z., Xue C., Feng Z., Chen Z., Han Z.;

"The full-length cDNA of S. japonicum genes.";

"The full-length cDNA of S. japonicum genes.";

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY223200; AAp6221.1;

ERBL, AX232200; AAP6221.1;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Becteroidaceae; Bacteroides.
NCBI_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.6%; Score 52; DB 16; Length 779; Best Local Similarity 61.5%; Pred. No. 39; Matches 8; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52; DB 5; Length 152;
Pred. No. 6.9;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87242 MW; FF30209278D8F430 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative tyrosine-protein kinase ptk.
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RESULT 681265 10 081265 10 081265 10 08126 10 08

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Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIB=cv. Nipponbare;
Sasaki T., Matsunoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum (isolate 3D7).
Eukaryodiu Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.5%; Score 50; DB 10; Length 386; 57.1%; Pred. No. 36; ive 2; Mismatches 4; Indels
Score 51; DB 2; Length 726;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003271; BAB89731.1; -.
EMBL; AP004366; BAB92930.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone:P0506B12.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPRO08972; Cupredoxin.
Interpro; IPRO04314; DUP239.
Pfam; PF03080; DUF239; L. SEQUENCE 386 AA; 42354 MW; DD4AED7939404EFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrENBLrel. 23, Created)
01-MAR-2003 (TrENBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Proposes
                                                                                                                                                                                                                                                                                                                                                                                                085179;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
P0506B12.3 protein (P0460C04.23 protein).
                                                                                                                                                                                                                                                                                                                                                                        386 AA
                                                                     Mismatches
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Best Local Similarity 57.1%;
   52.6%;
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709 GAGYSYNYAYAY 720
   Query Match
Best Local Similarity 75.0
Matches 9; Conservative
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Q811Q8
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Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
Harris B., Lennard N., Hall N., Atkin R., Chillingworth C., Doggett J.,
Demond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AL844509; CAD52401.1; -.
Hypothetical protein.
SEQUENCE 3519 AA, 419077 MW; 15C47FF2C08C5393 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=RAG-1;
Nakar D., Gutnick D.L.;
Nakar D., Gutnick D.L.;
required corganization of the wce region of Acinetobacter lwoffii RAG-1 required for emilsan biosynthesis.";
submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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"A protein tyrosine kinase of Acinetobacter lwoffii RAG-1 is involved in emulsan biosynthesis.";

submitted (UTN-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ243431; CAB57193.1; -.

EMBL; AJ243431; CAB57193.1; -.

GO; GO:0016320; C:membrane; IEA.

GO; GO:0016320; F:kinase activity; IEA.

GO; GO:001931; F:kinase activity; IEA.

InterPro; IPR003865; LPS Wzz_MPA.
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Moraxellaceae; Acinetobacter.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 5; Length 3519;
Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                          ul-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Hypothetical malaria antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Best Local Similarity 60.0%;
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                                                                         dydygygygydyd 769
                 1 GFGYSYNYDYYYG 13
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STRAIN=RAG-1;
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SEQUENCE
                                                                                757
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139 GY-FHYDEYYGLDV 151
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les 9; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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802 GYLFNYDYFY 811
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                                            NCBI_TaxID=76856;
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Q8SCTS
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Cronin A., Davies R., Dear P., Dearden F., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Hamper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Hamper S., Jagels K., James K.D., Ohnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., Mcican J., Mooney P., Moulte S., Murphy L.,
A Diver K., Ormond D., Price C., Quall M.A., Rabbinowitsch B.,
Rajandream M.A., Rutter S., Smith R., Squares R., Squares B., Stevens K.,
A Rajandream S., Smith R., Squares R., Squares S., Stevens K.,
A Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
R. Sulston J.B., Craig A., Newbold C., Barrell B.G,
R. "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
R. Nature 419:527-31(2002).
R. Pypothetical protein.
R. SEQUENCE 753 AA; 91152 MW, 477F6D4922EC2539 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea, Buryarchaeota, Thermococci, Thermococcales, Thermococcaceae;
Pyrococcus.
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STRAIN=Vol. / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AEO10176; AALSO661.1;
PiterPro; IPRO3165; Piwi.
Pfam: PF02111; Piwi; 1.
PROS1TE; PS58022; Piwi; 1.
PROSITE; PS58022; Piwi; 1.
SEQUENCE 770 AA; 90390 MW; E68D761BC3FC7D6D CRC64;
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Pred. No. 72;
3; Mismatches 3; Indele
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Bacteria, Fusobacteria, Pusobacterales, Fusobacteriaceae;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypochetical protein PF0537.
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01-UUN-2002 (TrEMBLrel. 21, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
SWF/SNF family helicase.
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Local Similarity 53.8%;
Los 7; Conservative
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547 YRFNYDYIIGIDV 559
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Best Local Similarity 61.5-
Best Local Similarity
8; Conservative
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MEDLINE=21914557; PubMed=11916376;
Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
Mesyanzhinov V.V., Sykillnda N.N., Krylov V.N., Volckaert G.;
Bourkaltseva M.V., Sykillnda N.N., Krylov V.N., Volckaert G.;
"The genome of bacteriophage phixZ of Pseudomonas aeruginosa.";
J. Mol. Biol. 317:1-19(2002).
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Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
Mesyanzhinov V.V., Sykilinda N.N., Krylov V.V., Volckaert G.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF399011, AaL83128.1; -.
SEQUENCE 171 AA, 19830 MW; 54877503302B5A9F CRC64;
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
NCBI_TaxID=169683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.5%; Score 50; DB 16; Length 1089; 70.0%; Pred. No. 1.1e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicase, Complete proteome.
SEQUENCE 1089 AA; 128870 MW; 9BB00D9FB478708F CRC64;
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Query Match
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A Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
A Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.; is solvent-producing
T. "Genome sequence and comparative analysis of the solvent-producing
T. bacterium Clostridium acetobutylicum.";
BMBL; AB00773; AAX80283.1;
J. Bacteriol. 183:4823-4838(2001).
RMBL; AB00773; AAX80283.1;
RMBL; AB00773; PAX80283.1;
RMBL; AB00773; DAV86.
GO; GO: 0016740; F: transferase activity; IEA.
RO; GO: 0016740; F: transferase activity; IEA.
RO; GO: DR01073; Glyco_trans I.
RICETPO: IPR001173; Glyco_trans I.
R Pfam; PF00534; Glyco_trans I.
R Pfam; PF00535; Glyco_trans I.
R Pfam; PF00535; Glyco_trans I.
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                                                                                                                                                                                                                                                                                                  Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Pred. No. 1.4e+02;
1; Mismatches 2; Indels 3
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PF14 0236.
Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase, Complete_proteome.
SEQUENCE 1044 AA; 121349 MW; CIF2F27E651C39F2 CRC64;
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Last annotation update)
                                                                                                                                                 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Glycosyltransferase domain containing protein.
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                                           PRT; 1044 AA
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
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MEDLINE=22255705; PubMed=1236864;
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Nature 419:498-511(2002).
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nes 9, Conservative
                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                             Clostridium.
NCBI_TaxID=1488;
                                                                                                                                             01-OCT-2001
01-JUN-2003
                                                                                                                 01-OCT-2001
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to hypothetical protein 9330175N02.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                50.5%; Score 49; DB 5; Length 1781; 50.0%; Pred. No. 2.5e+02; ive 3; Mismatches 4; Indels
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46.7%; Pred. No. 64;
tive 3; Mismatches 5; Indels
InterPro; IPR000571; Znf CCCH.
Pfam; PF00642; zf-CCH; 2.
SMART; SM00356; ZnF C3H1; 2.
Hypothetical protein.
SRQUENCE 1781 AA; 211749 WW; E4E19022A14C46F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stransberg R.;
Stransberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041775; AAH41775.1; -.
Hypothetical protein.
SEQUENCE 360 AA; 39183 MW; DA00242A347C7709 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                             Local Similarity 50.0
les 7; Conservative
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sapien musculu musculu musculu sapien musculu musculu musculu

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(Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal fecus.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035036; AAD56272.1; -.
PIR; A30601; A30601.
PIR; B30609; A30608.
PIR; B30607; B30607.
PIR; C30601; C30601.
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09JL74
09JM12
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Q91WF8
Q9JL82
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NCBI_TaxID=9606;
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Q9UL78;
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  29UL78
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Q91186 homo sapien
Q91183 homo sapien
Q91183 homo sapien
Q91177 homo sapien
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Q91170 homo sapien
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Q72374 homo sapien
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Q72413 homo sapien
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Q724181 homo sapien
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558
1 EIVLTQSPGTLSLSPGERAT.......CQQYGSSPCSFGQGTKLEIK 108
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Listing first 45 summaries
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sp_vertebrate:*
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Gapop 10.0 , Gapext 0.5
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No.
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Pfam; PF00047; 1g; 1.
SMART; SM00406; 1Gv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                    PRELIMINARY;
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RESULT 3
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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formunol. Immunopathol. 87:184-192(1998).

FIR: 130607; B30607.

FIR: 1306047; FIR: 130-1;

Fir: 1306047; FIR: 130-1;

Fir: 13060406; FIR: 130-1;

FIR: 130
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BEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 109
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
101-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
92.8%; Score 518; DB 4; Length 10
Best Local Similarity 93.5%; Pred. No. 3.2e-49;
Matches 101; Conservative 2; Mismatches 5; Indels
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109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
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PIR; PH0963; PH0963.
PIR; PH0965; PH0965.
PIR; S34096; S34096.
HSSP; P80362; JWTL.
INTERPRO; IPR007110; Ig-like.
INTERPRO; IPR007110; Ig-like.
PEam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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es 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
MEDILINE=88277139; PubMed=9614934;
WED.LINE=88277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                  Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 108;
                                                                                                                                                                                                                                [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE 58277139; PubMed=9614934; MEDLINE=98277139; Pubmed=9614934; Walls., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; --+*** autoantibodies in rheumatic carditis and n
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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1 Similarity 79.6%; Pred. No. 3.7e-40;
86; Conservative 10; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                      fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035031; AAD56267.1; -.
PIR; B30609; B30609.
PIR; C30609; D30609.
PIR; S34098; S34098.
PIR; S34099; S34098.
HSSP; P80362; IMT.
InterPro; IPR007110; Ig-like.
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EMBL, AF035029, AAD56265.1, ...
PIR, D30609, D30609.
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108 AA
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1 EIVLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
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                                                                                                                                                                                                                                                                                          X MEDLINE-98277139; PubMed=9614934;
X MEDLINE-98277139; PubMed=9614934;
A Wu X., Liu B., Van der Nerwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
T "Myosin-reactive autoantibodies in rheumatic carditis and normal
T fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
R PIR; 849047; B49047.
R PIR; 849047; B49047.
R PIR; 849047; B49047.
R InterPro; IPR00310; Ig-like.
R InterPro; IPR00310; Ig-like.
R InterPro; IPR00310; Ig-like.
R Pfam; PF00047; ig; 1.
R PR031TE; PS50835; IG_LIKE; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
70.0%; Score 390.5; DB 4; Length 108;
Best Local Similarity 69.4%; Pred. No. 3.3e-35;
Matches 75; Conservative 15; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 SRFSGSGGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK 107
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Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
01-WAY-2000 (TrEMBLrel. 13, Created)
U-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER 1 1 1
NON TER 108 108
SEQÜENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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EMBL; AF035044; AAD56280.1; -.
PIR; PH0863; PH0863.
HSSP; P01607; IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
PMOSTIF; PS50835; IGy: 1.
NON_TER: 1
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Amon sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
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                                                                                                                                                                                                                                                                                                   Query Match 76.3%; Score 426; DB 4; Length 109; Best Local Similarity 78.0%; Pred. No. 4.2e-39; Matches 85; Conservative 11; Mismatches 11; Indels
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Q9UL79;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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                                                                                          Pfam; PF00047; ig; 1. 5. SMART; SM00406; IGv; 1. 5. PROSITE; PS50835; IG_LIXE; 1. NON TER 109 109 SEQÜENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035035; AAD56271.1; -.
PIR; S23689 S23638.
HSSP; PO1607; IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                  InterPro, IPR007110; Ig-like.
InterPro, IPR003596; Ig_v.
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Q9UL77;
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Q9UL7
ID Q9UL7
AC Q9UL7
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P SEQUENCE FROM N.A.

TISSUE=Skeletal muscle;

X TISSUE=Skeletal muscle;

X Straubberg R.L.; Feligold E.A.; Grouse J.G.; Mediler G.D.;

A Straubberg R.L.; Colling F.S.; Wagner L., Shenmen C.M.; Schuler G.D.;

X Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

A Altschul S.F.; Jordan H.; Moore T., Max S.I.; Wang J., Heigh F.;

A Diatchenko L., Marusina K., Farmer A.A.; Rubin G.M.; Hong L.;

B Diatchenko L., Marusina K., Farmer A.A.; Rubin G.M.; Hong L.;

RA Diatchenko L., Modin T.B.; Toshiyuki S., Carninci P., Prange C.;

B Bronnetein M.J.; Usdin T.B.; Toshiyuki S., Carninci P., Prange C.;

RA Bata S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

RA Rohards S. Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

RA Nillalon D.K.; Muzny D.M.; Sodergren B.J.; Lu X.; Gibbs R.A.;

R Hitting M. M.; Madan A.; Young A.C.; Shevchenko Y.; Boulfard G.G.;

Mitting M. M.; Madan A.; Young A.C.; Shevchenko Y.; Boulfard G.G.;

RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;

R Krayninki M. I.; Skalska U.; Smailus D.E.; Schnerch A., Schein J.E.;

RA Jones S.J.; Marra M.A.;

RA Gones S.J.; Marra M.A.;

RA Gones S.J.; Marra M.A.;

RA Hons S.J.; Marra M.A.;

RA Hond S.J.;

RA Hond S.J.;
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                                            CTRAIN=WIL/Mpd-lpr/lpr; TISSUE=Spleen;

X MEDLINE=93156722; PubMed=8429833;
A Takhatashi S., Itch J., Nose M., Ono M., Yamamoto T., Kyogoku M.;
A Takhatashi S., Itch J., Nose M., Ono M., Yamamoto T., Kyogoku M.;
Tantibodies derived from an MRL/lpr lupus mouse.";
I mol. Immunol. 30:177-182(1933).
R EMBL; D14629; BAA03482-11 -.
R InterPro; IPR00110; Ig-like.
R InterPro; IPR00110; Ig-like.
R SMART; SM00409; Ig; 1.
R SMART; SM00406; IG; 1.
R PROMO40; IG; 1.
R PROSITE; PS50835; IG_LIKE; 1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCPI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMUNOGLOBULIN GAMMA-3 KAPPA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP-CSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Best Local Similarity 67.0%; Pred. No. 2.5e-34;
Matches 73; Conservative 16; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 22 POTENTIAL.
23 >131 IMMUNOGLOBULIN GAMMA-3 KAI
131 131 AA, 14083 MW, 5583556954666595 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SEQUENCE FROM N.A.
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                                   SECUENCE FROM N.A
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NON TER
SEQUENCE
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SIGNAL
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SIGNINE BALB/C; TISSUB=Hyperimmunized spleen;
STRAIN=BALB/C; TISSUB=Hyperimmunized spleen;
STRAIN=BALB/C; TISSUB=Hyperimmunized spleen;
A Zhou Y.-X.; Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
Timate proteolytic antibodies: Failed D-VIPase response to the D-
Innate proteolytic antibodies: Failed D-VIPase VL domains.";
Innate proteolytic antibodies: Failed D-VIPase VL domains.";
Is Submitter (MAY-2002) to the EMBL/GenBank/DDBJ databases.

REBL; AR516284; AAM64202.1;
REBL; A33933; A33933.
REBL; A33933; A33933.
REPROSOME TIPE TO THE TO THE
                                                                                                                                                                                                                                                                                              1 BIVLTOSPGTLISLSPGERATLSCRASOSVSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
                                                                                                                                                                                                                                                                                                                                           1 EIVLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBKIF1;
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Anota) Schordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
111 TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 AA; 12162 MW; 8BD9833DBF3EEFD1 CRC64;
             108 108
108 Aa; 11633 MW; B7BEDC3E41FCCA37 CRC64;
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                                                                                                                                      Query Match
Best Local Similarity 66.7%
Matches 72; Conservative
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RESULT 11 Q96SA9

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TISSUE-Lung;

XX MIDLINE-22388257, PubMed=12477932;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Feingold E.A., Grouse L.H., Schamen C.M., Schuler G.D.,

XI Strausberg R.L., Feingold E.A., Grouse C.F., Bhat N.K.,

A Alschul S.P., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peers G.J., Abramson R.D., Mullahy S.J.,

A Brownstein M.J., WcKerran K.J., Malek J.A., Gunaratne P.H.,

A Brown S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XI Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muray D.M., Sodergen E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bourffard G.G.,

Radriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.,

Young A. M., Smailus D.E., Schnerch A., Schein J.E.,

A Marra M.A.,

A Marra M.A.,

A Honge S.J., Marra M.J.,

A Honge S.J., Marra M.J.,

A Honge S.J., Marra M.J.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 IRWIQSPSSFSASTGDRVTITCRASQSI-GSYLAWYQQXPGKAPQLLIYAASTLQSGVPS
                                  Hypothetical protein.
Homo saplena (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
"Genetic and genomic tools for Xenopus research: The NIH Xenopus
intiative."
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Straubberg R.;
Straubberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO56256; AMH56256.1; -.
Hypothetical protein.
SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
          01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 67.8%; Score 378.5; DB 4; Local Similarity 67.3%; Pred. No. 1.8e-33; HB 72; Conservative 16; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences."
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                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                   23 DIQMTQSPSSLSASVGDTVTITCRASQDI-SNYLAWFQQKPGKAPKSLIYGASSLQSGVQ 81
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-streptococcail/anti-myosin immunoglobulin kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98375893; PubMed=9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
"Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                  61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                  SKFSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEIK 129
                                                                                                                                                                             Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRFSGSGSGTDFTLTISRLEPEDFAVYYCOOYGSSPCSFGOGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 107;
                                                                                                                                                                     68.5%; Score 382.5; DB 4; Length 66.7%; Pred. No. 6.7e-34; ive 16; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.3%; Score 381; DB 4; Length 10 69.4%; Pred. No. 3.6e-34; ive 14; Mismatches 17; Indels
                  Straubberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC005332; AAH05332.1; ... Hypochetical protein protein protein Protein 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4BB43E9C5B577F16 CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR007110, Ig-like.
InterPro, IPR003596, Ig-v.
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Best Local Similarity 69....
Best Local Similarity 69....
                                                                                                                                                                                          Local Similarity 66.7%
les 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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TISSUE=Skeletal muscle;
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PIR; S34083; S34083.
PIR; S34086; S34086.
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Q72473;
01-OCT-2003
01-CCT-2003
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                                                                                                                                                                        Query Match
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NON TER
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Ry Straubserg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ry Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Ry Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Ry Bopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hang L.,

Rapleton M., Soares M.B., Bonaldon M.F., Carninci P., Scheetz T.E.,

Rapleton M., Soares M.B., Bonaldon M.F., Carninci P., Prange C.,

Ry Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Ry Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Ry Haley J., Helton B., Ketteman M., Madan A.M., Gay L.J., Buiffard G.G.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouiffard G.G.,

Ry Rodriguez A.C., Gimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones J.J., Marra M.A.;

Ry Goneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

Ry Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIPDRESGSGSGTDFTLTISRLEPEDFAVYYCOQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
65.3%; Score 364.5; DB 13; Length 237;
Best Local Similarity 64.0%; Pred. No. 6.4e-32;
Matches 71; Conservative 16; Mismatches 21; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030814; AAH30814.1; -.
PIR; S234638; S23638.
PIR; S34091, S34091.
PIR; S40357; S40357.
                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054155; AAH54155.1; -.
Hypothetical protein Protein
SEQUENCE 237 AA; 26300 MW; 47BBDDD2639CB436 CRC64;
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Last sequence update)
Last annotation update)
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Interpro; IPR003597; Ig_cl.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
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TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A. ISSUE=Whole;
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                                                                                                                                                                                                                                                                   1 BIVLTOSPGTLSLSPGERATLSCRASOSVSSS----YLAWYQQKPGQAPRLLIYATSSRA
                                                                                                                                                                                                   4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                 57 TGIPDRESGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLBIK 108
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DRESGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLBIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.9%; Score 362; DB 4; Length 107; 65.7%; Pred. No. 4.4e-32; ive 16; Mismatches 19; Indels
                                                                                                                                                      Length 239;
                                                                                                                                                   Query Match
Best Local Similarity 62.5%; Pred. No. 7.4e-32;
Matches 70; Conservative 20; Mismatches 18; Indels
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107 AA; 11501 MW; 070549FDE0754748 CRC64;
SMART; SM00407; IGC1; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS00289; IG LIKE; 2.

PROSITE; PS01201 IG MHC; 1.

SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAY-2000 (TrEMBLrel. 13, Created)
--WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AP035033, AAD56269.1; -.
HNSP, PO1607, IREL.
HNSP, PO1607, IREL.
INTERPRO, IPRO7110; IG-like.
InterPro, IPRO03596; Ig-v.
PFAM, PP00047; ig; I.
PRART; SM00466; IGv; I.
PROSITE; PS50835; IG_LIKE; I.
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Job time : 33.9099 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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The kappa Human 4.1 Anti-IL-1 Anti-IL-4 Light cha Kappa cha Kappa cha Kappa cha Human HIV Human imm Human imm Anti-ILB Anti-ILB Anti-ILB Anti-huma Anti-huma

Ade35884 Abb60729 Abr55800 Abr55800 Abr55801 Abr6228 Abr6228 Abr6328 Abr6328 Abr6328 Abr6328 Abr6328 Abr6328 Abr63394 Abr63394 Abr621473 Abr621473

Human imm Anti-IL-4 Antibody Antibody

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Monoclonal antibody, MAb, envelope, glycoprotein, gp120, HIV; AIDS; CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light; chain; epitope; immune deficiency.
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110. .117
/label= CDR3
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44. 55
/label= CDR1
/label= CDR2
                                    ABB07229
ABR54800
ABR55804
ABR55804
ABR55804
ABR62228
ADA43061
ABR54304
AAR39334
AAR39334
AAR375027
AAR375027
AAR375027
AAR375027
ABR074736
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/label= sig_peptide
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/label= mat_protein
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/label= vk325
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/label= Jk2
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(first entry)
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Misc-difference
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01-NOV-1993
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Region
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                                                                                                                                                                                                                                                                                                                                 RESULT 1
AAR38672
  Aar38672 vk225-Jk2
Abj56930 Anti-CD40
Aam24101 Human EST
Aau14462 Human nov
Aau14463 Human nov
Aau14464 Human nov
Aau34661 Human nov
Aas38059 Human ant
Abp57366 Anti-TRAI
Aab99397 Human int
Aab52509 Human int
Aab6220 Human int
Abp62199 Human imm
Abb6139 Human imm
Abb62207 Human imm
Abb62207 Human imm
Abb62207 Human imm
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                                                                                                                                                US-10-041-860-49
558
1 BIVLTQSPGTLSLSPGERAT......CQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                     1586107
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AAM24101
ADD40551
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AAU14464
AAB38059
ADA89268
ABG32514
AAB9393774
AAB9939374
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AAB75030
AAB35209
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ADA89220
ADP62199
ABP62186
ABB67233
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1990s:*
2: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2003as:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
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Maximum DB seq length: 200000000
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                                                                                                                            DNA segments encoding monoclonal antibody - which binds to gp120 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV
                                                                                                                                                                                     The nucleotide sequence of F105 Vk (AAQ42707 - sequence differs from other F105 Vk sequences given elsewhere in the specification) was compared with germline gene Humvk325 (AAQ42706), showing 97.7% similarity. By nucleotide sequence analysis, F105 appears to be derived from a member of the Vk III subgroup gene family. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                      21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antiallergic; haemostatic; immunomodulator; cytostatic; antibody; human CD40; IL-12; LPS; lipopolysaccharide; ITMgamma; interferon gamma; dendritic cell; high G28-5; E cell line; immunoactivator; anti-tumour agent; immunosuppressant; allergy; autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.
                                                                                                                                                                                                                                                                                                                   1 EIVITQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                        61 DRFSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLBIK 108
                                                                                                                                                                                                                                                                                                                                                                        Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-CD40 monoclonal antibody related protein SEQ ID No 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takahashi N;
                                                                                                                                                                                                                                                                            Query Match
95.9%; Score 535; DB 2; Length 12
Best Local Similarity 96.3%; Pred. No. 1.8e-33;
Matches 104; Conservative 1; Mismatches 3; Indels
                                                                             Haseltine WA;
                                               (DAND ) DANA FARBER CANCER INST INC.
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen X,
                                                                                                                                                                  Disclosure, Page 74-75; 109pp; English.
                                                                               Posner MR,
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                                                                                                                                                                                                                                                                                                                                                                                                                              ABJ36930 standard; protein; 130
           92WO-US010928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2001; 2001WO-US013672.
11-MAY-22001; 2001JP-0014482.
05-OCT-2001; 2001JP-00310535.
26-OCT-2001; 2001US-00040245.
                              91US-00804652
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                                                                              Sodroski JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yoshida H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KIRI ) KIRIN BEER KK
                                                                                                WPI; 1993-214174/26.
N-PSDB; AAQ42706.
                                                                                                                                                                                                                                                         Sequence 129 AA;
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                             10-DEC-1991;
         10-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                              Marasco WA,
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                                                                                                                                                 infection.
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The invention relates to an antibody to human CD40, or its functional fragment, has at least one of the following properties: acting on dendritic cells to produce IL-12 in the presence of LP8 (lipopolysaccharide) and IRNgamma (interferon gamma); acting on dendritic cells to activate maturity of the dendritic cells with high G28-5 antibody against cells to activate maturity of the dendritic cells with high G28-5 antibody against B cell line. Such antibodies or functional fragments can be used as immunoactivators, anti-tumour agents, immunosuppressants, and as remedies for autoindmene diseases, allergy or coagniation factor VIII inhibitors syndrome. This sequence represents a protein relating to the anti-CD40 monoclonal antibody of the invention
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                                                                                         Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40 or functional fragment, is useful in the treatment of e.g. autoimmune diseases or cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DRFSGSGSGTDFTLTISKLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPITFGQGTRLEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 533; DB 6; Lengtn L. Pred. No. 2.56-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou F, Qian XB, Wang Z,
1, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human EST encoded protein SEQ ID NO: 1626.
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                                                                                                                                                                                                                 Claim 25; Page 51; 94pp; Japanese.
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17-JUL-2000; 2000US-0061746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-00663870.
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Best Local Similarity 95.4%;
Matches 103; Conservative
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WPI; 2003-120463/11.
N-PSDB; ABT31872.
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Cao Y, Drmanac RA,
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N-PSDB; AAH98760.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 130 AA;
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AAU14462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          systemic inflammatory response syndrome; sepsis;
multiple organ dysfunction syndrome; acute respiratory distress syndrome;
multiple organ dysfunction syndrome; acute respiratory distress syndrome;
trauma; graft-versus-host disease; organ rejection; multiple sclerosis;
lidiopathic pulmonary fibrosis; osteoarthritis;
inflammatory bowel disease; Crohn's disease; ulcerative collitis;
acute myocardial infarction; cardiomyopathy; cardiac reperfusion injury;
diabetes; cancer; HIV infection; influenza virus; hepatic disorder;
renal disorder; antiinflammatory; antibacterlal; cardiant; osteopathic;
virucide; anti-HIV; cytostatic; antidabetic; nephrotropic; hepatotropic;
immunosuppressive; vulnerary; gene therapy; vaccine;
light chain variable region; 3E1; 4G11.
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                                                                                                             The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeakt, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated anti-hFasL human antibody or its antigen-binding portion, useful for preparing a composition for neutralizing hFasL activity for treating or preventing a disorder in which hFasL activity is detrimental,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVBIK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                        Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 533; DB 4; Length 38. Pred. No. 6.9e-33; Indels 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human Fas ligand; hFasL; antibody;
                                                                          Claim 20; Page 1102-1103; 1275pp; English.
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10-SEP-2002; 2002US-0409768P.
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.4%;
Matches 103; Conservative ;
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N-PSDB; ADD40550.
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                                                                                                                                                                                                                                                                                                                                                          Sequence 384 AA;
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The present invention relates to anti-human Fas ligand (hFasL) antibodies or their antigen-binding portion (I). (I) are useful for preparing a composition for neutralizing FasL activity for treating or preventing a disorder in which FasL activity is detrimental, e.g. systemic inflammatory response syndrome, sepsis, multiple organ dysfunction syndrome, acute respiratory distress syndrome, trauma, graft-versus-host disease, organ rejection associated with organ transplant, multiple sclerosis, idiopathic pulmonary fibrosis, osteoarthritis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, acute myocardial confinence, acute myocardial confinence, inflammatory in the inflammatory andiomyopathy, cardiac reperfusion injury, diabetes, cancer, HY infaction, influenza virus infection, hepatic disorders including but not limited to fulminant viral hepatitis B or C, chronic hepatitis C virus, chronic hepatitis B virus, alcoholic hepatitis, hepatic cirrhosis or renal disorders. The present sequence is a light chain variable region (LCVR) of anti-FasL antibodies 3El or 4G11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, novel protein; Antianaemic, osteopathic, antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 532; DB 7; Le
Pred. No. 2.8e-33;
2; Mismatches 3;
                                                            Claim 1; SEQ ID NO 2; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU14462 standard; protein; 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2000; 2000US-00491404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.4%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-451939/48.
N-PSDB; AAS22767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200155437-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-2001
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e.g. sepsis.
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                          The invention relates to polymucleotides encoding novel human proteins or their active domains. The polypeptides, polymucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the abstrant protein.

CC expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides.

CC Polymucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a ctumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein cumour, as a statem markers, and to isolate receptors or ligands.

CC levels, as tissue markers, and to isolate receptors or ligands.

CC disorders, stem cell disorders, regenerating bone, cartilage, tendon, clampant and/or nerve tissue, wound healing, treating puris, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, allered to stems at the anaemia, and solarosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graftverminer's parkinson's and shemophilia, thrombosis, auti-inflammatory diseases, casen, and infection. The present sequence crepters or represents a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunomodulatory, cytostatic, meuroprotective, vulnerary, nootropic, anticonvulsant, antiarthritic, cerebroprotective, antifungal, antiaviral, antibacterial, antiallergic, dermatological, haemostatic, antiathmatic, thrombolytic, immunogen, antibody, gene therapy, neurological disorder; Parkinson's disease, inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIVLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

95.0%; Score 530; DB 4; Length 38.
Best Local Similarity 94.4%; Pred. No. 1.2e-32;
Matches 102; Conservative 3; Mismatches 3; Indels
 Example 4; Page 825-826; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU14463 standard; protein; 384 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human novel protein #334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 384 AA;
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The invention relates to polymuclectides encoding novel human proteins or their active domains. The polymetides, polymuclectides and antibodies cataled against the polymetides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein of expression or activity. The polymetides can be used as molecular weight expression or activity. The polymetides can be used as molecular weight or expression or activity. The polymetides can be used as probes and primers, for markers, food supplements, and in antibody production. The polymetides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polymetides of the invention can be used to target drugs to a therapy, polymetides of the invention can be used to target drugs to antibodise/alicit an immune response, to determine quantitative protein can be used to target drugs to antibodise/alicit an immune response, to determine quantitative protein can be used to target drugs to antibodise/alicit an immune response, to determine quantitative protein can be useful in treating platelet company describes, treating, and its generating one, carrilage, trendon, cligament and/or nerve tissue, wound healing, treating burns, promocing the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporoals and osteoarthritis, anamemia, chingament infaction or from autodimmunity, cancer, allergy, asthmy grand disease, eczema, haemopolia, attromosty disease, nervous system disorders, and infection. The present sequence con represents a protein of the invention
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                                                                                                                                                            Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 530; DB 4; Length 384; 94.4%; Pred. No. 1.2e-32; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                      Example 4; Page 826-827; 894pp; English.
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Drmanac RT;
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Best Local Similarity 94.4<sup>†</sup>
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human novel protein #332.
                                                                     WPI; 2001-451939/48.
N-PSDB; AAS22768.
Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200155437-A2
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Tang YT,
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The invention relates to polymucleotides encoding novel human proteins or their active domains. The polymeptides, polymucleotides and antibodies caised against the polymeptides are used in a method of treatment of a manmal and prevention of disorders caused by the aberrant protein care used supplements, and in antibody production. The polymeptides are used as molecular weight are used to identify compounds which bind to the polypeptides.

CC dequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in generating for chromosome or gene mapping, in the production of the recombinant proteins, and in generating anti-sense DNA or RNA and in generating believes, elicit an immune biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands.

CC polymeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, cligament and/or nerve tissue, wound healing, treating burns, promocing contraceptive, treating osteoporosis and osteoarthritis, and an experial or fere proliferation or fiferentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis aneamia, cligaments, so parkinson's and Huntington's diseases, amylotrophic lateral cliesaes, nervous system disorders, and infection. The present sequence represents an orders, and infection. The present sequence
                                                                                                                                                                                                                                                                                                      Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases, nervous system disorders, ar
represents a protein of the invention
                                            25-JAN-2001; 2001WO-US002623.
                                                                                         25-JAN-2000; 2000US-00491404
                                                                                                                                                                                      Liu C, Drmanac RT;
                                                                                                                                                                                                                                   WPI; 2001-451939/48.
                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                            N-PSDB; AAS22766
  02-AUG-2001
                                                                                                                                                                                      rang YT,
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Sequence 384 AA;

9 1 BIVITQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP Gaps Query Match

95.0%; Score 530; DB 4; Length 384;
Best Local Similarity 94.4%; Pred. No. 1.2e-32;
Matches 102; Conservative 3; Mismatches 3; Indels

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AAU14464 standard; protein; 384 AA

AAU14464;

24-OCT-2001

(first entry)

Human novel protein #335.

Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; RESULT 8
ANU14464
ID AAU1
XX
AC AAU1
XX
DT 24-C
XX
XX
KW Huma
XX
KW Huma
KW immu
KW anti

The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies are assed in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein carposession or activity. The polypeptides can be used as molecular weight expression or activity. The polypeptides can be used as molecular weight care used to identify compounds which bind to the polypeptides.

CC sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-ense DNA or RNA and in generating combinant proteins, and in generating anti-ense DNA or RNA and in generating combinant proteins, and in generating anti-ense DNA or RNA and in generating complexed, as tissue markers, and to isolate receptors or ligands.

CC tumour, in assays to determine biological activity, to raise threapy. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, classacers, stem cell disorders, regenerating bone, cartilage, tendon, cligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, chingament's, parkinson's and Huntingfon's diseases, may infection or from autoinmounty, cancer, allery, asthma, graft-coversue-host disease, eczema, haemophila, thrombosis, anti-inflammatory diseases nervous system disorders, and infection. The present sequence thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder. Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage. Example 4; Page 827; 894pp; English. 25-JAN-2001; 2001WO-US002623. Tang YT, Liu C, Drmanac RT; 25-JAN-2000; 2000US-00491404 WPI; 2001-451939/48. (HYSE-) HYSEQ INC. N-PSDB; AAS22769 WO200155437-A2. Homo sapiens 02-AUG-2001 

Sequence 384 AA;

ö 95.0%; Score 530; DB 4; Length 384; illarity 94.4%; Pred. No. 1.2e-32; Conservative 3; Mismatches 3; Indels Query Match Best Local Similarity Matches 102, Conserv

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170 BIVITOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229 9 1 EIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 셤 ઠ ઠ

61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVDIK 277

AAE38059

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AAE38059 standard; protein; 108 AA

AAE38059 SXXX

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systemic lupus exythematosus; systemic sclerosis; grave's disease; ALCL; acupic dematitis, Hashimoto's thyroiditis; chronic renal failure; ALLD; acute infectious monouncesis; angioimmunoblastic lymphadenopathy; HTV; Hodgkin's disease; Castleman's disease; Kaposi's sarcoma; Lymphoma; ATL; Wednit T call lymphoma; human immunodeficiency virus; carcinoma; therapy; Wegner's granulomatosis; anaplastic large cell lymphoma; Omen's syndrome; light chain variable domain; VL.
                                   antibody; CD30; tumour; autoimmune disease; rheumatoid arthritis;
                  Human 17G1 CD30 antibody light chain variable domain (VL) protein.
                                                                                                                                                           "Complementarity determining region
                                                                                                                                                                                                  "Complementarity determining region
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                                                                                                                                          Location/Qualifiers
(first entry)
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/note= "C
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                                                                                                                         Homo sapiens
06-NOV-2003
                                      Human;
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WO2003059282-A2.

24-JUL-2003

07-JAN-2003; 2003WO-US000440.

09-JAN-2002; 2002US-0347649P.

2002US-0404427P. 19-AUG-2002; 06-DEC-2002;

(MEDA-) MEDAREX INC

Treml J; Graziano R, Keler T,

WPI; 2003-598476/56. N-PSDB; AAD57371 New human monoclonal antibody that binds to human CD10, useful for treating or preventing tumor or autoimmune disease, e.g., rheumatoid treating on arthritis.

Claim 18; Fig 8; 122pp; English.

The invention relates to human monoclonal antibody that binds to human CD30. The antibody is useful for treating or preventing tumour or autoimmune disease e.g. rheumatoid arthritis, systemic lupus erythematosus, systemic sclerosis, atopic dermatitis, Grave's disease, flashimoto's thyroiditis, Wegner's granulomatosis, Omen's syndrome, chronic renal failure, acute infectious mononucleosis, herpes or HIV (human immunodefaciency virus) virus-associated diseases. The antibody is also useful for treating Hodgkin's disease, anaplastic large cell lymphoma (ALCI), andioimmunoblastic lymphoma (ALCI), adult T cell lymphoma (ATL), angioimmunoblastic lymphoma (ALCI), adult T cell lymphoma (ATL), angioimmunoblastic lymphomas, embryonal carcinomas, undifferentiated carcinomas of the himo-pharynx (e.g. schmincke's tumour), castleman's disease, Kaposi's Sarcoma and other T-cell or B-cell lymphomas. The present sequence is human CD30 antibody VL (light chain variable domain) protein

Sequence 108 AA;

0; Gaps Length 108; Query Match
94.3%; Score 526; DB 6; Length 10:
Best Local Similarity 94.4%; Pred. No. 7.2e-33;
Matches 102; Conservative 2; Mismatches 4; Indels

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DRESGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108 61

d 8

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61 DRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108

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Z ADA89268 standard; protein; 109

ADA89268;

(first entry) 20-NOV-2003

Human antibody 3G3 light chain amino acid sequence SEQ ID NO:112.

immunoglobulin; Ig; heavy chain variable domain;
light chain variable domain; major histocompatibility complex; MHC;
gpl00; MUC1; TAX; hTERI; cytostatic; gene therapy; cancerous disorder;

cancer.

Homo sapiens. Synthetic

<u>.</u> ۳ 2 (CDR) 1"

28-AUG-2003

WO2003070752-A2.

20-FEB-2003; 2003WO-US005128

20-FEB-2002; 2002US-0358994P

(DYAX-) DYAX CORP. (TECR ) TECHNION RES & DEV FOUND LTD.

Hoogenboom HRJM, Reiter Y;

WPI; 2003-663847/62. N-PSDB; ADA89267 New protein comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, useful for preparing a composition for treating or preventing a cancerous disorder.

Disclosure, Fig 27A, 224pp, English.

The present invention describes a protein comprising an immunoglobulin (Ig) heavy chain variable (WH) domain and an Ig light chain variable (VL) domain. The protein blinds a complex comprising a major histocompatibility complex. (MHC) and a peptide, does not substantially bind the MHC in the absence of the bound peptide, and does not substantially bind the peptide in the absence of the MHC. The peptide is a peptide fragment of gp100, MUC1. TAX or hTERT. Also described: (1) a pharmaceutical composition comprising the novel protein and a carrier; (2) a cytotoxic T cell comprising one or more nucleic acids for expressing the Ig that binds a complex having an MHC and a peptide, and does not substantially bind the MHC in the absence of the bound peptide, and does not substantially bind the comprising a first segment that macodes the Ig variable domain; (4) a host cell comprising heterologous nucleic acid sequences that encodes the comprising a first segment that encodes the Ig variable domain; (4) a host of protein; (5) a transgenic animal whose genome includes heterologous nucleic acid sequences that encode the protein; (6) identifying the protein; (8) ablating or killing a target cell that an austigen-binding protein; (8) ablating or killing a target cell that can a surface MHC molecule; (9) treating or preventing a cancerous disorder in a subject; and (10) detecting an MHC-peptide complex in a semple. A protein of the invention has expected a cell for nreparing a complex in a semple. The present and can be used in gene therapy. The protein is useful for preparing a composition for treating or preventing a cancerous disorder. The present sequence represents the light chain of an antibody which binds to an Mi peptide complex where the peptide component in as peptide fragment of 

Sequence 109 AA;

Query Match

Length 109; 9 <u>B</u> 94.3%; Score 526; DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLYTFGGGTKLEIK 129

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Ā.

ABG32514 standard; protein; 109

RESULT 12

ABG3251

disease;

Human VK region of monoclonal antibody for CD89, CD89 8.2 VK.

(first entry)

15-NOV-2002

ABG32514;

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The present invention describes antibodies or their functional fragments that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies have cytostatic and apoptotic activities, and can be used in antibody therapy. The antibodies can be applied as remedies and preventives of diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful in the therapy of malignant tumours. Remedies produced with the sequence represents an anti-TRAIL-R1 and TRAIL-R2, which are useful sequence represents an anti-TRAIL-R antibody amino acid sequence from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer cells and without exerting an effect on normal cells expressing TRAIL-Rs nor inducing injury to hepatocytes, for use in therapy of malignant
                                                                                                                             9
                                                                                                                                                                                   9
                                                                                                                                                               1 ETTLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIP
                                                                                                                      1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; TRAIL-R1; TRAIL-R2; antibody; cytostatic; apoptotic; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-TRAIL-R antibody related clone H-48-2 protein SEQ ID NO:27.
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                                                                                                                                                                                                                                                   61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLBIK 108
                                                                                                                                                                                                                                                                                     DRFSGSGSGTDFTLTISRLEPEDFAVYYCOOYGSSPYTFGGTKLEIK 108
                                                            Indels
7.3e-33;
5;
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Pred. No. 9.4e-33;
1; Mismatches 3
                                                            Mismatches
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                                 Pred.
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09-AUG-2001; 2001JP-00243040.
11-OCT-2001; 2001JP-00314489.
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Best Local Similarity 95.4%;
Matches 104; Conservative
                              94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                            Conservative
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N-PSDB; ABZ59697.
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                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody therapy
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                                                            102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor.
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ABB97366
ID ABB97366
ID ABB97366
ID ABP97366
                                                            Matches
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The invention relates to an isolated human monoclonal antibody which binds to human CD89 (an IgA receptor also called Fcalpha), comprising the least one characteristic selected from: (i) a binding equilibrium cleast conscioution constant (K a) to human CD89 of at least about 10^7 M^-1; (ii) a dissociation constant (Kd) from human CD89 of about 10^-88^-1 or less; (iii) absence of in vivo complement activation upon binding to the man CD89; (iv) the antibody binds to an epitope on human CD89 which does not inhibit human IgA binding to the receptor; and (v) the antibody complises heavy chain and light chain components and their encoding nucleic acids appearing as ABS2470-ABS3473 and ABG3211 -ABG32114. The human antibodies of the present invention that modulates CD89 levels, blocks or inhibits IgA binding to CD89 are useful in the treatment of complexes such as cancer, bacterial, viral and parasitic infections, autoimmune diseases (diabetes, arthritis, multiple sclerosis, psoriasis, crohn's disease, asthma, and allergies), chronic hepatitis. Hench-schooling of the present sequence represents the light chain variable region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Fig 4; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibody CD89 8.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases.
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useful as

New isolated human monoclonal antibody that binds to human CD89, for in the treatment of diseases related to CD89 expression such cancer, bacterial, viral and parasitic infections and autoimmune

Van Dijk MA;

Hudson D, Van De Winkel J,

(MEDA-) MEDAREX INC.

WPI; 2002-643459/69.

N-PSDB; ABS52473

11-FEB-2002; 2002WO-US004024. 12-FEB-2001; 2001US-0268075P. 05-NOV-2001; 2001US-0338956P.

WO200264634-A2. Homo sapiens.

22-AUG-2002.

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Indels

94.0%; Score 524.5; DB 5; 95.4%; Pred. No. 9.5e-33; ive 1; Mismatches 3;

Matches 104; Conservative Query Match Best Local Similarity

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1; Gaps

Indels

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1 BIVLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60

EIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP

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В

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61

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DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPC-SFGQGTKLEIK 108

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Length 109;

1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60

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the present invention describes a method for detecting an analyte in a human sample containing human antibodies that specifically bind to antibodies from a nonhuman species. The method involves contacting the ample with a human antibody (I) which specifically binds to antibodies from a nonhuman species and detecting the binding between (I) and the analyte to indicate presence of the analyte. The method is used for detecting an analyte in a human sample containing human anti-mouse antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes, type of target antigen including bacterial, fungal and viral pathogens that cause human antibodies can be used as detection reagents for performing claims, Leishmania, Staphylococcus aureus, Steudomons acruginosa. Human antibodies can be used as detection reagents for performing claims all diagnostic tests and for performing other in vitro detection assays, including for research purposes. (I) can be used in qualitative assays designed to indicate the presence of one or more target antigen in a sample that usually correspond to the sensitivity limitations of the assays for each target antigen. Also, (I) is used to determine the amount of target antigen in a sample in a semi-quantitative or relative sense. Contarget antigen in a sample in a sample or antigen in a sample carried out using (I). AM441652, and AAB99361 to AAB93399, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting analyte in human sample containing human antibodies binding to nonhuman-antibodies, involves contacting sample with human antibody which binds to antibodies from nonhuman species and detecting binding.
Human antibody; detection; Fab; immunoglobulin; heterophilic antibody; human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes; targer antigen; bacterial; fungal; viral; pathogen; human disease; hepatitis A; hepatitis B; hepatitis C; infilunza; diardia; Malaria; Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.
                                                                                 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS-PCSFGQGTKLEIK
                                                                                                                                                                                                                                                                                                                          Human interleukin 8 antibody protein sequence M2_33L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 22; Page 96; 135pp; English.
                                                                                                                                                                                                      AAB99397 standard; protein; 226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gray J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOS-) BIOSITE DIAGNOSTICS INC. (GENP-) GENPHARM INT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-2000; 2000WO-US033042.
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                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
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the present invention describes a method for detecting an analyte in a human sample containing human antibodies that specifically bind to antibodies from a nonhuman species. The method involves contacting the sample with a human antibody (I) which specifically binds to antibodies from a nonhuman species and detecting the binding between (I) and the analyte to indicate presence of the analyte. The method is used for detecting an analyte in a human anti-mouse idiotype antibodies and/or heterophilic antibodies). The method can also be used for detecting any type of target antigen including bacterial, fungal and viral pathogens that cause human diseases e.g., hepetitis (A,B and C), influenza, Herpes, CC diardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas that cause human antibodies can be used as detection reagents for performing clinical diagnostic tests and for performing other in vitro detection assays including for research purposes. (I) can be used in qualitative assays designed to indicate the presence of one or more target antigens above minimally detectable amounts of antigen in the sample that usually correspond to the sensitivity limitations of the assays for each target antigen. Also, (I) is used to determine the amount
                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting analyte in human sample containing human antibodies binding to nonhuman-antibodies, involves contacting sample with human antibody which binds to antibodies from nonhuman species and detecting binding.
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                                                                                                                    1 EİVLİÇSPGİLİSLSPGERATLSCRASÓSVSSSYLAWYQQKPGQAPRILLIYGASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human antibody; detection; Fab; immunoglobulin; heterophilic antibody; human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes; targer antigen; bacterial; fungal; virtal; pathogen; human disease; hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria; Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis.
                                                                            1 BIVLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                        Gapa
                                        1;
                                                                                                                                                                 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS-PCSFGQGTKLEIK 108
                                                                                                                                                                                            61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIK 109
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human interleukin 8 antibody protein sequence M1_23L.
Query Match

94.0%; Score 524.5; DB 4;
Best Local Similarity 95.4%; Pred. No. 1.9e-32;
Matches 104; Conservative 1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                  AAB99374 standard; protein; 226 AA
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valkirs G,
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(GENP-) GENPHARM INT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                             AAB99374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunised nonhuman transgenic animals, and from this a population of antibodies may be prepared. Production of a human monoclonal antibodies display library using this method means there is no need to immunise humans with antigens, and the difficulties faced with immortalising B cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056 represent sequences used in the exemplification of the present invention
of target antigen in a sample in a semi-quantitative or relative sense. Quantification of one or more target antigens in a sample can also be carried out using (I). AMH1612 to AAH41686, and AAB99361 to AAB9939, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                               1 EIVLŢQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
                                                                                                                                                                                                                                                            Producing a human antibody phage display library comprises providing a transgenic animal whose genome comprises human immunoglobulin genes and isolating nucleic acids encoding antibody chains from lymphatic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; antibody; immunoglobulin; interleukin 8; II8; immunogen; human antibody phage display library; immunisation; transgenic animal.
                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                               DRFSGSGSGTDFTLTISRLEPEDFAVYYCQOYGSS-PCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                        61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIK 109
                                                                                                                                                DB 4; Length 226;
                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-IL8 monoclonal antibody protein fragment M1_23L
                                                                                                                                           Query Match

94.0%; Score 524.5; DB 4
Best Local Similarity 95.4%; Pred. No. 1.9e-32;
Matches 104; Conservative 1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOS-) BIOSITE DIAGNOSTICS INC.
(GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gray J, Lonberg N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB75007 standard, protein; 226 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0157415P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buechler J, Valkirs G,
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                                                                                                     Sequence 226 AA;
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                                                                                                                                                 1 EIVLTÖSPÖTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRILIYGASSRATGIP 60
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                                                                                    1; Gaps
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                                                                                                                                                                                                61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOOYGSS-PCSFGOGTKLEIK 108
                                                 Length 226;
                                                                                    Indels
                                                 DB 4;
                                               Query Match 94.0%; Score 524.5; DB 4; Best Local Similarity 95.4%; Pred. No. 1.9e-32; Matches 104; Conservative 1; Mismatches 3;
               Sequence 226 AA;
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Search completed: April 21, 2004, 17:01:54 Job time : 49.279 secs

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Sequence 9, App
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Sequence 112, A
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                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-041-860-49
558
1 BIVLTQSPGTLSLSPGERAT......CQQYGSSPCSFGQGTKLEIK 108
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('Ggn2_6')ptodata/2'/pubpaa/USO7_NEW_PUB.pep:*
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('Ggn2_6')ptodata/2'/pubpaa/USO6_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-041-860-225
US-10-041-860-325
US-10-041-860-359
US-10-309-762-156
US-10-307-724-123
US-10-291-265-804
US-10-291-265-806
US-10-291-265-806
US-10-291-265-806
US-10-291-265-806
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US-10-338-366-4
US-10-338-366-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1133595 seqs, 276475211 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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                                                                                                                                                                                                                                                    Run on:
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equence 1	equence 150	equence 8,	equence 50	equence 86	43	금	equence 8,	equence 7,	equence 64	equence 7,	equence 13	equence 32	36	13	80	34,	17	70	Ď	38,	e 14	equence 4,	equence 36	9 74	equence 39	equence 42	equence 33%	ednence 33,	equence 47	
9-762-163	7-890-150	3-644C-8	3-234-50	3-234-86	9-762-43	2-088-113	3-880-8	8-939-7	1-942-64	3-382	1-085B-	9-805-32	9-805-36	1-085B-133	-234-80	-053-34 S	-798-178	7-800-70	1-942-104	053-38	0-648-14	0-648-4	1-942-36	3-234-74	9-762-39	-42	1-265-332	ñ	4	
-10-3	US-10-1	US-10-0	US-09-4	US-09-4	US-10-3	US-10-2	US-10-2	0S-09-9	US-10-3	-10-1	US-10-2	US-10-2	US-10-2	US-10-2	US-09-4	85	US-09-8	-0	2 US-10-3	85	2 US-10-1	2 US-10-1	2 US-10-3	0 US-09-4	5 US-10-3	US-09-4	5 US-10-2	5 US-10-2	4 US-10-0	
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16	17	18	19	70	21	22	23	24	52	56	27	78	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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WESULT 1

WESULT 1

WESULT 1

WESULT 1

WESULT 1

SEQUENCE 49, Application US/10041860

PUBLICANT Corvalan, Jose R.F.

APPLICANT Servalan, Jose R.F.

APPLICANT Feng, Xiao-Chi

APPLICANT Chen, Francine

APPLICANT Chen, Francine

APPLICANT Chen, Francine

APPLICANT Chen, Francine

APPLICANT Chen, Francine

APPLICANT HOBER 1

APPLICANT BEAZAPH, SINYAM

APPLICANT BEAZAPH, SINYAM

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APPLICANT HOBER 2

APPLICANT SECOND NO SERVICE 2010/041,860

CURRENT PILLING DATE: 202-01-07

NUMBER OF EGO ID NOS: 377

CURRENT FILLING DATE: 202-01-07

SOFTWARE FEASTER for Windows Version 4.0

SEQ ID NO 49

LENGTH: 108

CUBTY MATCH

BEST Local Similarity 100.0%; Score 558; DB 14; Length 108;

MATCHES 108; CONSERVATISEREPERATISCRASOSVESSYLAWYQOKPGQAPRILIYATSSRATGIP

DE TYPE: PRT

ORGANISM: NOW SETILSERFERATISCRASOSVESSYLAWYQOKPGQAPRILIYATSSRATGIP

I BIVITQSRGTISISPERATISCRASOSVESSYLAWYQOKPGQAPRILIYATSSRATGIP

DE THE FESSEG STOFFILTISRIEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108

61 DRFSGSGGTDFTILTISRIEPEDFAVYYCQQYGSSPCSFGGGTKLEIK 108

61 DRFSGSGGTDFTILTISRIEPEDFAVYYCQQYGSSPCSFGGGTKLEIK 108

61 DRFSGSGGTDFTILTISRIEPEDFAVYYCQQYGSSPCSFGGGTKLEIK 108
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61 DRESGSGSGTDFTLTISRLEPEDFAVYYCQOYGSSPCSFGQGTKLEIK 108
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ORGANISM: Homo sapiens
US-10-309-762-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRGANISM: homo sapiens US-10-041-860-375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-10-309-762-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 BIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
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100.0%; Score 558; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 108; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 558; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 108; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                         Sequence 225, Application US/10041860

Fublication No. US20030157109A1

GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Weber, Kiao-Dong
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX. 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 225
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-10-041-860-259
i US-10-041-860-259
i Publication No. US20030157109A1
i GANERAL INFORMATION:
i APPLICANT: Corvalan, Jose R.F.
i APPLICANT: Feng, Xiao-Chi
i APPLICANT: Yang, Xiao-Chi
i APPLICANT: Yang, Xiao-Dong
i APPLICANT: Peng, Xiao
i APPLICANT: Peng, Xiao
i APPLICANT: Gazit, Gadi
i APPLICANT: Gazit, Gadi
i APPLICANT: Bezabeh, Binyam
i TITLE OF INVENTION: ANTHEODIES DIRECTED TO PDGFD AND USES
i TITLE OF INVENTION: THEREOF
i TITLE OF INVENTION: THEREOF
i TITLE OF INVENTION: THEREOF
i TITLE OF INVENTION: THEREOF
i TITLE OF INVENTION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
i NUMBER OF SEQ ID NOS: 377
i SOUTHARE: FESTSEQ for Windows Version 4.0
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CORGANISM: homo sapiens
US-10-041-860-259
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; ORGANISM: homo sapiens
US-10-041-860-225
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LENGTH: 108
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1 BIVLTQSPCTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
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publication No. US20040018198A1

publication No. US20040018198A1

j GENERAL INFORMATION:

APPLICANT: Guida, Masahisa

APPLICANT: Foltz, Ian

APPLICANT: Gallo, Michael

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

TORRENT APPLICATION NUMBER: US/10/309,762

PRIOR APPLICATION NUMBER: 60/337275

PRIOR APPLICATION NUMBER: 60/337275

PRIOR PILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 156

IENGTHAN 108

TENGTHAN 108
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95.5%; Score 533; DB 15; Length 108;
Best Local Similarity 95.4%; Pred. No. 2.8e-41;
Matches 103; Conservative 2; Mismatches 3; Indels (
Sequence 375, Application US/10041860
; Publication No. US2020157109A1
; GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Gravalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Reng, Xiao-Chi
APPLICANT: Wang, Xiao-Chi
APPLICANT: Wang, Xiao-Chi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
ITILE OF INVENTION: ATMIBODIES DIRECTED TO PDGFD AND USES
ITILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 3772-01-07
SEQ ID NO 375
LENGTH: 108
LENGTH: 108
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Best Local Similarity 100.0%; Score 558; DB 14; Length
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 108; Conservative 0; Mismatches 0; Indels
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1 EIVLIQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60

Gaps

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Sequence 804, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INPORMATION:
; APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al.
ITILE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides
; TILE REPERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR PILING DATE: 2000-01-25
; PRIOR PILING DATE: 2000-01-25
; PRIOR PILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,461
; PRIOR PILING DATE: 2000-09-03
; PRIOR PILING DATE: 2000-09-03
; PRIOR PILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: PSESEQ for Windows Version 3.0
; SEQ ID NO 804
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APPLICANT: Tang et al
TITLE OF INVENTION: No. US20030232054Alel Nucleic Acids and Polypeptides
FILE REFERNCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
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                                                                                                                                                                                                                                                                                                                                           Query Match 95.3%; Score 532; DB 15; 1
Best Local Similarity 95.4%; Pred. No. 7.1e-41;
Matches 103; Conservative 2; Mismatches 3;
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95.0%; Score 530; DB 15
Best Local Similarity 94.4%; Pred. No. 2e-40;
Matches 102; Conservative 3; Mismatches
                                                                                                                                                                                                                       OTHER INFORMATION: antibody light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 805, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
   SOFTWARE: Patentin version 3.2
SEQ ID NO 122
SENGTH: 215
TYPE: PRT
                                                                                                                                                   ORGANISM: artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
                                                                   1 BIVLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 123, Application US/10307724

Publication No. US2003023297241

GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
ITILE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFRENCE: 1097-2cip
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT APPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2000-105-04
PRIOR FILING DATE: 2001-05-29
PRIOR PRIOR APPLICATION NUMBER: US 10/006,593
PRIOR FILING DATE: 2001-05-29
PRIOR PRIOR DATE: 2001-05-29
PRIOR PRIOR DATE: 2001-05-29
PRIOR PRIOR DATE: 2001-05-39
PRIOR PRIOR DATE: 2001-05-39
PRIOR PRIOR DATE: 2001-05-39
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Publication No. US20030232972A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
ITILE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFRENCE: 1087-2cip
CURRENT APPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/286,889
PRIOR FILING DATE: 2000-105-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 134
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ORGANISM: artificial sequence
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JS-10-269-711-21
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Publication No. US20030232054A1

GENERAL INFORMATION:

APPLICANT: Hyaeq. Inc.

APPLICANT: Hyaeq. Inc.

APPLICANT: Hyaeq. Inc.

PILE REFERENCE: 21272-017 (785)

CURRENT APPLICATION NUMBER: US/10/291,265

CURRENT APPLICATION NUMBER: US/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-25

PRIOR PILING DATE: 2000-01-3

PRIOR PILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

SOUTHWER OF SEQ ID NOS: 944

SOUTHWER OF SEQ ID NOS: 944

SEQ ID NOS 944

LENGTH: 384
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95.0%; Score 530; DB 15; Length 384;
Best Local Similarity 94.4%; Pred. No. 2e-40;
Matches 102; Conservative 3; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: PASTEREQ for Windows Version 3.0
SEQ ID NO 805
LENGTH: 384
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CORGANISM: Homo sapiens
US-10-291-265-806
                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-805
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US-10-291-265-807
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; Sequence 807, Application US/10291265 ; Publication No. US20030232054A1

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APPLICANT: "Jordy at al TITLE OF INVENTION: "Jordy and Polypeptides TITLE OF INVENTION: No. US20030232054Alel Nucleic Acids and Polypeptides TILE OF INVENTION: No. US20030232054Alel Nucleic Acids and Polypeptides TILE REPERENCE: 21272-017 (785)
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-09-15
PRIOR PLING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 807
LUMBER OF SEQ ID NOS: 944
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 229
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APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Beilly, Edward B.
APPLICANT: Reilly, Edward B.
APPLICANT: Weller, James
APPLICANT: Weller, James
APPLICANT: Weller, James
APPLICANT: Weller, James
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APPLICANT: Weller, James
APPLICANT: Weller, James
APPLICANT: WATISODIES
FILE REFERNCE: 699 US.01
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT FILING DATE: 2002-10-14
NUMBER OF SED ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 108
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.0%; Score 530; DB 15; Best Local Similarity 94.4%; Pred. No. 2e-40; Matches 102; Conservative 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 94.8%; Score 529; DB 12; Best Local Similarity 94.4%; Pred. No. 6.5e-41; Matches 102; Conservative 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/10269711 Publication No. US20040071694A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRGANISM: Homo sapiens
US-10-291-265-807
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US-10-269-711-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: light chain variable region predicted sequence for OTHER INFORMATION: 4B6 from VK A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOS-LU-338-356-4

JOS-LU-338-356-4

JOS-LU-338-356-4

JOSTICATION OF US20040006215A1

JOSTICANT: Keler, Tibor

APPLICANT: Keler, Tibor

APPLICANT: Tream, John

TILE OF INVENTION: HONOR MONOCLONAL ANTIBODIES AGAINST CD30

FILE REFERENCE: MXI-180

FILE REFERENCE: MXI-180

CURRENT FILING DATE: 2003-01-07

PRIOR FILING DATE: 2002-01-09

PRIOR FILING DATE: 2002-08-19

PRIOR FILING DATE: 2002-08-19

PRIOR FILING DATE: 2002-08-19

PRIOR FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 53

SEQ ID NO 4

LENGTH: 108

WANDER PRIOR TOWN HONOR VERSION 4.0

SEQ ID NO 4

LENGTH: 108
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Sequence 9, Application US/09948939;
Publication No. US2020086014A1
GENERAL INFORMATION:
APPLICANT: Korman, Alan J.
APPLICANT: Halk, Edward L.
APPLICANT: Horberg, Nils
APPLICANT: Horberg, Nils
APPLICANT: Horberg, Nils
APPLICANT: Horberg, Nils
APPLICANT: Horberg, Nils
APPLICANT: Horberg, Nils
APPLICANT: Horberg, Nils
APPLICANT: Medarex, Inc.
TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
FILE REFERENCE: 014643-010520US
CURRENT APPLICATION NUMBER: US 60/150,452
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 1999-08-24
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

94.6%; Score 528; DB 12; Length 108;
Best Local Similarity 94.4%; Pred. No. 8e-41;
Matches 102; Conservative 3; Mismatches 3; Indels (
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ORGANISM: Homo sapiens
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US-10-338-366-4
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1 EIVLTGSPGTLSLSPGERATLSCRASGSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP

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Db 1 EIVLTOSPGTLSLSPGERATISCRASQSVSSSYLAWYQOXPGGAPRLLIYGASSRATGIP 60

G1 DRFSGSGSGTDFTLTISSLEPEDFAVYYCQCYGSSPCSFGGGTKLEIK 108

RESULT 15

US-10-371-942-112

SGQUENCE 112, Application US/10371942

SGQUENCE 112, Application US/10371942

SGQUENCE 112, Application US/10371942

SGQUENCE 112, Application US/10371942

SGRUENCE 112, Application US/10371943

SPELICANT: Realest.

SPELICANT: REALEST.

SGRUENCE 11280-001401

CUTRENT PELLONG NAMER: US/10/371,942

CUTRENT PELLONG NAMER: US/10/371,942

CUTRENT PELLONG NAMER: US/10/371,942

SETIL REPERBACE: 10280-001-20

SETIL REPERBACE: 10280-001-20

SETIL REPERBACE: PARTICAL NAMER: US/10/371,942

CUTRENT PELLONG NAMER: US/10/371,942

SETIL NAMER: PARTICAL NAMER: US/10/371,942

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SETIL NAMER: US/10/371,942-112

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SETIL NAMER: US/10/371

SETIL NAMER
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Sequence Seq

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EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42, Application US/08232081B
| Sequence 42, Application US/08232081B
| Patent No. 5886152
| GENERAL INFORMATION:
| APPLICANT: WAKATAIN, TOMOYUKI
| APPLICANT: WIJDENES, JOHN
| APPLICANT: WIJDENES, JOHN
| APPLICANT: WIJDENES, JOHN
| APPLICANT: WIJDENES, JOHN
| APPLICANT: WIJDENES, JOHN
| APPLICANT: WIJDENES, JOHN
| APPLICANT: WIJDENES, JOHN
| APPLICANT: WIJDENES: 42
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADD
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ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATION NUMBER: US/08/232,081B
                                         US-08-472-788A-14-
US-08-472-788A-14-
US-09-456-090A-38-
US-09-456-090A-52-
US-09-456-090A-52-
US-08-276-82-99-
US-08-276-82-99-
US-08-99-575-99-
US-08-99-575-99-
US-08-99-575-99-
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SYENSSON, LECONARD R
REGISTRATION NUMBER: 30,330
REFRENCE/DOCKET NUMBER: 30-3484
TELECOMMUNICATION INFORMATION:
TELEPRANCE/OCKET NUMBER: 20-3484
TELEPRANCE/OCKET NUMBER: 30,330
INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: acids
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Best Local Similarity 94.4%;
Matches 102; Conservative
  TOPOLOGY: linear
MOLECULE TYPE: peptide
  US-08-232-081B-42
\begin{array}{c} 2 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\ 0 & 0 \\
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                                                                                                                                                               ; Search time 15.2961 Seconds (without alignments) 364.511 Million cell updates/sec
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                                                                                                                                                                                                                                                            US-10-041-860-49
558
1 EIVLTQSPGTLSLSPGERAT......CQQYGSSPCSFGQGTKLEIK 108
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1. /GGTZ 6/ptodata/2/iaa/5A_COMB.pep:*

2. /GGMZ 6/ptodata/2/iaa/5B_COMB.pep:*

3. /GGMZ 6/ptodata/2/iaa/6A_COMB.pep:*

4. /GGMZ 6/ptodata/2/iaa/6B_COMB.pep:*

5. /GGMZ 6/ptodata/2/iaa/PCTUS COMB.pep:*

5. /GGMZ 6/ptodata/2/iaa/PCTUS COMB.pep:*

6. /GGMZ 6/ptodata/2/iaa/PGTUS COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-08-488-16
US-08-488-150
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US-09-136-150
US-09-136-150
US-09-456-090A-86
US-09-472-087-65
US-09-472-087-65
US-09-472-087-65
US-09-456-090A-86
US-09-456-090A-86
US-09-456-090A-42
US-09-456-090A-42
US-09-456-090A-42
US-09-456-090A-42
US-09-456-090A-42
US-09-456-090A-42
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US-08-480-090A-42
US-08-480-090A-42
US-08-480-090A-42
US-08-480-090A-42
US-08-480-090A-42
US-08-480-090B-86
US-08-487-200-86
US-08-487-200-86
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                     61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGQGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Raappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Pack, Peter
APPLICANT: Cd. Limin
APPLICANT: Cd. Limin
APPLICANT: Gd. Limin
APPLICANT: Gd. Limin
APPLICANT: Bluckthun, Andreas
ITILE OF INVENTION: Protein/(Poly)peptide libraries
ITILE OF INVENTION: Protein/(Poly)peptide libraries
ITILE OF INVENTION: Protein/(Poly)peptide libraries
APPLICANT: Pluckthun, Andreas
ITILE OF INVENTION: Protein/(Poly)peptide libraries
APPLICANT: New York
STREET: 1251 Avenue of the Americas
CITY: New York
STREET: 1251 Avenue of the Americas
CITY: New York
STREET: 1251 Avenue of the Americas
CITY: New York
CONPUTER: IBM PC compatible
OFFRATION (SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ploppy disk
COMPUTER: IBM PC compatible
OFFRATION NUMBER: BP-B1998
APPLICATION NUMBER: BP-B1998
APPLICATION NUMBER: BP-B1998
APPLICATION NUMBER: BP-B1998
APPLICATION NUMBER: MORPHO/5
TELEFORMURICATION N
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61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
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2.08-488-113B-150
3. Sequence 150, Application US/08488113B
3. Patent No. 5744580
3. GENERAL INFORMATION:
3. APPLICANT: Better, Marc D.
3. APPLICANT: Carroll, Stephen F.
                                                                                                                                                                                                                                          US-09-025-769B-16; Sequence 16, Application US/09025769B; Patent No. 6300064
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MOLECULE TYPE: protein
US-09-025-7698-16
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        Studnika, Gary M.
VENTION: Immunotoxins Comprising Ribosome-Inactivating
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                                                                                                                                                                                                                                                                                                                                                                                                         CURTAIN CONTRACT CONTRACT CONTRACT CONTRACT COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-UN-1995
CLASSIFICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
FILING DATE: 18-APR-1995
FILING DATE: 18-APR-1995
FILING DATE: 10-WAY-1993
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-WAY-1993
FILING DATE: 12-WAY-1993
FILING DATE: 12-WAY-1993
FILING DATE: 10-WAY-1993
FILING DATE: 10-WAY-1993
FILING DATE: 09-DEC-1992
FILING DATE: 09-DEC-1992
FILING DATE: 19-UNH-1992
FILING DATE: 19-UNH-1993
FILING DATE: 10-UNH-1993
FILING DATE: 1
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribor TITLE OF INVENTION: Immunotoxins Comprising Ribor TITLE OF INVENTION: 169
CORRESPONDENCE ADDRESS: 169
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: CORREST: 500 West Madison Street, 34th floor STREET: Illinois SCUNTRY: Illinois
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Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-150
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US-08-477-484B-150
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
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        TITLE OF INVENTION: Pronumber of SEQUENCES: 1'CORRESPONDENCE ADDRESS:
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STRANDEDNESS: do
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US-08-839-765-150
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Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Garry M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
WOMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STRIE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
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                                                                                                                                                                                                                                                            COMPUTER: BUBBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: The PC-DOS/MS-DOS
COMPUTER: The PC-COMPACIBLE
COMPUTER: The PC-COMPACIBLE
COMPUTER: The PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/4691
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/91,707
FILING DATE: 19-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCNICATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELEFORMAUNICATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.CZA
TELEFRAX: 312/707-8889
TELEFRAX: 312/707-8889
TELEFRAX: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11022US07/200-70.P3.C2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-477-484B-150
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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSXLAWYQQXPGQAPRLLIYGASSRATGIP
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Sequence 150, Application US/08819765
Patent No. 6146611
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
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Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4; Indels
                                                                                                                                                             COMPUTER: PORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: EN PC compatible
COMPUTER: EN PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION NUMBER: BCT/US94/05348
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BCT/US94/05348
PRIOR APPLICATION NUMBER: US 08/064,691
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,430
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,707
FILING DATE: US 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: US 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: US 07/787,567
FILING DATE: US 07/787,567
FILING DATE: US 07/787,567
FILING DATE: US 07/787,567
FILING DATE: US 07/787,567
FILING NUMBER: US 07/787,567
FILING NUMBER: 32,918
REFERENCE/DOCKET NUMBER: Z00-70.P4
TELEPRAK: 312/707-8889
TELEFRAK: 312/707-8889
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-389-150
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-610-838-150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
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Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Batter, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DRFSGSGGTDFTLITISRLEPGDFAVYYCQQYGSSPXTFGQGTKVEIX 108
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NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSE: MANDAGEWS, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 60661
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 15-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 32,918
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: 32,918
FILING DATE: 19-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WANACHOLAS: Janet M
REGISTRATION NUMBER: 32,918
REFERRENCE/DOCKET NUMBER: 32,918
REFERRENCE/DOCKET NUMBER: 32,918
REFERRENCE/DOCKET NUMBER: 32,918
REFERRENCE/DOCKET NUMBER: 32,918
REFERRENCE/DOCKET NUMBER: 32,918
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REFERRENCE/DOCKET NUMBER: 32,918
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TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-839-765-150
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1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP
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) Patent No. 6376217
) GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studinka, Garry M.
APPLICANT: Studinka, Garry M.
TITLE OF INVENTION: Proteins
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
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94.1%; Score 525; DB 3; Length 108;
Best Local Similarity 94.4%; Pred. No. 3.3e-42;
Matches 102; Conservative 2; Mismatches 4; Indels
CORRESPONDENCE ADDRESS:
ADDRESSE:
RCHAGGE Madison Street, 34th floor
STREET: 500 West Madison Street, 34th floor
STREET: 500 West Madison Street, 34th floor
STREET: 111inois
CUNTRY: USA
ZIP: 60661
COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: PROBABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTE: PREDABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTE: PREDABLE FORM:
MEDIUM TYPE: PROSPER: PC-DOS/MS-DOS
OFFRATION NUMBER: US/09/136,389
FLING DATE: 12-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FLING DATE: 12-MAY-1996
APPLICATION NUMBER: US 08/064,691
FLING DATE: 12-MAY-1996
APPLICATION NUMBER: US 07/984,430
FLING DATE: 19-MAY-1993
RRIOR APPLICATION NUMBER: US 07/984,430
FLING DATE: 19-UNH-1992
APPLICATION NUMBER: US 07/981,567
FLING DATE: 19-UNH-1992
APPLICATION NUMBER: US 07/981,567
FLING DATE: 19-UNH-1992
APPLICATION NUMBER: 32-918
REFERENCE/DOCKET NUMBER: 32-918
REFERENCE/DOCKET NUMBER: 32-918
REFERENCE/DOCKET NUMBER: 32-918
REFERENCE/DOCKET NUMBER: 32-918
REFERENCE/DOCKET NUMBER: 32-918
REFERENCE/DOCKET NUMBER: 32-918
REFERENCE/DOCKET NUMBER: 32-918
TELEFRAK: 312/707-9155
TELEFRAK: 312/707-9155
TELEFRAK: 312/707-9159
TELEFRAK: 108-MIND OCIDS
INFORMATION FOR SEQ 1D NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108-MIND OCIDS
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1 EIVLTQSPGTLSLSPGBRATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proceedins NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSES: MACHAGE MAGISON Street, 34th floor CITY: Chicago STRTE: 100 West Madison Street, 34th floor CITY: Chicago STRTE: 101inois COUNTRY: USA
ZIP: 60661
COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
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PRICK APPLICATION DATA:
PRICK APPLICATION DATA:
APPLICATION UNBER: US 08/064,691
FILLING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 07/901,707
PILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
PILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: 13-918
ATTORNEY/AGENT INFORMATION:
NAME: MCNICCholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/;
TELECHONE: 312/707-9889
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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; Sequence 50, Application US/09456090A
; Patent No. 6680209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIETCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-09-711-485-150
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                                                                                                                                                                                                   ZUNTAIL O'SA

ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
SOUTWARE: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FLING DATE: 10-MG-1998
APPLICATION NUMBER: US/09/136,389
FLING DATE: 11-MAY-1998
APPLICATION NUMBER: PCT/US94/05348
FLING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FLING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING APPLICATION DATA:
APPLICATION NUMBER: 32,918
REGISTRATION NUMBER: 200-70.P4
TELEBRONE: 312/70.01.01.689
            NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
STREET: MCANDTEWS, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-09-711-485-150
; Sequence 150, Application US/09711485
; Patent No. 6649742
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: 312/707-9155
TELEAX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150: SEQUENCE CHARACTERISTICS: LENGTH: 108 amino acids
TYPE: amino acids
STRANDEDNESS: double
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TILLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-00020008

CURRENT APPLICATION NUMBER: US/09/456,090A

CURRENT PILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 110

SOOTWARE: Patentin Ver. 2.1

LENGTH: 226

TYPE: n=2
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94.0%; Score 524.5; DB 4; Length 226;
Best Local Similarity 95.4%; Pred. No. 8.3e-42;
Matches 104; Conservative 1; Mismatches 3; Indels 1;
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US-09-456-090A-86

Sequence 86, Application US/09456090A

Sequence 86, Application US/09456090A

Ratent No. 6680209

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
CARENT GRAY, Jeff
CURRENT APPLICATION TOWNER: US/09/456,090A

CURRENT APPLICATION TOWNER: US/09/456,090A

CURRENT APPLICATION TOWNER: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
CURRENT FILING DATE: 1999-12-06
CURRENT FILING DATE: 1999-12-06
CURRENT RIPORMATION: NAC-331.
US-09-456-090A-86
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NUTLIER, BILLER B.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
                                                                                                                                                                                                                                                                                                           TYPE: PRT Homo sapiens CHANISM: HOMO SAPIENS TOTHER INFORMATION: M1-23L US-09-456-0908-50
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US-09-472-087-14
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93.4%; Score 521; DB 4; Length 235;
Best Local Similarity 91.7%; Pred. No. 1.8e-41;
Matches 99; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                         Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
APPLICANT: CORVALAN, JOSE R.

TILE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR PILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SEQ ID NOS: 147
SEQ ID NO 14
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.7%; Pred. No. 1.8e-41;
Matches 99; Conservative 6; Mismatches 3
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US-09-456-090A-80
; Sequence 80, Application US/09456090A
; Partent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Homo sapiens
US-09-472-087-14
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ACS-04-274-178
; Sequence 178, Application US/09240274
; Sequence 178, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; TITLE OF INVENTION: SORTION
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION WHRER: 08/09/240,274
; CURRENT APPLICATION WHRER: 60/081,380
; EARLIER APPLICATION WHRER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER FILING DATE: 1998-04-10
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SEQ ID NO 178
; SEQ ID NO 178
; LENGTH: 108
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APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nish
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
LENGTH: 226
TYPE: PRT
ORGANISM: HOMO Sapiens
CHER INPORMATION: M2-20L
US-09-456-090A-80
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US-09-240-274-178
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Search completed: April 21, 2004, 17:05:19 Job time : 16.2961 secs

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MEDLINE=88171307; PubMed=3127527;
Kipps T.J., Tombave E., Chen P.P., Carson D.A.;
Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852 (1988).
-i. DISBASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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BY SIMILARITY.
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Local Similarity 94.4%; Pred. No. 3.3e-48;
tes 102; Conservative 3; Mismatches 3; Indels
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region HAH precursor.
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SWART; SW00406; IGv; 1.
SROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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PIR; PL0022; K3HUHA.
HSSP; P80362; 1WTL.
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129 AA;
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RX MEDLINE=7188439; PubMed=5027703;

RX Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein rT i). IV. The complete amino acid sequence and its significance for RT Th. IV. The complete amino acid sequence and its significance for RT the mechanism of antibody production.";

RL HOPPE-SEVIE'S Z. Physiol. Chem. 353:189-208(1972).

CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) WARKER.

CC -I- MISCELLANEOUS: This is a Bence-Jones protein.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR GO; GO:0006956; IG-1.

DR SMART; SMO0406; IGV; I.

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DR SMART; SMO0406; IGV; I.

DR PROSITE; PS50315; IGILIKE; I.

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DR SMART; SMO0406; IGILIKE; I.

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DR SMART; SMUDLED STATILARITY.
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-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOUGHN ACTIVITY.

PIN: A01892; K3HUSI.

HSSP, P80362; NWIL.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005557; F:antigen binding; NAS.

GO; GO:0005955; P:antigen binding; NAS.

InterPro; IPR007110; Ig-11ke.

InterPro; IPR007110; Ig-11ke.

Ffam; PF00047; 1g; I.

SMART; SM00406; IGv; I.
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Best Local Similarity 92.6%; Pred. No. 7.1e-48;
Matches 100; Conservative 5; Mismatches 3.
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-III region SIE.
Homo sapiens (Human)
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MEDLINE=8871307; PubMed=3127527;
Midper T.J., Tomhave E., Chen P.P., Carson D.A.;
Midper T.J., Tomhave E., Chen P.P., Carson D.A.;
Mutcantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-i- DISERASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo Sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
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                DRFSGSGSGTDFTLTISRLEPEDFAVYCQQYGTSPRTFGQGTKVEIK 128
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 Appa chain V-III region Ti.
Homo sapiens (Human).
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region HIC precursor.
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HSSP; PR0362; 1WTL.
GO; GO:0005576; Centracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Igl-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
SWART; SW00406; IGv; 1.
IMMAT; SW00406; IGV; 1.
Immunoglobulin, V region; Signal.
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129 AA;
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Matches 102; Conserv
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P18136;
01-NOV-1990 (
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AC 21-52,

DT 21-70L-1986

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Pfan; PR00047; 1g; 1.
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOCAMINA ACTIVITY.

BR GLOBELS: KSHUWI.

BR 90: GO: 00005576; KSHUWI.

BR GO; GO: 00005576; C: extracellular; NAS.

BR GO; GO: 0000582; F: antigen binding; NAS.

BR GO; GO: 0000582; F: antigen binding; NAS.

BR GO; GO: 0000582; F: antigen binding; NAS.

BR GO; GO: 0000582; F: antigen binding; NAS.

BR GO; GO: 0000595; P: antigen binding; NAS.

BR GO; GO: 0000595; P: antigen binding; NAS.

BR GO; GO: 0000595; F: antigen binding; NAS.

BR GO; GO: 0000595; F: antigen binding; NAS.

BR GO; GO: 0000595; F: antigen binding; NAS.

BR GO; GO: 0000595; F: antigen binding; NAS.

BR GO; GO: 0000595; F: antigen binding; NAS.

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BR GO; GO: 0000595; F: antigen binding; NAS.

BR GO; GO: 0000595; F: antigen binding; NAS.

BR GO; GO: 0000595; F: antigen binding; NAS.

BR GO; GO: 000595; F: antigen binding; NAS.

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BR GO: 000595; F: antigen binding; NAS.

BR GO: 00059
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                                                                                                                                                                                                                                                                                                                                                                                1 EIVIJQSPGTISISPGERATISCRASQSVSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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                                                                                                                                                                                                                                       Length 109;
                                                                                                                                                                                                                                   Query Match 93.4%; Score 521; DB 1; Length 10
Best Local Similarity 92.6%; Pred. No. 1.5e-47;
Matches 100; Conservative 5; Mismatches 3; Indels
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                                                                                 23 89 BY SIMILARITY.
109 109
109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-III region WoL.
Homo sapiens (Human)
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MEDLINE=82046598; Pubmed=6794615;
PROSITE, PSS0835, IG LIKE, 1.
Immunoglobulin V region.
DISULFID 23 89
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P01623;
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P01619;
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SEQUENCE
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Miletein C.;

Miletein C.;

"The basic sequences of immunoglobulin kappa chains: sequence studies of Bence Jones proteins Rad, Fr4 and B6.";

FEBS Lett. 201301-304(1968).

C. -1- MISCELLANEOUS: This is a Bence-Jones protein.

PIR; A01891; K3HUB6.

R HSSP; P80362; 1WTL.

R InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

R FAMR; SW00406; IGV.

R FAMR; SW00406; IGV.

R PRART; SW00406; IGV.

M Immunoglobulin V region; Bence-Jones protein.

DISULEID

23 89

BY SIMILARITY.
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Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Newkirk M., Chen P.P., Carson J.A., Man idiotypic group, in part predicted by its reactivity with antipeptide antibodies.";
Mol. Immunol. 23:239-244(1986).
Mol. Immunol. 23:239-244(1986).
Mol. Immunol. 23:239-244(1986).
Mol. Go.0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000555; P:immuno response; NAS.
InterPro; IPR007110; Ig-like.
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20-MRR-1987 (Rel. 04, Last sequence update)
20-MR-1989 (Rel. 04, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-III region GOL (Rheumatoid factor).
19 kappa chain V-III region GOL (Rheumatoid factor).
19 kappa chain V-III region GOL (Rheumatoid factor).
19 kappota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
10 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-III region B6.
19 kappa ins (Human).
19 kappa chains (Human).
19 kappa chains (Briman).
19 kappota; Metazoa; (Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Match 90.1%; Score 503; DB 1; Length 16 Local Similarity 86.1%; Pred. No. 1.1e-45; Pred 93; Conservative 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 BIVLTQSPGTLSLSPGESATLSCRASQSVSN-LAWYQQKRGQSPRLLIRDASSRANGIP 79
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1g kappa chain V-III region POM.
1g kappa chain V-III region FOM.
50-NKaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SEQUENCE FROM N.A.

BEDLINES 86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
Human immunoglobulin kappa light chain genes of subgroups II and
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14070 MW; CC8957F0FE3B9012 CRC64;
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Pred. No. 1.1e-41;
4; Mismatches 9
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GO, GO:0005576, C:extracellular; NAS.
GO, GO:0005576, C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003596; IG_V.
Pfam; PF00047; ig; IGV; I.
SMART; SW00406, IGV; I.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                      Nucleic Acids Res. 13:6499-6513(1985).
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Best Local Similarity 87.0
Matches 94; Conservative
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-III region NG9 precursor (Fragment).
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                 Length 109;
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                                               89.6%; Score 500; DB 1; Length 10
89.8%; Pred. No. 2.38-45;
ive 3; Mismatches 8; Indels
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    109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;
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Best Local Similarity 94.7%; Pred. No. 7.1e-42;
Matches 90; Conservative 2; Mismatches 3:
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(Rel. 06, Last sequence update)
(Rel. 38, Last annotation update)
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MEDLINE=84093600; PubMed=6419127;
Bentley D.L.;
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97; Conservative
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01-JAN-1988
15-JUL-1999
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KV3K HUMAN
ID KV3K HUMAN
AC P063I1;
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       SEQUENCE
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               **Riapper D.G., Capra J.D.;

"The amino acid sequence of the variable regions of the light chains
"The amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive 19M anti-gamma globulins.";

"In manual. (Paris) 127C:261-271(1976).

"In MSCELLANBOUGS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

PIR, A1897; KSHUDM.

PIRSP, PROBGS: 1 WHT.

RO; GO:0005576; C:extracellular; NAS.

GO; GO:0005576; P:immune response; NAS.

RO; GO:000595; P:immune response; NAS.

RILEPPRO 1 PROBOTIO; 1g-like.

RILEPPRO 1 PROBOTIO; 1g-like.

RILEPPRO 1 PROBSS; IG_V.

RESPART; SMO0406; IGy.

RESPART; SMO0406; IGy.

RESPART; SMO406; IGY.

RESPART; SMO406; IGY.

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MIDLINES 86177570; PubMed=3083417;

JIXIK F.R., SOTGE J., FONG S., Heitzmann J.G., Curd J.G., Chen P.P.

Goldfien R., Carson D.A.;

"Cloning and sequence determination of a human rheumatoid factor

light-chain gene.";

Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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01-MOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
19 kappa chain V-lir region CLL precursor (Rheumatoid factor).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                                                                                                                                                                                                                                                                        109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           79.9%; Score 446; DB 1; 78.7%; Pred. No. 9.6e-40; iive 12; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; I.
SMART; SM00406; IGv; I.
   MEDLINE=76276460; PubMed=60899;
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tes 85; Conserva
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P04207;
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                                                                                                                                                                                                                                                                                                                                                                                                                    21 EIVWTQSPATLGVSPGERATLSCRASQSVSNN-LAWYQQKPQQPPRLLIYGASTRATGIP 79
                                                                                                                                                                                                                                                                                                                                                                                           1 BIVLTOSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=85087932; PubMed=6440122;
Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups are interdigitated within the VK locus.";
Nucleic Acids Res. 12:9229-9236(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 ARFSGSGSGTEFTLTISKLOSEDFAVYYCQOYNNWEPWTFGQGTRVEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCOOYGS-SPCSFGOGTKLEIK 108
                                                                           FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
GOMPLEMENTARITY-DETERMINING-3.
JKI. SEGMENT.
BY SIMILARITY.
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PRAMEMORK-1.
COMPLEMENTARITY-DETERMINING-1.
PRAMEMORK-2.
                                                          IG KAPPA CHAIN V-III REGION CLL
                                                                                                                                                                                                                                                                                                             Length 129;
                                                                                                                                                                                                                                                                                                           78.7%; Score 439; DB 1; Length 12
79.8%; Pred. No. 6.3e-39;
ive 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                     14275 MW; 5C13B411BE60CC14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain V-III region VG precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 AA
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PIR; A01900; K3HUVG.
HSSP; R80562; UT.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005955; F:antigen binding; NAS.
GO; GO:0005955; P:immune response; NAS.
InterPro; IPR007110; IG-1ke.
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Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                     Local Similarity 79.8
les 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                129 AA;
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                          Immunoglobulin
SIGNAL
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DOMAIN
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HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1996) to Swiss-Prot.
-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-1- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=76004342; PubMed=50995; Schneider M., Hilschmann N.; Schneider M., Hilschmann N.; "The primary structure of a monoclonic immunoglobulin-L-chain of subgroup IV of the kappa type (Bence-Jones protein Len)."; Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
                                                                                                                                                                              1;
                                                                                                                                        DB 1; Length 115;
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COMPLEMENTARITY-DBTERMINING-1.
FRAMEWORK-2.
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                   FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NART, SM00406; 1GV; 1.
PROSITE; PSS0835; IG LIKE; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
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  COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                            8; Indels
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76 COMPLEMENTARITY-DETERMININ
108 FRAMEWORT-3.
115 COMPLEMENTARITY-DETERMININ
108 BY SIMILARITY.
115
12575 MW, 2DE47CDA3A17D555 CRC64;
                                                                                                                                                                                                                                                                                                                           80 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 115
                                                                                                                                      Score 420.5; DB 1
Pred. No. 4.7e-37;
2; Mismatches 8
                                                                                                                                                                                                                                                                                                 61 DRFSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update).
10-OCT-2003 (Rel. 42, Last annotation update).
Ig kappa chain V-IV region Len.
                                                                                                                                                                                                                                                                                                                                                                                                                                            114 AA
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PDB; IEEQ; 03-FEB-01.
PDB; IEEQ; 09-FEB-01.
PDB; IEEQ; 09-FEB-01.
PDB; IECA; 06-MAR-01.
PDB; ILVE; 21-JAN-98.
PDB; SLVE; 28-MAR-01.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; F:antigen binding; NAS.
INCETERO; IPR003110; IG-11ke.
InterPro; IPR003110; IG-11ke.
                                                                                                                                        75.4%;
88.5%;
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Best Local Similarity
Best Local Similarity
Best Conservative
Trapy
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SMART; SM00406; IGv; 1
PROSITE; PS50835; IG L
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                                                         43 1
115 1
115 AA;
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                     DOMAIN
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Length 114;

DB 1;

74.5%; Score 415.5;

Query Match

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                                                             0; Gaps
                     5; Gaps
                                                                                                                                                                                    56 ATGIPDRESGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTXLEIK 108
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups are interdigitated
within the VK locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG KAPPA CHAIN V-III REGION VH. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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Pred. No. 2.2e-36;
4; Mismatches 11; Indels
Similarity 70.8%; Pred. No. 1.5e-36; 80; Conservative 16; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-AUG-1999 (Rel. 38, Last annotation update)
15-AUG-1999 (Rel. 38, Last annotation update)
16 kappa chain V-III region VH precursor (Fragment).
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                        116 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 12:9229-9236(1984)
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SMART; SM00406; 1Gv; 1.
PROSITE; PS50835; 1G LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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Local Similarity 84.4%;
es 81; Conservative
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70
77
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1116
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Best Local Similarity
Matches 80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 DIVWIQSPDSLAVSLGERATINCKSSQSILYSSDNKNYLAWYQQKPGQPPKLLIYWASTR
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01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 Kappa chain V-IV region B17 precursor.
Eukarpota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINES 86601885, Gould H.;
March P., Mills F., Gould H.;
"Detection of a unique human V kappa IV germline gene by a cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
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FRAMENORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMENORK-2.
COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14966 MW; 6413A22FD0738832 CRC64;
81 ARFSGSGGTDFTLTISSLQPEDFAVYCCQDHNLP 116
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                                                                                                                                                                                      134 AA
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GO; GO:0003825; F:antigen binding; NAS.
GO; GO:0003825; F:antigen binding; NAS.
InterPro; IPR00110; Iglike.
InterPro; IPR003596; Ig_v.
Ffan; PF00047; ig; 1.
SWART; SW0046; IGv.
IRR03596; IG v.
IRR03515; PS0835; IG LIKE; 1.
IRRNDG1Dbulin V region; signal.
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                                                                                                                                                                                      PRT;
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Best Local Similarity 66.4%
Matches 75; Conservative
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P06314;
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Search completed: April 21, 2004, 17:02:35 Job time : 10.7339 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 21, 2004, 16:59:07; Search time 12.515 Seconds (without alignments) 830.097 Million cell updates/sec

Title: Perfect score:

US-10-041-860-49 558 1 EIVLTQSPGTLSLSPGERAT.......CQQYGSSPCSFGQGTKLEIK 108 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Descrip	Ig kappa chain V-I	Ig kappa chain V-I	kappa	Ig kappa chain V-I	kappa	Ig kappa chain V-I	kappa chain V-	IG light chain var	kappa	kappa	anti-Sm antibody V	kappa chain		g kappa chain	kappa chain	kappa chain		g kappa chain	kappa chain	b	g kappa chain V	g kappa chain V-	g kappa	g kappa chain -	g kappa chain V-	g kappa chain V	g kappa cha	g kappa chain V-	
5	C30608	H30601	F30601	B30601	0	D30601	C30601	846369	S38643	G30601	S49532	K3HUHA	520636	КЗНОНІ	K3HUTI	F30607	S46375	K3HUSI	A30608	G30607	PH0965	B30608	S20633	S40327	K3HUWL	S20635	E30609	E30607	K3HUB6
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F44151	H441	K	8206	A322	S441	S471	PH0964	JE0242	840325	A3060	B27594	A2374	T0303	8333988	C27
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109	108	109	130	129	110	109	104	215	129	96	116	215	118	108	116
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						88	87	87	87	86	86	86	85	85	82
502	501.5	500	200	499	497.5	495	488.5	488	486.5	485	485	484	479	477	475

## ALIGNMENTS

```
C;Accession: C30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solu M. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IGM autoant: A;Reference number: A30601; MUD:89215279; PMID:2496160
A;Accession: C30608
                                      C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                              A/Status: preliminary
A/Molecule type: protein
A/Ratus: preliminary
A/Molecule type: protein
A/Ratus: 1.108 <60N.
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-91/Domain: immunoglobulin homology <1MM>
kappa chain V-III region (Pie) - human (fragment)
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.. 0 Length 108; 3; Indels Similarity 96.3%; Score 535; DB 2; Similarity 96.3%; Pred. No. 5.3e-38; 94; Conservative 1; Mismatches 3. Query Match Best Local Simi Matches 104;

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Gaps

1 BIVLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP g ઠે

DRFSGSGSGTDFTLIISRLEPEDFAVYYCQQYGSSPWTFGQGTKLEIK 108 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108 61 ઠ 셤

Ig kappa chain V-III region (Gar and Flo) - human (fragment)

D.; Sol

C'Species: Howo sapiens (man)
C'Species: Howo sapiens (man)
C'Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 21-Jan-2000
C'Accession: H30601; E30601
R'Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol. A. Jammunol. 142, 3158-3159, 1889
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoant A;Reference number: A30601; MUID:89215279; PMID:2496160

A,Accession: H30601 A,Status: preliminary A,Molecule type: protein A,Residuss: 1-109 cGON1> A,Accession: E30601

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Cyaccession: D30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solo J. Immunol. 142, 3158-3163, 1989
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoant: A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: D30601
A;Status: preliminary
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| Species 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
                                                                                                      Ig kappa chain V region (G6+ CLL-SMI) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C;Accession: PH0963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EIVLTÖSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP
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J. Exp. Med. 175, 983-991, 1992
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0963
A;Atatus: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-109 < WAR>
61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGQGTKVEIK 108
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A;Residues: 1-109 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
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C;Keywords: heterotetramer; immunoglobulin
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95.2%; Score 531; DB 2; Length 10

Best Local Similarity 95.4%; Pred. No. 1.1e-37;

Matches 103; Conservative 2; Mismatches 3; Indels
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Best Local Similarity 95.4%; Pred. No. 1.1e-37;
Matches 103; Conservative 2; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      File 91/Domain: immunoglobulin homology <IMM>F;24-34/Region: complementarity-determining 1 F;35-50/Region: framework 2 F;51-56/Region: complementarity-determining 2 F;57-89/Region: framework 3 F;57-89/Region: complementarity-determining 3 F;90-97/Region: complementarity-determining 3
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RyGoni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold J. Immunol. 142, 3158-3163, 1369
A; Timmunol. 142, 3158-3163, 1369
A; Title: Structural and idiotypic characterization of the L chains of human IgM autoanti A; Reference number: A30601; MUD:89215279; PMID:2496160
A; Reference number: A30601; MUD:89215279; PMID:2496160
A; Reference number: A30601, MUD:89215279; PMID:2496160
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A; Reference number: A30601, MUD:89215279; PMID:2496160
A; Residual Eype: protein
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C; Reywords: heterotetramer; immunoglobulin
F; 16-91/Domain: immunoglobulin homology < IMM>
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C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
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                               Length 109;
                          Score 535; DB 2; Length 10
Pred. No. 5.3e-38;
1; Mismatches 3; Indels
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Pred. No. 6.5e-38;
4; Mismatches 3;
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species: Homo sapiens (man)
                             Similarity 96.3%;
14; Conservative
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al Similarity 93.5%;
101; Conservative
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Best Local Similarity
Matches 101; Conserv
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Best Local Similarity
Matches 103; Conserv
                               Query Match
Best Local Simil
Matches 104; (
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Journ-1989 #text_change 21-Jan-2000
C;Accession: G30601
R;Goni, P.R; Chen, P.P; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solk
C;Accession: G30601
A;Title: Structural and idiotypic of paracterization of the L chains of human IgM autoant:
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: G30601
A;Accession: G30601
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A;Accession: G30601
A;Accession: G30601
A;Status: preliminary
A;Molecule type: procein
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           A,Molecule type: mRNA
A,Residues: 1-134 <BEN>
A,Residues: 1-134 <BEN>
A,Residues: 1-134 <BEN>
C,Superferences: EMBL: 227170; NID:g415955; PIDN:CAA81694.1; PID:g415956
C,Superfamily: immunoglobulin V region; immunoglobulin
C,Keywords: heteroretramer; immunoglobulin
P;41-116/Domain: immunoglobulin homology <IMM>
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94.8%; Score 529; DB 2; Length 10
Best Local Similarity 95.4%; Pred. No. 1.7e-37;
Matches 103; Conservative 1; Mismatches 4; Indels
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95.0%; Score 530; DB 2;
Best Local Similarity 95.4%; Pred. No. 1.7e-37;
Matches 103; Conservative 1; Mismatches 4
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Pred. No. 2e-37;
1; Mismatches
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Best Local Similarity 95.4%;
Matches 103; Conservative
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Ig kappa chain V-III region (Pay) - human (fragment)
C;Species: Home agains (man)
C;Species: Home agains (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: (30601
T; R.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold J. Immunol. 142, 3158-3163, 1989
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti A;Title: Droliminary
A;Accession: (30601
A;Status: protein
A;Status: protein
A;Status: protein
A;Residues: 1-109 cGON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <INM>
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[G light chain variable region (VU) - human

[G species: Homo sapiens (man)

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S38643
Likappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38643
R;Bensimon, C; Chastagner, P; Zouali, M.
Bibensimon, C; Chastagner, P.; Zouali, M.
A;Bensimon, C.; Chastagner, P.; Zouali, M.
A;Bensimon, C.; Chastagner, P.; Zouali, M.
A;Bensimon, C.; Chastagner, Bata Library, November 1993
A;Bescription: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A;Accession: S38643
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
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Best Local Similarity 95.4%; Pred. No. 1.6e-37;
Matches 103; Conservative 1; Mismatches 4.
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A map position: 2012-2011

G. Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaj facomplex: An immunoglobulin heterotetramer subunit consists of two identical light (kaj haid disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into le Superfamily: immunoglobulin V region; immunoglobulin homology

G. Keywords: autoantipody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin P;1-20/Domain: signal sequence #status predicted <SIGs
F;21-117/Region: V segment
F;21-117/Region: V segment
F;36-111/Domain: immunoglobulin homology <IMM>
F;44-55/Region: complementarity-determining 2
F;71-77/Region: complementarity-determining 3
F;110-117/Region: Complementarity-determining 3
F;118-118/Region: J segment (JKI)
F;43-109/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         );Residues: 1-129 «KIP»
();Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
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Cispectes: 184-Apr-1884 #text_change 21-Jan-2000
Cipate: 24-Apr-1884 #sequence_revision 24-Apr-1884 #text_change 21-Jan-2000
Cipate: 24-Apr-1884 #sequence_revision 24-Apr-1884 #text_change 21-Jan-2000
Cipates: 24-1884 #sequence_revision 23, 189-208, 187-2184
Hoppe-Seyler's 2. Phybaiol. Chem. 353, 189-208, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, A;Reference number: A91651; MUID:72188439; PMID:5027703
A;Reference number: A01885
A;Rocession: A01895
A;Rocession: A01895
A;Rocession: Antological Antological Aproperation A;Residues: 1-109 csUT>
A;Residues: 1-109 csUT>
A;Rocession: Aproperation A;Residues: 1-109 csUT>
C;Comment: This is a Bence Jones protein.
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                                                                                                                                        21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSGYLAWYQQKPGQAPRLLIYAASSRATGIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0021
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                                                                                    1 BIVLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP
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                          Gaps
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J. Exp. Med. 167, 840-852, 1988
A;Title: Autoantibody-associated kappa light chain variable region gene
A;Reference number: PL0021; MUID:88171307; PMID:3127527
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                          Indels
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Pred. No. 2.9e-37;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                       kappa chain precursor V-III region (Hic) - human
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Similarity 94.4%; 32; Conservative
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Best Local Similarity 94.4
Matches 102; Conservative
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                             102;
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Best Local
Matches 10
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap distulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Complex: An immunoglobulin V region; immunoglobulin homology
C;Complex: An immunoglobulin V region; immunoglobulin homology
C;Complex: An immunoglobulin V region; immunoglobulin homology
C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
C;Keywords: utcoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F;21-129/Product: V segment
F;21-117/Region: V segment
F;34-111/Domain: immunoglobulin homology <IMM>
F;34-111/Domain: immunoglobulin homology <IMM>
F;34-111/Region: complementarity-determining 2
F;110-117/Region: complementarity-determining 3
F;110-117/Region: complementarity-determining 3
F;118-129/Region: Josephen (VKI)
F;33-109/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                            Ig kappa chain precursor V-III region (Hah) - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0022
R;Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
A;Kipps, T.J.; Rombave, E.; Chen, P.P.; Carson, D.A.
A;Title: Autcantibody-associated kappa light chain variable region gene expressed in chr
A;Reference number: PL0021; MUID:88171307; PMID:3127527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: PL0022
A, Molecule type: mRNA
A, Residues: 1-129 < KIP>
C, Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C, Genetics:
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   EIVLTOSPGTLSLSPGERATLSCRASOSVSSSYLAWYQQKPGQAPRLLIYATSSRATGIP 60
                                                    21 EIVLTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80
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Cispecies: Homo sapiens (man)
Cipace: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
Cipacesion: S20636
R:Lee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
submitted to the BMSL Data Library, April 1992
A;Reference number: S20631
A;Reference number: S20636
A;Reference number: S20636
A;Reference number: S20636
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A;Reference number: S20631
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                                                                                                                                                            DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPQTFGQGTKLEIK 128
                                                                                                                           DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPCSFGQGTKLEIK 108
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2.4e-37;
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Best Local Similarity 94.4%;
Matches 102; Conservative
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Ig kappa chain V region - human
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A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
A;Cross-references: GDB:136266
A;Cross-references: GDB:136266
A;Cross-references: GDB:136266
A;Map position: 25p12-25p13
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-91/Domain: immunoglobulin homology <IMM>
F;13-89/Disulfide bonds: #status predicted
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Search completed: April 21, 2004, 17:04:25 Job time : 13.515 secs

86, Appl 65, Appl 65, Appl 1, Appli 6, Appli 8, Appli 14, Appl 14, Appl 41, Appl 38, Appl

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APPLICANT: Knappik, Achim
APPLICANT: Rappik, Achim
APPLICANT: Rack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ilag, Vic
APPLICANT: Bock, Deter
APPLICANT: Bock, Peter
APPLICANT: Pucchtum, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STRATE: New York
CONTRY: USA
ZIP: 10021
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY, AGENT INFORMATION:
NAME: James F. Halley, Jr., ERG.
REGISSATION NUMBER: 27, 77,94
REGISSATION NUMBER: 27,794
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llarity 84.0%; Pred. No. 1.4e-44;
Conservative 5; Mismatches 10;
US-08-473-503-86
US-08-483-932-86
US-08-714-017-86
US-08-714-017-86
US-08-300-3868-65
US-08-311-646-65
US-08-911-646-65
US-08-652-816A-6
US-08-652-816A-6
US-08-652-816A-8
US-08-652-816A-8
US-08-652-816A-8
US-08-911-59-16
US-08-910-59-16
US-08-910-59-41
US-08-910-59-41
US-08-910-386A-64
US-08-910-386A-64
US-08-910-386A-64
US-08-911-64-44
US-08-910-386A-64
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEPAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-09-205-769B-36
Sequence 36, Application US/09025769B
Patent No. 6300064
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TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity
Matches 105; Conserv
         April 21, 2004, 17:00:06 ; Search time 17.7039 Seconds (without alignments) 364.511 Million cell updates/sec
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1 QVQLVQSGAEVKKPGASVKV......XDYYYGMDVWGQGTTVTVSS 125
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-1025-769B-22
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US-08-102-121-145
US-08-102-121-145
US-08-102-121-10
US-08-102-121-10
US-08-102-110
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-08-487-113D-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                           OM protein - protein search, using sw model
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Gaps

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-22
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US-09-199-149-3
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                                                                                                   61 AQKPQGRVTMTRDTSISTAYMELSSLRSEDTAVYYCARWGG-----DGFYAMDYWGQGTL 115
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                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYXMHWYRQAPGQGLEWMGWINPNSGGTNY 60
1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIN#VRQATGQGLEWMGWINPNSGNTDY 60
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Pred. No. 1.4e-44;
5; Mismatches 10; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: AOR-1995

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1251 Avenue of the Americas
CITY: New York
CCUNTRY: USA
ZIP: 10021
                                                                                                                                                                                                                                                                             Sequence 59, Application US/09025769B
Fatent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: 1lag, Vic
APPLICANT: Inlag, Vic
APPLICANT: October, Peter
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEC ID NO: 59: SEQUENCE CHARACTERISTICS: LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 84.0%;
Matches 105; Conservative
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                    121 VTVSS 125
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US-09-025-769B-59
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| RESULT 4 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 |
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 AQKFQGRVTITADISTSTAYMELSSLRSEDTAVYYCARPGYGYGGGCYGY-WYWG--VWG 116
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; Sequence 22, Application US/08202047
; Patent No. 5800815
; GENERAL INFORMATION:
    APPLICANT: CHESNUT, Robert W.
    APPLICANT: PAULSON, Margaret J.
    APPLICANT: PAULSON, Jase W.
    APPLICANT: BALDHA, Jose W.
    APPLICANT: BALDHA, Jose W.
    APPLICANT: ALLADHA, Jose W.
    APPLICANT: ALLADHA, Jose W.
    TITLE OF INVENTION: Mary M.
    TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses NUMBER OF SEQUENCES: 4
    CORRESPONDENCE AMERICAL ADDRESS: ADDRESSE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.3%; Score 513; DB 3; Length 125; Best Local Similarity 80.6%; Pred. No. 7.5e-42; Matches 104; Conservative 8; Mismatches 9; Indels
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ZIF: 94105
COMPUTER ERADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
COMPUTER: TEM PC COMPUTER:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 124
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-77
TELECOMMUNICATION INFORMATION:
TELEFORM 115-326-2400
TELEFERNICE/DOCKET NUMBER: 14137-77
TELEFORM FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acide
TYPE: amino acide
TYPE: amino acide
APPLICANT: Jonak, Zdenka L.
APPLICANT: Taylor, Alexander H.
APPLICANT: Traylor, Alexander H.
APPLICANT: Trulli Jr., Stephen H.
APPLICANT: Johanson, Kyung O.
ITILE OF INVENTION: Humanized Monoclonal Antibodies
FILE REPERBACE: P50860
CURRENT APPLICATION: 1998-11-24
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 125
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; ORGANISM: Kabat VH subgroup I
US-09-199-149-3
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60 YAOKEQGEVIMIRDISISTAYMELSSLRSEDIAIYYCVRGFGYS----YNYDYYYGMDV 114
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                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN 60
                                                                                                                                                                                                                                                                                    APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERTANI, ROBERTO L.
APPLICANT: CERTANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: Mc3 ANTI-BA46 ANTIBODY, MCFHODS OF USE THEREOF, AND
TITLE OF INVENTION: MFHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVXVSCKASGYTFTSYDINWVRQATGQGLEWMGWINP-NSGNTD
                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINP-NSGNTD
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Pred. No. 1.5e-41;
7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTY: USA

ZIP: 94304-1018

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATCRNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELEPAN: (415) 494-0792
TELEPAN: (415) 494-0792
ITELEX: 706141
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LEMGTH: 22 main a acids
                                                                                                                                                                                                                                  Sequence 77, Application US/08525539A Patent No. 6309636 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.9%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 WGOGTTVTVSS 125
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                    115 WGOGTTVTVSS 125
                                                                                                                                                                  119 WGOGTLVTVSS 129
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TOPOLOGY:
US-08-525-539A-77
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                                                                                                                                                                                                                  60 YAQKEQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYS----YNYDYYYGMDV 114
                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINP-NSGNTD 59
                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWYRQAPGQGLEWMGWINPYGNGDTN 60
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                                                                                      Query Match 76.0%; Score 510.5; DB 3; Length 128; Best Local Similarity 77.9%; Pred. No. 1.3e-41; Matches 102; Conservative 7; Mismatches 13; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.9%; Score 510; DB 2; Length 129; larity 77.9%; Pred. No. 1.5e-41; Conservative 7; Mismatches 14; Indels
; NAME/KEY: Protein
; LOCATION: 1.128
; OTHER INFORMATION: /label= HUMAN_I
US-08-964-690-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                             115 WGQGTTVTVSS 125
                                                                                                                                                                                                                                                                                                             118 WGQGTLVTVSS 128
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Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGYIFIGSYMHWVRQAPGQGLEWMGRINPNSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.7%; Score 502; DB 1; Length 12:
78.1%; Pred. No. 8.2e-41;
tive 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Human Amu 5-3 heavy chain variable region.
      CORRESPONDENCE ADDRESS:
ADDRESSE: Carella, Byrne, ADDRESSE: Carella, Byrne, ADDRESSE: Cacchi, Stewart & Olstein STRET: 6 Becker Farm Road CITY: Roseland START: New Jersey COUWTRY: U.S.A.
ZIP: 07068
COWPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: New Jersey SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/417,877B
FILING DATE: 07-UTM-1995
CLASSIFICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
APPLICATION NUMBER: 08/119,032
APPLICATION NUMBER: 08/119,032
APPLICATION NUMBER: 08/27,008
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION: NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseein, Ellich M. NAME: Olseei
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INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 78.1:
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201-994-1744
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 GTTVTVSS 125
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Sequence 94, Application US/0847787B

Sequence 94, Application US/0847787B

Sequence 94, Application US/0847787B

GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa
NUMBER OF SEQUENCES: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 YAQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYS----YNYDYYYGMDV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YAQKFQGRVIITADISISTAYMELSSLRSEDTAVYYCARAPGYGSGGCYRGDYXF--DY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGASVKVSCKASGYTFISYDINWVRQATGQGLEWMGWINP-NSGNTD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAIS#VRQAPGQGLEHMGWINPYGNGDTN 60
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                                                                                                                                                                                                                                        APPLICANT: Bendig, Mary M.
APPLICANT: Bendig, Mary M.
APPLICANT: Bendig, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STRIE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.9%; Score 510; DB 5; Length 129; Best Local Similarity 77.9%; Pred. No. 1.5e-41; Matches 102; Conservative 7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01219

FILNG DATE: 25-JAN-1995

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/186,269

FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: SMAITH WIlliam L.

REGISTRATION NUMBER: 1570-14

TELEPHONE: 415-543-9600

TELEPHONE: 415-543-9600

TELEPRA: 415-543-9600

TELEPRA: 415-543-9600

TELEPRA: 415-543-9600

TELEPRA: 415-543-9600

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TELEPRA: 415-543-9600

TELEPRA: 415-543-9600

TYPE: AMINORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: LENGTH: 129 AMINO acids

TYPE: AMINORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: LENGTH: 129 AMINO acids

TYPE: AMINORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: LENGTH: 129 AMINO acids

TYPE: AMINORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: LENGTH: 129 AMINO acids

TYPE: AMINORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: LENGTH: 129 AMINO acids

TYPE: AMINORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: LENGTH: 120 AMINO acids

TYPE: AMINORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE
                                                                                                                                                        Sequence 45, Application PC/TUS9501219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 WGQGTTVTVSS 125
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                                                                                                       PCT-US95-01219-45
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ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,989B
FILING DATE: US/08/477,989B
FILING DATE: OF-UN-1995
CLASSIFICATION NUMBER: 08/407,009
FILING DATE: 29-MAR.1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 24,025
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 GITVIVSS 125
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             CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-561-521-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AQKFQGRVTMTRDTSISTAYMELSRIRSDDTAVYYCARG-----RTEXIVVAEGFDYWGQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 OVOLVOSGAEVKKPGASVKVSCKASGYTFTSYDINWVROATGOGLEWMGWINPNSGNTDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLVQSGAEVKKFGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGRINPNSGGINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 78.1%; Pred. No. 8.2e-41;
Matches 100; Conservative 6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , NAME/KEY: Human Amu 5-3 heavy chain variable region. US-08-472-281A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
APPLICANT: Latinne, Dominique
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Witte-Scharf, Mary
TITLE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carella, Byrne, Bain, Gilfillan,
Cecchi, Stewart & Olstein
                                                                    COMPUTER REABBLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPBERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,281A
FILLING DATE: 07-UN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61750-142
                                                                                                                                                                                                                                                                                               PRICKASIFICATION 1443
PRICKASIFICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MRR-1995
APPLICATION NUMBER: 08/19,032
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-14
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 9 SEQUENCE CHARACTERISTICS: LENGTH: 123 amino acida TYPE: amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 GTTVTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 GTLVTVSS 123
STATE: New Jersey COUNTRY: U.S.A. ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-477-989B-94
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61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYY---GMDVWGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARG-----RTEYIVVAEGFDYWGQ 115
                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYXMHWVRQAPGQGLEMMGRINENSGGINY
                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Bendig, Mary M.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: APPLICANT: Aldaha, Jose
APPLICANT: APPLICANT: Aldaha, Jose
APPLICANT: APPLICANT: Adhesion Molecule VLA-4
ITILE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Commend and Townsend Khourie and Crew
CITY: San Francisco
CITY: San Francisco
                                                                                                                                               Query Match 74.7%; Score 502; DB 2; Length 123; Best Local Similarity 78.1%; Pred. No. 8.2e-41; Matches 100; Conservative 6; Mismatches 14; Indels
NAME/KEY: Human Amu 5-3 heavy chain variable NAME/KEY: region.
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61 AQKEQGRVIMTRDTSISTAYMBLSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AQKFQGRVTMTRDTSISTAYMBLSSLRSEDTALYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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| Sequence 41, Application US/09438954
| Sequence 41, Application US/09438954
| GENERAL INFORMATION:
| APPLICANT: HONG:
| APPLICANT: FANG, Woung Jun
| APPLICANT: KANG, Young Jun
| APPLICANT: KANG, Chang-Yuil
| APPLICANT: YOON, Sung Kwan
| TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
| TITLE OF INVENTION: HUMANIZED COMPOSITION COMPRISING SAME
| TITLE OF INVENTION: HUMANIZED LOSS OF THE REPERENCE: 1303-124P
| CURRENT APPLICATION NUMBER: US/09/438,954
| CURRENT FILING DATE: 1999-11-12
| SEQ ID NO 41
| SEQ ID NO 41
| LENGTH 119
| WADER OF THE TENDER OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMGWINAGNGNTKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Variable OTHER INFORMATION: region of heavy chain of human antibody (M17750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.1%; Score 498; DB 4; Length 119; 78.4%; Pred. No. 1.9e-40; tive 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 74.6%; Score 501; DB 5; Length 119; Best Local Similarity 79.2%; Pred. No. 9.9e-41; Matches 99; Conservative 7; Mismatches 13; Indels.
FILING DAID.

CLASSIPTCATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
RESENCE/DOCKET NUMBER: 15270-14
TELEPHONE: 415-543-960
FILEPHONE: 415-543-960
FILEPAX: 415-543-960
FILEPAX: 415-543-960
FILEPAX: 415-543-960
FILEPAX: 415-543-960
FILEPAX: 415-419-960
FILEPAX: 415-43-960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 78.4*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein PCT-US95-01219-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VTVSS 125
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US-09-438-954-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEMMGWINAGNGNTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OVOLVOSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
74.6%; Score 501; DB 2; Length 119;
Best Local Similarity 79.2%; Pred. No. 9.9e-41;
Matches 99; Conservative 7; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                PCT-US95-01219-10
Sequence 10, Application PC/TUS9501219
GENERAL INFORMATION:
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
          California
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61 SQKPQGRVTITRDISASIAYMELSSLRSEDTAVYYCARG-GY----YGSGSNYWGEGTL 114 121 VTVSS 125 |||||| 115 VTVSS 119 

Search completed: April 21, 2004, 17:05:18 Job time : 26.7039 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 21, 2004, 16:55:26; Search time 54.721 Seconds (without alignments) 645.427 Million cell updates/sec Run on:

672 1 QVQLVQSGABUKKPGASUKV......YDYYYGMDVWGQGTTVTVSS 125 US-10-041-860-48 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\* Database :

geneseqD1990s:\* geneseqD200s:\* geneseqD2001s:\* geneseqD2001s:\* geneseqD2002s:\* geneseqD2003bs:\* geneseqD2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	_	-	Ada89120 MS-Pro-26	Ada89122 MS-Pro-29	Ada89202 Human ant	4	6 MS-Pro		Aaw22841 Human ant	0	Aay34301 IgM antib	~		Abr55813 Heavy cha		Abp44908 Human BLy				Abj18673 Antibody	Aab53510 Human col		Aay34302 IgM antib		Abp45885 Human BLy
SUMMARIES	ΩI	ABR55829	ABP57367	ADA89120	ADA89122	ADA89202	AAW88464	ADA89116		AAW22841	·	•			ABR55813	ADA89115	ABP44908	AAB67619		ABJ18719	ABJ18673	AAB53510	·	AAY34302	AAU74296	ABP45885
	Length DB	122 6				128 6																				Z.
ع ع ع		83.6	83.1	82.4	4	81.5	81.0	80.7	80.6	80.5	80.1	79.9	79.8	79.8	79.8	79.5	79.5	79.3	79.2	78.8	78.8	78.5	78.3	78.3	78.3	78.1
	Score	561.5	558.5	53	551	547.5	544	ď	541.5	541	538	537	536.5	536.5	536	534.5	534.5	533	532.5	529.5	529.5	527.5	526.5		N	524.5
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Abp45396 Human BLy Abp44916 Human BLy Abp44397 Human BLy Ada84194 MS-Pro-55	Human Human Heavy	Human HLA-DR Human Human	Human Human Human	Abp46020 Human BLy Aay71447 Human hea Abp45710 Human BLy Abp44915 Human BLy
ABP45396 ABP44916 ABP44937		AAB62747 ABB5755 ABP45624 ABP45279		ABP46020 AAY71447 ABP45710 ABP44915
			252 251 251 221 5	
78.0 77.9 77.9		77.1	76.7	76.4 76.3 76.2 76.1
523.5 523.5	519.5	518 517.5 517.5	515.5 515.5 515.5	513.5 513 512 512 511.5
22 2 2 2 2 4 6 4 6 4 6 4 6 6 6 6 6 6 6 6	, o n o o	3 <b>60 60</b> 60 3 4 70 40 5	338 399 110	4 4 4 4 2 4 4 4 2 5 4 4 3

## ALIGNMENTS

Heavy chain variable region of anti-Ang-2 antibody IP-2C11 HC. Ŕ ABR55829 standard; protein; 122 02-SEP-2003 (first entry) Homo sapiens ABR55829; ABR55829 

Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic; gynaecological; antinflammatory; osteopathic; antipsoriatic; cancer; angiogenesis; antibody.

2 <u>د</u> -26. .36
/note= "complementarity determining region (CDR)
50. .66
/note= "complementarity determining region (CDR)
96. .112
/note= "complementarity determining region (CDR) Location/Qualifiers Key Region Region Region

WO2003030833-A2 17-APR-2003

11-OCT-2002; 2002WO-US032613

11-OCT-2001; 2001US-0328604P.

(AMGE-) AMGEN INC

Oliner JD;

WPI; 2003-504963/47.

New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.

Claim 1; Page 93; 161pp; English.

The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55769-830) or its fragment. The binding agents are antibodies that recognize and bind to

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New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer cells and without exerting an effect on normal cells expressing TRAIL-Rs nor inducing injury to hepatocytes, for use in therapy of malignant
                                                                                                                                                                                                                                                                                                                  61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTALYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
angiopojetin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, traating cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-2 activity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease, inflammatory disease, inflammatory disease, inflammatory disease, bone-related disease, or psoriasis) in a mammal. The present sequence represents a heavy chain variable region of an anti-Ang-2
                                                                                                                                                                                                                                                                                                                                     The present invention describes antibodies or their functional fragments that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies have cytostatic and apoptotic activities, and can be used in antibody
                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                               1 OVOLVOSGABVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRAIL-R1; TRAIL-R2; antibody; cytostatic; apoptotic; tumour;
                                                                                                                                                                                                                              ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-TRAIL-R antibody related clone 0304 protein SEQ ID NO:29.
                                                                                                                                                                                                   Length 122;
                                                                                                                                                                                                                             Indela
                                                                                                                                                                                                83.6%; Score 561.5; DB 6;
86.4%; Pred. No. 3.2e-44;
ive 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP57367 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 54; Page 62; 92pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-2001; 2001JP-00150213.
09-AUG-2001; 2001JP-00243040.
11-OCT-2001; 2001JP-00314489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAY-2002; 2002WO-JP004816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KIRI ) KIRIN BEER KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-120790/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kataoka S;
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                VTVSS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody therapy
                                                                                                                                                                        Sequence 122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                         antibody
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Matches
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ABP57367
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therapy. The antibodies can be applied as remedies and preventives of diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful in the therapy of malignant tumours, Remedies produced with the antibodies are highly safe, and avoid hepatotoxicity. The present sequence represents an anti-TRAIL-R antibody amino acid sequence from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPTK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a molecule (I) comprising the antigen binding portion of an isolated antibody which has specific binding affinity for a receptor protein tyrosine kinase (RPTK), particularly for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor protein tyrosine kinase; RPTK; receptor protein tyrosine kinase; RPTK; receptor protein tyrosine kinase inhibitor; fibroblast growth factor receptor; FGFK; osteopathic; cytostatic; ophthalmological; bone disorder; cartilage disorder; skeletal dysplasia; achondroplasia; thanatophoric dysplasia; hypochondroplasia; traniosynostosis disorder; thanatophoric dysplasia; malignant cell proliferative disease; dancer; tumour; vision disorder; non-neoplastic angiogenic pathologic condition.
                                                                                                                                                                                                                                                                     61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGY-SYNYDYYYGMDVWGQGT
                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                           20 QVQLVQSGAEMKKPGASVKVSCKTSGYTFTNYKINWVRQAPGQGLEWMGWNNDTDSTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies which have specific binding affinity for a receptor protein tyrosine kinase (RPTK) and block constitutive activation of useful for treating bone and cartilage disorders, or malignant cell proliferative diseases.
                                                                                                                                                                             Gaps
                                                                                                                                                                             1,
                                                                                                                                               Length 145;
                                                                                                                                                                             11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen binding; antibody; specific binding affinity;
                                                                                                                                               DB 6;
                                                                                                                                             Score 558.5; DB 6,
Pred. No. 7.3e-44;
9; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MS-Pro-26-VH amino acid sequence SEQ ID NO:108
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA89120 standard; protein; 126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 52; Page 19; 122pp; English.
                                                                                                                                                83.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2002; 2002WO-IL000495
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                                                                                                                                                                                105; Conservative
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                                                                                                                                                                                                                                                                                                                                          120 TVTVSS 125
                                                                                                                                                                                                                                                                                                                                                                      145
                                                                                                                                                                 Local Similarity
                                                                     sequence represen
present invention
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                                                                                                                    Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                        TVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2003
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                                                                                                                                                  Query Match
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activation of an RPTR. Also described: (1) pharmaceutical constitutive comprising (1) as an active ingredient and a pharmaceutical carrier. Comprising (1) as an active ingredient and a pharmaceutical carrier. Comprising (1) as an active ingredient and a pharmaceutical carrier. Comprising (1) as an active ingredient and a pharmaceutical carrier. Comprising (1) as the presence of (1) when bound to the RPTK, and instructions for use; (3) a method for treatment of bone and cartilage correlated disorders by administering a composition of (1) to the subject; (4) a method for treating the composition of (1); (5) a method for cartilage correlated disorders by administering a composition of (1); (5) a method for contribution of an artibody which blocks ligand-dependent activation of RPTK; (6) an antibody which blocks ligand-dependent activation of RPTK; (6) an antibody which blocks ligand-dependent activation of RPTK; (6) and (9) host cells transformed with the vector. (1) have calls call disorders and ophthalmological activities, and can be used correlators disorders including skeletal disorders such as skeletal disorders disorder (1) and cartilage disorders including skeletal disorders (1) and cartilage disorders including skeletal disorders (1) cartinos ingricans displasia, thanatophoric dysplasia, and cartilage disorders disorders associated with abnormal cartivity, including a heamatoposteic associated with abnormal cartivity, including a heamatoposteic malignant cell proliferative disorders associated with abnormal call carcinoma or mammary carcinoma, tumour formation, primary cull carcinoma or mammary carcinoma, tumour formation, primary cull carcinoma or mammary carcinoma, tumour formation of an explandent cell proliferative disorder may be used for tre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conditions (e.g. haemangiomas, angiofibromas and psoriasis). The F
sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , and non-neoplastic angiogenic pathologic
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diabetic retinopathy)
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Query Match

82.4%; Score 553.5; DB 6; Length 126;
Best Local Similarity 82.9%; Pred. No. 1.8e-43;
Matches 107; Conservative 7; Mismatches 8; Indels 7. Sequence 126 AA;

1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60

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61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSY----NYDYYYGMDVWG 116 61 AQKFQGRVTWTRDTSISTAYMELSSLRSEDTAVYXCARGYWYAYFTYINYGYF---DNWG 117 117 OGTTVTVSS 125 118 QGTLVTVSS 126 占 ઠે g ઠે 엄

MS-Pro-29-VH amino acid sequence SEQ ID NO:110. ADA89122 standard; protein; 127 AA. 20-NOV-2003 (first entry) ADA89122; ADA89122 **2222222222222** 

antigen binding; antibody; specific binding affinity; receptor protein tyrosine kinase; RPTK; receptor protein tyrosine kinase inhibitor; fibroblast growth factor receptor; FGFR; osteopathic; cytostatic; ophthalmological; bone disorder; cartilage disorder; skeletal disorder;

skeletal dysplasia; achondroplasia; thanatophoric dysplasia; hypochondroplasia; craniosynostosis disorder; malignant cell proliferative disease; cancer; tumour; vision disorder; non-neoplastic angiogenic pathologic condition. 

Homo sapiens. Synthetic

WO2002102973-A2

27-DEC-2002.

20-JUN-2002; 2002WO-IL000495.

(PROC-) PROCHON BIOTECH LTD.

20-JUN-2001; 2001US-0299187P.

Yayon A,

WPI; 2003-175236/17.

New antibodies which have specific binding affinity for a receptor protein tyrosine kinase (RPTK) and block constitutive activation of RPTK, useful for treating bone and cartilage disorders, or malignant cell proliferative diseases.

Claim 52; Page 19; 122pp; English.

The present invention describes a molecule (1) comprising the antigen binding portion of an isolated antibody which has specific binding of a fifth of the control of an isolated antibody which has specific binding or a fifth of a receptor protein tyrosine kinse (RPTK), particularly for a fifth of a receptor protein tyrosine kinse specific binding or affith of a receptor protein tyrosine kinse and a carial and actival independent and a pharmaceutical compositions comprising (1) as an actival independent activation of the RPTK, and instructions for use; (3) a method for treatment of those and cartilage reagent for detecting the presence of (1) when bound to the RPTK, and instructions for use; (3) a method for treatment of (1) to the subject; (4) a method for treatment of composition of (1); (4) a method for treatment or antibody which blocks Ingand-dependent activation of an antibody which blocks Ingand-dependent activation of RPTK; (6) an antibody which blocks Ingand-dependent activation of RPTK; (6) or closed mucleic acid molecule encoding a Vi-CR3 DBA region and a VH region; (9) vectors comprising a nucleic acid molecule encoding a Vi-CR3 DBA region and a VH region; (9) vectors comprising a nucleic acid molecule of (6) or cost-coptantic, cycostatic and ophthalmological activation of RPTK; (6) or cost-coptantic, cycostatic and ophthalmological activation of RPTK; (7) and (9) host cells transformed with the vector. (1) have

Cost-coptantic, cycostatic and ophthalmological activation of RPTK; (8) and a VH region; (9) weeters including an activation of yaptasis and composition and prolification of acanthosis injeriens dysplasis, than activated and activation of instances and individual and prolificative disease or disorder with describer the composition and prolificative disorder may be associated with the action of a conspicition may also be used for treating or inhibiting conscient, unmour progression (particularly progression of transitional conscient and pendent references and disorder may be used for treating

Sequence 127 AA

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The present invention describes a protein comprising an immunoglobulin (IG) heavy chain variable (VH) domain and an IG light chain variable (VL) domain. The protein binds a complex comprising a major histocompatibility complex (RHC) and a peptide, does not substantially bind the peptide in the absence of the MHC. The peptide is a peptide fragment of gp100, MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition comprising the novel protein and a carrier; (2) a cytocxic T cell comprising the novel protein and a carrier; (2) a cytocxic T cell comprising one or more nucleic acids for expressing the Ig that binds a complex having an MHC and peptide, does not substantially bind the MHC in the absence of the MHC; (3) an isolated nucleic acid peptide in the absence of the MHC; (3) an isolated nucleic acid comprising a first segment that encodes the Ig variable domain; (4) a comprising a first segment that encodes the Ig variable domain; (4) a novel protein; (5) a transgenic animal whose genome includes heterologous nucleic acid sequences that encodes the novel protein; (6) identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protein comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, useful for preparing a composition for treating or preventing a cancerous disorder.
                                                                                                                                                               61 AQKFQGRUTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNY--DYYYGMDVWGQG 118
                                                                                                                                                                                     61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAVYXCARTWQYGYFYYLDGGYYFDIWGQG 120
                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWYRQAPGQGLEWMGWINPNSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin, Ig; heavy chain variable domain,
light chain variable domain; major histocompatibility complex; MHC;
gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human antibody 2F1 heavy chain amino acid sequence SEQ ID NO:46.
                                           5
    Length 127;
                                        12; Indels
ch 82.0%; Score 551; DB 6; Il Similarity 84.3%; Pred. No. 3.1e-43; 107; Conservative 6; Mismatches 12;
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(TECR ) TECHNION RES & DEV FOUND LTD.
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                                                                                                                                                                                                                                                                                                                                                                                       ADA89202 standard; protein; 128 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                             119 TTVTVSS 125
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  Query Match
Best Local S:
Matches 107,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibody 4B5 polynucleotides and polypeptides - used to develop products for the diagnosis and treatment of cancers and for prophylactic therapy to reduce risk of recurrence.
protein that specifically binds the WHC-peptide complex; (7) expressing an antigen-binding protein; (8) ablating or killing a target cell that displays a peptide on a surface MHC molecule; (9) treating or preventing a cancerous disorder in a subject; and (10) detecting an MHC-peptide complex in a sample. A protein of the invention has cytostatic activity, and can be used in gene therapy. The protein is useful for preparing a composition for treating or preventing a cancerous disorder. The present sequence represents the heavy chain of an antibody which binds to an MHC-peptide complex where the peptide component in as peptide fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma; lung carcinoma; metastasis; anti-idiotype antibody; GD2 antigen; human.
                                                                                                                                                                                                                                                                                                                           1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPQQGLEWMGAINPSGGSTPY
                                                                                                                                                                                                                                                                                                                                                                                61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGY---SYNYDYYYGMDVWGQ
                                                                                                                                                                                                                                                                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises the heavy chain variable region of the recombinant human monoclonal antibody (MAb) 4B5. 4B5 recognises antibodies specific for GD2 antigen antibodies. Antibodies specific for SD2 recognise various cancers including glioblastoma, neuroblastoma, malignant and/or metastatic melanoma, breast adenocarcinoma, lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
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                                                                                                                                                                                                                                  Length 128;
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                                                                                                                                                                                                                                  Score 547.5; DB 6;
Pred. No. 6.6e-43;
5; Mismatches 13;
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.6%;
Matches 107; Conservative
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N-PSDB; AAX06951.
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                                                                                                                                                                                                    Sequence 128 AA;
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prostate adenocarcinoma. The invention encompasses 4B5 derivatives with immunologic specificity for antibodies specific for GD2. These derivatives, or antigen binding fragments, comprise regions of the 4B5 CD4 junction and regions spanning the 4B5 CD8. Coher derivatives include Pab, F(ab')2, Fab', scFv and isolated heavy and light chains (see also AAW8845). Polymucleotide fragments (see AAX06591-54) encoding 4B5 cartiolated heavy and light chains (see also AAW8845). Polymucleotide fragments (see AAX06591-54) encoding 4B5 cortises, including vaccinia virus vectors, comprising these and operating a host immune response to cancer. Products of the invention can be used in the detection and treatment of e.g. astrocytoma, cludeful in generating a host immune response to cancer. Products of the invention can be used in the detection and treatment of e.g. astrocytoma, cludedendrogilona, pependymona, medulloblastoma, printitive neural cetodermal tumour (PNET), pancreatic ductal adenocarcinoma, small and large cell lung adenocarcinoma, squamous cell carcinoma, and liver metastases, bronchoalveoarcarcinoma, breast tumours such as ductal and lobular adenocarcinoma, prostatic adenocarcinoma, cholangiocarcinoma of the bladder, B and T cell ymphoma (nodular and diffuse), plasmacytoma, acute and chronic leukemia, malignant melanoma, soft tissue sarcoma and leiomyosarcoma
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Sequence 476 AA;

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61 AQKEQGRVTMTRDTSISTAYMELSSLRSEDTALYYCVRGFGYSYNYD-----YYYGM 112
                                                                                                                                                                                               80 AQKEQGRUTMIRNISIRIAYMELSGLRSEDTAVYFCAR-----NADNVEMAAIXHYYGM 133
                                                                                                              20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSFDLNWVRQAPGQGLEWMGWMPNSGKTGY 79
                                                                                     1 QVQLVQSGABVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                              Gaps
                                              14;
Length 476;
Query Match 81.0%; Score 544; DB 2; Length 47 Best Local Similarity 78.9%; Pred. No. 5.8e-42; Matches 105; Conservative 7; Mismatches 7; Indels
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MS-Pro-11-VH amino acid sequence SEQ ID NO:104. ADA89116 standard; protein; 126 AA. (first entry) 20-NOV-2003 ADA89116; RESULT 7 ADA8911 

antigen binding; antibody; specific binding affinity; receptor protein tyrosine kinase; RPTK, receptor protein tyrosine kinase inhibitor; receptor protein tyrosine kinase inhibitor; fibroblast growth factor receptor; fGFR; osteopathic; cytostatic; ophthalmological; bone disorder; cartilage disorder; skeletal disorder; hypochondroplasia; thanatophoric dysplasia; hypochondroplasia; traniosynostosis disorder; tumour; vision disorder; non-neoplastic angiogenic pathologic condition.

Homo sapiens. Synthetic

#02002102973-A2.

27-DEC-2002

20-JUN-2002; 2002WO-IL000495

20-JUN-2001; 2001US-0299187P.

(PROC-) PROCHON BIOTECH LTD.

Yayon A,

WPI; 2003-175236/17.

New antibodies which have specific binding affinity for a receptor protein tyrosine kinase (RPTK) and block constitutive activation of RPTK, useful for treating bone and cartilage disorders, or malignant cell proliferative diseases.

Claim 52; Page 18; 122pp; English

The present invention describes a molecule (I) comprising the antigen binding portion of an isolated antibody which has specific binding ordination of an isolated antibody which has specific binding ordinates growth factor receptor (FGFR), and which blocks constitutive affinity for a receptor protein tyrosine kines (EFFR), particularly for a cutiliary agent; (2) \* kit comprising (I), at least one crivation of an active ingredient and a pharmaceutical compositions comprising for use; (3) a method for treatment of bone and artiliage research for detecting the presence of (I) when bound to the RPFK, and instructions for use; (3) a method for treating or inhibiting a cell proliferative disease or clisolated mucleic caid molecule emodality of (1); (5) a method for recenting an entitle comprising the antigen-binding portion of antibody which blocks Ilgand-dependent activation of RPFK; (6) and WH-comparing the antigen-binding portion of an inhibition antibody which blocks Ilgand-dependent activation of RPFK; (6) or clostated mucleic acid molecule emodaling a VI-CRN 3DNA region and WH-comparing by region; (8) vectors comprising an ancivities, and can be used on an artiforage of socrates of socra

Sequence 126 AA;

Gaps 3, DB 6; Length 126; Indels 11; Query Match

80.7%; Score 542.5; DB 6
Best Local Similarity 83.5%; Pred. No. 1.9e-42;
Matches 106; Conservative 7; Mismatches 11

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAVYYCARWGG-----DGFYAMDYWGQGTL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPQQGLEMMGMINPNSGGTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the human antibody heavy chain variable region synthetic sequence VHIB, used in the preparation of a human derived antibody gene library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 80.6%; Score 541.5; DB 2; Length 120; Best Local Similarity 84.0%; Pred. No. 2.2e-42; Matches 105; Conservative 5; Mismatches 10; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCXASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparation of human derived antibody gene library - using synthetic consensus sequences, and signal consensus antibody gene as universal framework for highly diverse antibody libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour antigen; cancer; monoclonal; antibody; heavy chain;
variable region; medicine; pharmacology; biochemistry; CDR;
complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human anti-tumour antigen antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                        Ge L, Moroney S, Plueckthun A;
                                                                                                                                               Human, antibody, preparation, library, VH1B, variable region,
heavy chain, consensus.
                                                                                                                  Human Ab heavy chain variable region VHIB consensus.
                                                                                                                                                                                                                                                                                                                                           (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
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                             AAW27551 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 5B; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Knappik A, Pack P, Ilag V,
                                                                                                                                                                                                                                                                                  96WO-EP003647.
                                                                                                                                                                                                                                                                                                               95EP-00113021
                                                                                     23-JAN-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-179277/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 VTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT87949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 120 AA;
                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                              18-AUG-1995;
                                                                                                                                                                                                                                                                                19-AUG-1996;
                                                                                                                                                                                                                      WO9708320-A1
                                                                                                                                                                                                                                                   06-MAR-1997.
                                                        AAW27551;
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              AAW27551
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80 AQKFQGRVTMTRDTSISTAYMELSRLKSDDTAVYYCARGPKGYCSSTSCYFDYYYYGMDV 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AQKEQGRVIMIRDISISTAYMELSSLRSEDIAIYYCVRG-FGY----SYNYD-YYYGMDV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a human anti-tumour antigen monoclonal antibody (MAb) heavy chain variable region, useful in medicine, pharmacology and blochemistry. The isotype of a MAb secreted by the human/human hybridoma HT was determined to be mu and kappa. Human MAb was purified, and the antigen recognised by human MAb CLN"-IgM identified by western blotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWYRQAPGQGLEMMGWINPNSGGTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human heterodimeric antibody heavy chain variable region SEQ ID NO:108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anticancer human monoclonal antibody variable region sequences - and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.5%; Score 541; DB 2; Length 146; Best Local Similarity 83.5%; Pred. No. 3e-42; Matches 106; Conservative 6; Mismatches 9; Indels
                             . .19
label= sig_peptide
                                                                          20. .146
/label= mat_peptide
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 10; 14pp; Japanese.
                                                                                                                                                                                      69. .85
/label= CDR_2
118. .139
                                                                                                                                50. .54
/label= CDR_1
                                                                                                                                                                                                                                            95JP-00278266.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 WGOGTTV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 WGQGTTV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-276726/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         related DNA and RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HAGI/) HAGIWARA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT75422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 146 AA;
                                                                                                                                                                                                                                                                                                                             JP09100300-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                   15-APR-1997.
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Key
Peptide
                                                                             Peptide
                                                                                                                                   Region
                                                                                                                                                                                         Region
                                                                                                                                                                                                                                               Region
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Hales J;

Corvalan JR, Culwell AR, Green LL, Ha Lipani JA, Liu Q, Weber RF, Yang X;

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This sequence represents the heavy chain of an antibody of the invention. The antibody is a monoclonal antibody (MAD) with an isotype that fixes complement and a variable region that binds to the epitope on CD147 bound by the IGM MAD ABX-CBL, providing that the antibody is not CB11. The MAD can selectively kill activated T-cells, activated B-cells or resting or diseases involving activated T-cells or B-cells or reacting diseases involving activated T-cells or B-cells or monocytes, e.g. graft versus host disease (GVHD), organ transplant rejection diseases (e.g. can all transplant, cancers (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and panoreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases (e.g. arthritis)
                                                                                                                                                                                                                                                                                                     New monoclonal antibody, used for treating e.g. graft versus host disease, cancers, autoimmune diseases and inflammatory diseases.
                                                                                                                                                                                                                                                                                                                                                    Claim 60; Fig 26; 245pp; English
                                                                                                       99WO-US004583.
                                                                                                                                  98US-00034607.
                                                                                                                                                                                                              Blacher RW,
, Ivanov VE,
                                                                                                                                                                                                                                                            WPI; 1999-540816/45.
                                                                                                                                                                                (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                          N-PSDB; AAZ20402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 203 AA;
                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-NOV-2003
                                            W09945031-A2
                                                                                                        03-MAR-1999;
                                                                                                                                                     03-FEB-1999;
                                                                                                                                                                                                               Davis CG, B.
Havrilla N,
                                                                                                                                    03-MAR-1998;
                                                                           10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA89123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a human heterodimeric antibody (I) fragment) having a binding affinity of at least 1x10-8 M to the protective antigen of Bacillus anthracis or a molecule involved in anthrax infection that blocks binding of the antigen or molecule to cell receptors, edema factor and lethal factor. (I) has virucide and antibacterial activities, and can be used in immunotherapy. The antibactive agents, such as anti-toxins or anti-infectives with respect to infective agents, such as anthrax, bornlinum, smallpox, vanezuelan equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The present sequence represents a human heterodimeric antibody heavy chain which is region amino acid sequence, which is used in the exemplification
                                                                                                                                                                                                                                                                                                        New human heterodimeric antibodies or their antibody fragments, useful as anti-toxins or anti-infectives with respect to infective agents, e.g. anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West Nile virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AQXEQGRVTMTRDISISTAYMELSSLRSEDTAIYYCVRGF-----GYSYNYDYYYGMDVW 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AQNFQGWVIMTRDISIRIAYTBLSRLRSDDTAVYXCARDFYSDSSGYYGY-YSYGMDVW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEMMGMINPNTGDTNY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody, CD147; IgM; ABX-CBL; activated T-cell killing, leukaemia; activated B-cell; monocyte; graft versus host disease; therapy; cancer; organ transplant rejection disease; lymphoma; pancreatic disease; autoimmune disease; inflammatory disease; arthritis; binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 538; DB 7; Length 136;
Pred. No. 5.3e-42;
7; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgM antibody CEM 10.12 F3 heavy chain sequence.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 108; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY34301 standard; protein; 203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.1%;
                                                                                                                                    11-FEB-2002; 2002US-0356086F.
29-AFF-2002; 2002US-0376408F.
27-SEP-2002; 202US-0414659F.
25-NOV-2002; 2002US-0428807F.
                                                                                                          11-FEB-2003; 2003WO-US004206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 80.0
Matches 104; Conservative
                                                                                                                                                                                                                 (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQGTTVTVSS 125
                                                                                                                                                                                                                                             Bowdish KS, Wild MA;
                                                                                                                                                                                                                                                                          WPI; 2003-722327/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 136 AA;
                                               WO2003076568-A2.
                  Homo sapiens.
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                                                                           18-SEP-2003
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 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
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                                                                                                                                             12 KKPGASVKVSCKASGYTFTSYDINWYRQATGQGLEMMGWINPNSGNTDYAQKFQGRVTWT
                                                                                                                                                                                           2; Gaps
                                                                                                                                                                                                                                                                                              72 RDISISTAYMELSSLRSEDIAIYYCVRGFGYSYNYDY-YYGMDVWGQGTTVTVSS 125
                                                                                                                                                                                                                                                                                                                                61 RNTSISTAYMELSSLRSEDTAVYYCARG-GHGGSYFYSYYGMDVWGQGTTVTVSS 114
Query Match
79.9%; Score 537; DB 2; Length 203;
Best Local Similarity 88.7%; Pred. No. 1e-41;
Matches 102; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MS-Pro-54-VH amino acid sequence SEQ ID NO:111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA89123 standard; protein; 126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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The present invention describes a molecule (I) comprising the antigen binding affinity for a receptor protein tyrosine kinase (RPTK), particularly for a fibroblast growth factor receptor (FGFR), and which blocks constitutive activation of an active ingredient and a pharmaceutical carrier.

Comprising (I) as an active ingredient and a pharmaceutical carrier.

excipient, or auxiliary agent; (2) a kit comprising (I), at least one carrier to detecting the presence of (I) when bound to the RPTK, and instructions for use; (3) a method for treatment of bone and cartilage comprising the composition of (I) to the subject; (4) a method for treating the composition of (I) to the subject; (5) a method for treating the composition of (I); (5) a method for creating the composition of (I); (5) a method for creating the composition of (I); (5) a method for creating the composition of (I); (5) an instructions for use; (7) and (9) hose ligand-dependent activation of RPTK; (6) an antibody which blocks ligand-dependent activation of RPTK; (6) and a VH region; (7) and (9) hose cells transformed with the vector. (I) have calls transformed with the vector. (I) have (6) or correctly comprising (I) are useful for treating cast and a VH region; (3) and solated mucleic acid molecule encoding VL region and a VH region; (3) and solated mucleic acid molecule encoding VL region and a VH region; (2) and (2) hose and cartilage disorders; including skeletal disorders such as Refer inhibitor. Compositions comprising (I) are useful for treating bene and cartilage disorders; including skeletal disorders such as cannotroplasia, severe achondroplasia, thanatophorate disorder as a RPTK inhibitor. Composition may also be used for treating cast mannary call under Section and a carnical delay and acanthosis ingricans dysplasia or a cranicynostosis disorder (e.g. mannary, colon, cervical, chondroplasia, conference and services and such associated with the action of a constructurely acidated RPTK. The composition may further be associated with the action 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dependent FGFR signaling, such as vision disorders (e.g. neovascular glaucoma, macular degeneration and proliferative retinopathy including diabetic retinopathy), and non-neoplastic angiogenic pathologic conditions (e.g. haemanglomas, anglofibromas and psoriasis). The present
                                                                                                                                                                                                                                                                                                                                                                               New antibodies which have specific binding affinity for a receptor protein tyrosine kinase (RPTK) and block constitutive activation of useful for treating bone and cartilage disorders, or malignant cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions (e.g. haemangiomas, angiofibromas and psoriasis). The psequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 52; Page 19; 122pp; English
                                                                                                                                                                                          20-JUN-2001; 2001US-0299187P.
                                                                                                                                            20-JUN-2002; 2002WO-IL000495
                                                                                                                                                                                                                                        (PROC-) PROCHON BIOTECH LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative diseases.
                                                                                                                                                                                                                                                                                                                                    WPI; 2003-175236/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 126 AA;
                                             WO2002102973-A2.
  Homo sapiens
                                                                                           27-DEC-2002
                                                                                                                                                                                                                                                                                        Yayon A,
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QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY Score 536.5; DB 6; Length 126; Pred. No. 6.7e-42; 5; Mismatches 14; Indels 3: Query Match

Best Local Similarity 82.7%; Promatches 105; Conservative 5;

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61 AQKFQGRVTWTRDTSISTAYWELSSLRSEDTAVYYCARNWAYT-NYQYVNWPHFDYWGG 119 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGWINPNSGGTNY 119 TTVTVSS 125 120 TLVTVSS 126 8 ઠે 원

BLys, B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunombulatory; antirheunatic; antiAIDS; vaccine, cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erychematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome. Human BLyS binding scFv SEQ ID 1729. ABP45718 standard; protein; 247 AA, (first entry) 19-AUG-2002 ABP45718;

of RPTK,

15-JUN-2001; 2001WO-US019110. 16-JUN-2000; 2000US-0212210P WO200202641-A1. Homo sapiens. 10-JAN-2002. 

17-OCT-2000; 2000US-0240B16P. 16-MAR-2001; 2001US-0276248P. 21-MAR-2001; 2001US-0277379P. 25-MAY-2001; 2001US-0293499P.

CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY. HUMA-) HUMAN GENOME SCI INC

Hilbert D; Choi GH, Vaughan T, Ruben SM, Barash SC,

WPI; 2002-114799/15.

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

Claim 1; Page 2465-2466; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides: BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell correction and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS on seasociated with aberrant expression of BLyS. They may to diagnose disease associated with aberrant expression of BLyS. They may also be amontal to treat diseases associated with aberrant ELyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lipus erythematosus, theumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the interpolates and fragments of the antibodies described in the method of invention

Sequence 247 AA;

The present

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55769-830) or its fragment. The binding agents are antibodies that recognize and bind to anglopoietin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired anglogenesis, treating cancers, inhibiting undesired anglogenesis, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangloblastoma, haemangloblastoma, arteriosclerosis, inflammatory disease, inflammatory disease, inflammatory disease, inflammatory disease,
                                                                                                                                       AQKFQGRVTWTRDTSISTAYWELSRLRSDDTAVYYCARGY-YDILTGYYDAFDIWGKGTM 119
                                                                                                                        61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                            9
                                                                   60
                                                                                  1. QVQLVQSGAEVKKFGASVKVSCKASGYTFTSYYMHWVRQAFQQGLEWMGWINPNSGGTNY
                                                                   QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                      Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic;
gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
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                                         1;
              Length 247;
                                                                                                                                                                                                                                                                                                                                                              Heavy chain variable region of anti-Ang-2 antibody FJ-G11 HC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96. .115
/note= "complementarity determining region
                                         Indels
                       .4e-41;
              DB 5;
              Score 536.5;
Pred. No. 1.4e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                             ABR55813 standard; protein; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 92; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001; 2001US-0328604P.
             79.8%;
ilarity 81.6%;
Conservative 6
                                                                                                                                                                                                                                                                                                                                    (first entry)
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96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26. .36
/note= "
                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-504963/47.
                                                                                                                                                                                VIVSS 125
                             Similarity
                                                                                                                                                                                                         124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003030833-A2
                                                                                                                                                                                                        VIVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                    02-SEP-2003
                                       102;
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                Query Match
                              Local
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Region
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Matches
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The present invention describes a molecule (I) comprising the antigen binding portion of an isolated antibody which has specific binding affinity for a receptor protein tyrosine kinase (RPTK), particularly for a tibroblast growth factor receptor (FGFR), and which blocks constitutive activation of an RPTK. Also described: (I) pharmaceutical compositions comprising (I) as an active ingredient and a pharmaceutical carrier,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibodies which have specific binding affinity for a receptor protein tyrosine kinase (RPTK) and block constitutive activation of RPTK, useful for treating bone and cartilage disorders, or malignant cell proliferative diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor protein tyrosine kinase; RPTK; receptor protein tyrosine kinase inhibitor; receptor protein tyrosine kinase inhibitor; receptor protein tyrosine kinase inhibitor; cytostatic; ophibaloplast growth factor receptor; descoptor; ophibaloplasta; barder; cartilage disorder; skeletal displasia; achondroplasia; thanatophoric dysplasia; hypochondroplasia; caniosynostocais disorder; hypochondroplasia; caniosynostocais disorder; haliomat cell proliferative disease; cancer; tumour; vision disorder; non-neoplastic angiogenic pathologic condition.
                                                                                                                                                                                                                                                                     61 AQKFQGRVTMTRDISISTAYMELSSLRSEDTALYYCVRGFGYSYNYDYYYGMDVWGQGTT
                                                                                                                                                                                                                                                                                        61 AQKLQGRVIMITDISISIAYMBLRSLRSDDJAVYXCARDRGIAARSAYYKMDVWGQGTT
                                                                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPQQGLEWMGWISAYNGNTNY
                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                Gaps
disease, bone-related disease, or psoriasis) in a mammal. The prest
sequence represents a heavy chain variable region of an anti-Ang-2
antibody
                                                                                                                                                                ö
                                                                                                                            Length 125;
                                                                                                                                                                16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen binding, antibody; specific binding affinity;
                                                                                                                           Score 536; DB 6;
Pred. No. 7.4e-42;
7; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MS-Pro-2-VH amino acid sequence SEQ ID NO:103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA89115 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 42; Page 18; 122pp; English.
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                                                                                                                                79.8%;
                                                                                                                                             Best Local Similarity 81.6%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PROC-) PROCHON BIOTECH LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-175236/17.
                                                                                                                                                                                                                                                                                                                                              VIVSS 125
                                                                                                                                                                                                                                                                                                                                                                                  VTVSS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                Sequence 125
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                                                                                                                                Query Match
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reagent for detecting the presence of (1) when bound to the RPTK, and reagent for detecting the presence of (1) when bound to the RPTK, and instructions for use; (3) a method for treatment of bone and cartilage related disorders by administering a composition of (1) to the subject; (4) a method for treating or inhibiting a cell proliferative disease or disorder by administering the antigon-binding portion of an antibody which blocks ligand-dependent activation of RPTK; (6) an isolated nucleic acid molecule encoding a VL-CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VL-CDR3 DNA region; (8) vectors comprising nucleic acid molecule of (6) or (7), and (9) host cells transformed with the vector. (1) have controlled transformed with the vector. (1) have cost expands. (2) cost expands (2) and (3) host cells transformed with the vector. (1) have cost expands (2) and (3) host cells transformed with the vector. (1) have cost expands (2) and (3) host cells transformed with the vector. (1) have cost expands (2) and (3) host cells transformed with Anatophoric dysplasia, expression for treating of a propersion of a craniosynostosis of counthosis nigricans dysplasia or a craniosynostosis disorder (e.g. hypochondroplasia, severe achondroplasia with developmental delay and acanthosis nigricans). The composition may also be used for treating or inhibiting malignant cell proliferative disease or disorder associated with abnormal RPTK activity, including a haematopotesic of cranical, chondrosarcoma or osteosarcoma), tumour formation, primary tumour formations and mammary carcinarly progression of transitions and cell carcinoma or mammary carcinarly progression of cell carcinoma or mammary carcinarly dependent formations and further be used for treating constitutively activated RPTK, or with ligand-dependent extraorlar degeneration and proliferative dependent or mammary described with ligand-dependent formations and incorder as sociated with ligand-dependent formations as vision and sociated with ligand-dependent 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conditions (e.g. haemangiomas, angiofibromas and psoriasis). The j
sequence is given in the exemplification of the present invention
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Sequence 118 AA;

1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60 Gaps Query Match 79.5%; Score 514.5; DB 6; Length 118; Best Local Similarity 82.5%; Pred. No. 9.6e-42; Matches 104; Conservative 6; Mismatches 7; Indels 9 ઠ

120 TVTVSS 125

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셤 ઠ 113 LVTVSS 118

Search completed: April 21, 2004, 17:01:52 Job time : 60.721 secs

Sequence 349, App Sequence 205, App Sequence 242, App Sequence 211, App Sequence 219, App Sequence 219, App Sequence 216, App Sequence 217, App Sequence 213, Appl Sequence 239, App Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 46, App Sequence 1729, App Sequence 1729, App Sequence 1729, App Sequence 213, Appl Sequence

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61 AQKFQRVIMTRDISISTAYMBLSSLRSEDIAIYYCVRGFGYSYNYDYYYGMDVMGQGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQKFQGRVTMTRDTSISTAYMELSSLBTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 672; DB 14; Length 125; Best Local Similarity 100.0%; Pred. No. 1e-56; Matches 125; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Peng, Xiao-Chi
APPLICANT: Peng, Xiao-Chi
APPLICANT: Peng, Xiao-Dong
APPLICANT: Peng, Xiao-Dong
APPLICANT: Peng, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Bazabeh, Binyam
ITILE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
ITILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FREESE for Windows Version 4.0
SEQ ID NO 48
ILBNGTH: 125
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 48, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
    ORGANISM: homo sapiens
US-10-041-860-48
    JS-10-041-860-48
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544
                                     TYPE: PRT
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Sequence 237, App
Sequence 237, App
Sequence 203, App
Sequence 203, App
Sequence 240, App
Sequence 240, App
Sequence 201, App
Sequence 238, App
Sequence 238, App
Sequence 238, App
Sequence 238, App
Sequence 238, App
                                                                             April 21, 2004, 17:03:52 ; Search time 41.309 Seconds (without alignments) 836.607 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 48, F
                                                                                                                                       672
1 QVQLVQSGAEVKKPGASVKV......YDYYYGMDVWGQGTTVTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/BEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*

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6: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-041-860-200

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US-10-041-860-372

US-10-041-860-38

US-10-041-860-203

US-10-041-860-240

US-10-041-860-240

US-10-041-860-288

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US-10-041-860-288

US-10-041-860-288

US-10-041-860-288

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US-10-041-860-204

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US-10-041-860-204
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Maximum Match 100%
Listing first 45 summaries
                                                         - protein search, using sw model
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Maximum DB seq length: 200000000
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                                                           protein
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61 AQKFQGRVTMTRDTSISTAYMBLSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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                                                                                                                                                                                                                                                                                               61 AQKEQGRVTMTRDISISTAYMELSSLRSEDTALYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                                                                    61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNXDYYYGMDVWGQGTT 120
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Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 125; Conservative 0; Mismatches 0; Indels 0;
                      DB 14; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 372. Application US/10041860

Publication No. U920030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Reng, Xiao-Chi
APPLICANTION: Reng, Xiao-Chi
APPLICANTING PRINTING Reng, Xiao-Chi
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                                                                                           Indels
                      Query Match 100.0%; Score 672; DB 14; Best Local Similarity 100.0%; Pred. No. 1e-56; Matches 125; Conservative 0; Mismatches 0;
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GENERAL INFORMATION: APPLICANT: Corvalan, Jose R.F., APPLICANT: Toffa, Xiao-Chi, APPLICANT: Feng, Xiao, APPLICANT: Yang, Xiao-Dong, APPLICANT: Gazit, Gadi, APPLICANT: Gazit, Gadi, APPLICANT: Weber, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
, ORGANISM: homo sapiens
US-10-041-860-372
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Publication No. US20030157109A1

GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Teng, Xiao-Dong
APPLICANT: Rencine
APPLICANT: Razit, Gadi,
APPLICANT: Razit, Gadi,
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ATTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
TILE REFERENCE: ABGENIX: 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FRAISEQ for Windows Version 4.0
SED ID NO 237
LENGTH: 125
                                                                                                                                                                                                                              Sequence 2000, Application US/10041860
Fublication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Gravian, Jose R.F.
APPLICANT: Chan, Xiao-Chi
APPLICANT: Chan, Xiao-Chi
APPLICANT: Chan, Francine
APPLICANT: Chan, Francine
APPLICANT: Gait, Gadi
APPLICANT: Beaber, Richard
APPLICANT: Beaber, Binyam
TITLE OF INVENTION: THEREOF
FILE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX: 051A
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 672; DB 14; Length :
Best Local Similarity 100.0%; Pred. No. 1e-56;
Matches 125; Conservative 0; Mismatches 0; Indels
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; ORGANISM: homo sapiens
US-10-041-860-237
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; ORGANISM: homo sapiens
US-10-041-860-200
                                             VIVSS 125
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US-10-041-860-200
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94.9%; Score 638; DB 14; Length 125;
Best Local Similarity 94.4%; Pred. No. 1.9e-53;
Matches 118; Conservative 3; Mismatches 4; Indels (
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Best Local Similarity 94.4%; Pred. No. 1.9e-53;
Matches 118; Conservative 3; Mismatches 4; Indels
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| Publication No. US20030157109A1
| GENERAL INFORMATION:
| APPLICANT: Corvalan, Jose R.F.
| APPLICANT: Peng, Xiao-Chi
| APPLICANT: Yang, Xiao-Dong
| APPLICANT: Yang, Xiao-Dong
| APPLICANT: Yang, Xiao-Dong
| APPLICANT: Real (Applicant) APPLICANT: APPLICANT: Hancine
| APPLICANT: Real (Applicant) APPLICANT: Richard
| APPLICANT: Bezabeh, Binyam
| TITLE OF INVENTION: ATHEREOF;
| TITLE OF INVENTION: THEREOF;
| TITLE OF INVENTION: THEREOF;
| TITLE OF INVENTION: THEREOF;
| TITLE OF INVENTION: AND USER: US/10/041,860
| CURRENT APPLICATION NUMBER: US/10/041,860
| CURRENT APPLICATION NUMBER: 2002-01-07
| NUMBER OF SEQ ID NOS: 377
| SOFTWARE: FREESEQ for Windows Version 4.0
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENTX: 0514
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 125
                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: homo sapiens
US-10-041-860-38
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ORGANISM: homo sapiens

US-10-041-860-203
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LENGTH: 125
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Sequence described and the sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of seq
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APPLICANT: COTVALAIN, JOSE R.F.
APPLICANT: Teng, Xiao-Chi
APPLICANT: Peng, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Annoine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Rezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION UNDERS: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOCTWARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 343
LENGTH: 125
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CORGANISM: homo sapiens
US-10-041-860-240
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ORGANISM: homo sapiens
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CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 201
LENGTH: 126
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 288, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
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US-10-041-860-238
; Sequence 238, Application US/10041860
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; ORGANISM: homo sapiens
US-10-041-860-288
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                                                                                                                                                               61 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYGXDYYYGMDVWGQGTT 120
                                                                                                                                  61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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                                                                                  1 QVQLVQSGAEVKKFGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWMNFNSGNTGY 60
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APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Peng, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Reber, Richard
APPLICANT: Reber, Richard
APPLICANT: Resabeh, Binyam
TITLE OF INVENTION: THEREOF
FILE REPERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 3772-01-07
SEQ ID NOS: 3772-01-07
SEQ ID NOS: 3772-01-07
SEQ ID NOS: 3772-01-07
SEQ ID NOS: 3772-01-07
SEQ ID NOS: 3772-01-07
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| Publication No. US20030157109A1
| GENERAL INFORMATION:
| APPLICANT: Corvalan, Jose R.F.
| APPLICANT: Feng Xiao-Chi
| APPLICANT: Yang, Xiao-Chi
| APPLICANT: Yang, Xiao-Dong
| APPLICANT: Yang, Xiao-Dong
| APPLICANT: Rendine
| APPLICANT: Rancine
| APPLICANT: Rancine
| APPLICANT: Reber, Richard
| APPLICANT: Rezabeh, Binyam
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| FILE REFERENCE: ABGENIX.051A
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
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US-10-041-860-201
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61 AQKFQGRVTWIRNTSISTAYMELSSLRSEDTAVYYCAREGIAVAGTYYYYYGMDVWGQGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Feng, Xiao
APPLICANT: Feng, Xiao-Dong
APPLICANT: Then, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazir, Gadi
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOUTHARR: FastSEQ for Windows Version 4.0
SEQ ID NO 288
LENGTH: 126
Query Match

88.3%; Score 593.5; DB 14; Length

Best Local Similarity 89.7%; Pred. No. 3.4e-49;

Matches 113; Conservative 4; Mismatches 8; Indels
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Query Match
Best Local Similarity 87.3
Matches 110; Conservative
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ORGANISM: homo sapiens
US-10-041-860-204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 FOGRVTMTRDTSISTAYMELSSLRSEDTALYYCVR-GFGYSYNYDYYYGMDVWGQGTTVT 122
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US-10-041-860-40

Sequence 40, Application US/10041860

Publication No. US20030157109A1

GENERAL INFORMATION

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Find, Xiao-Chi

APPLICANT: Find, Xiao-Chi

APPLICANT: Fend, Xiao-Chi

APPLICANT: Gadi

APPLICANT: Gadi

APPLICANT: Gazir, Fancine

APPLICANT: Gazir, Fancine

APPLICANT: Bezabeh, Binyam

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES

TITLE REFERENCE: ASSENIX, 051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT APPLICATION NUMBER: US/10/041,860

MUMBER OF SEQ ID NOS: 377

SOFTWARE: FastSEQ for Windows Version 4.0

TENDENCE: TENDENCE: ANTIBODIES

SEQ ID NO 40
                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Reber, Richard
APPLICANT: Beber, Binyam
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: US/200-01-07
NUMBER OF SEQ. ID NOS: 377
NUMBER OF SEQ. ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 86.2%; Score 579.5; DB 14; Length Best Local Similarity 89.4%; Pred. No. 7.3e-48; Matches 110; Conservative 4; Mismatches 8; Indels
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Publication No. US20030157109A1 GENERAL INFORMATION:
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ORGANISM: homo sapiens
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ORGANISM: homo sapiens
US-10-041-860-238
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; SEQ ID NO 241
; LENGTH: 126
; LENGTH: 126
; ORGANISM: home sapiens
US-10-041-860-241

Query Match
Best Local Similarity 87.3%; Pred. No. 1.86-47;
Matches 110; Conservative 5; Mismatches 10; Indele 1; Gaps 1;
Matches 110; Conservative 5; Mismatches 10; Indele 1; Gaps 1;
Matches 110; Conservative 5; Mismatches 10; Indele 1; Gaps 1;

Qy | QVQLVQSGABYKKPGASVKVSCKASGYFFYSYDINWYRQATGQGLEWMGWNIPNSGNIPY 60

Qy | QVCQCABVKKRGASVKVSCKASGYSFTSYDINWYRQATGQGLEWMGWNIPNNGNITCY 60

Qy | GI AQKFQGRVTMTRDTSISTAYMELSSLRSEDTALYYCCARDIVVVVTATDYYYGMDVWGQGT 120

Qy | 120 TVTVSS 125

Db | 121 TVTVSS 125

Db | 121 TVTVSS 126

Search completed: April 21, 2004, 17:13:22
Job time: 42.309 secs
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1 QVQLVQSGABVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Homo sapiens putative microfibrillar protein with Ig-like domain 3 mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
Submitted (UUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY039025; AAK82649.1;
InterPro; IPR003596; Ig-.
InterPro; IPR003596; Ig-.
Pfam; PR00447; ig1.
PRART; SM04406; IGV: 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 159 AA; I7497 MW; 5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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74.0%; Score 497.5; DB 4; Length 159;
Best Local Similarity 74.0%; Pred. No. 1.2e-42;
Matches 97; Conservative 12; Mismatches 15; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
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  PRELIMINARY;
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SEQUENCE FROM N.A.
NCBI_TaxID=9606;
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672
1 QVQLVQSGAEVKKPGASVKV......YDYYYGMDVWGQGTTVTVSS 125
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Q921WT1
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Gapop 10.0 , Gapext 0.5
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Gaps

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RESULT 2 Q9UL94

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61 AQKFOGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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Homo saplens (Human).
Elwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin reactive autoantibodies in rheumatic carditis and normal
fetus",
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                                                                                                                                                                                                                                                                                                                                                                                                        4; Length 125;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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EMBL; AF035022; AAD56258.1; -.

EMBL; AF035022; AAD56258.1; -.

INESP; POIT72; 2F84.

InterPro; IPR00310; Ig-like.

InterPro; IPR0047; ig-like.

FRAM; PR00407; ig-like.

PROSITE; PS50835; IG-like; 1.

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SEQÜENCE 124 AA; 13580 MW; IBAAACBD96ACD2A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Indels
                                                                                                                                                                                                                                                                                                                                      125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
Query Match
73.5%; Score 494; DB 4;
Best Local Similarity 76.0%; Pred. No. 2.1e-42;
Matches 95; Conservative 9; Mismatches 21;
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Homo sapines (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCDI_TaxID=9606;
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fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.5%; Score 494; DB 4; Length 119; Best Local Similarity 76.0%; Pred. No. 2e-42; Matches 95; Conservative 10; Mismatches 14; Indels
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01-WAY-2000 (TrEMBLrel. 13, Created)
10-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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119 AA; 13205 MW; 13E64F5345F4A16E CRC64;
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EMBL; AF035020; AAD56256.1; -
HSSP; PO1810; 2FBG.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; FR00407; Ig; 1.
SMART; FR00406; IGv.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER
II9 119 119
SEQÜENCE 119 AA; 13205 MW; 13E64F5345F4A16E
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                    139 WGQGTTVTVSS 149
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Q96GA6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
"Identification and characterization of SNG66, a Ig-like gene which is submitted (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (JUN-2000) to the EMBL, Path Solor (J
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Best Local Similarity 70.0%; Pred. No. 1.2e-39;
Matches 91; Conservative 13; Mismatches 16; Indels 10; Gaps
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo săpiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
111—12xID=9606;
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TISSUE-Prostate;
Strausberg R.;
Strausberg R.;
Submitted (AFR-2001) to the EMBL/GenBank/DDBJ databages.
EMBL; BC005951; AAH05951.1; -.
INERP. PO1789; IMCR.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003106; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
SNCG6 protein.
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    VIVSS 125
                                                                         VIVSS 124
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Strauberg R.;
Strauberg R.;
Submitted (UTL-2001) to the EMBL/GenBank/DDBJ databases.

B. EMBL; BC009851. AAH09851.1;
P. EMBL; BC009851.3 AAH09851.1;
P. EMBL; BC00085290. S15590.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0006352; P:tregulation factor activity; IEA.

GO; GO:0006355; P:tregulation of transcription, DNA-dependent; IEA.

InterPro; IPR00110; Ig-like.

R. InterPro; IPR00110; Ig-like.

InterPro; IPR001596; Ig-V.

R. PROSTIE; PR00041; HTH ARAC_FAMILY_1; 1.

PROSTIE; PS00041; HTH ARAC_FAMILY_1; 1.

R. PROSTIE; PS00041; HTH ARAC_FAMILY_1; 1.

R. PROSTIE; PS00041; HTH ARAC_FAMILY_1; 1.

R. PROSTIE; PS000290; IG-MC; 3.

R. PROSTIE; PS000290; IG-MC; 3.

R. Hypothetical protein.

SOUTH OF THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO THE PROSTIES TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OVOLVOSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                         Query Match 70.0%; Score 470.5; DB 4; Length 500; Best Local Similarity 71.9%; Pred. No. 2.8e-39; Matches 92; Conservative 11; Mismatches 22; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 69.6%; Score 468; DB 4; Length 614; Best Local Similarity 73.6%; Pred. No. 6.4e-39; Matches 92; Conservative 14; Mismatches 15; Indels
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 1.
HYPOCHELIOTOCLEIN.
SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             096GA6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human)
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TISSUE=B-cell;
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Gunaratne P.H

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Richards S., Worley K.C., Hale S., Garcia A.N., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gabbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mass and mouse coln Research A.S., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra M.A., Schemes S.J., Marra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AQKEQGRVTMTRDTSISTAYNELSSLRSEDTAIYYCV---RGFGYSYNYDYYYGMDVWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVHLVQSGAEVKKPGASVKLSCKTSGINFSSYDLIWVRQAPGGLEWMGWISAHNGDTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

Best Local Similarity 66.4%; Pred. No. 1.5e-35;
Matches 85; Conservative 13; Mismatches 19; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO51328; AAH51328.1; -.
Hypothetical protein.
SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
., McKernan K.J., Malek J.A.,
                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Spleen;
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MEDLINE=2238257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Bustevow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hatch F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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                                                                                                                                                                                                                                                                                                                          (Fragment).
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annoration update)
Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SONG X.T., Feng Z.O., Guan X.H.;
SAMPlification, clloning and sequence analysis of the heavy chain "Amplification, clloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum.";
Schistosoma japonicum.";
Schistosoma japonicum.";
Schistosoma japonicum.";
Schistosoma japonicum.";
Schistosoma japonicum.";
Schistosoma japonicum.";
Schistosoma japonicum.";
INFN0152, 2FB4.
InterPro; IPR007110; Ig-like.
InterPro; IPR007566; Ig-v.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.7%; Score 455; DB 5; Length 11
69.6%; Pred. No. 1.8e-38;
tive 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 119
119 AA; 13567 MW; BA893873FD5FA6AB CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                       119 AA
                                                                                                                       PRT;
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 69.67
watches 87; Conservative
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SEQUENCE
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                                                                                                                       Q9GYZ2
                                            RESULT 8
09GYZZ
1D 09GYZZ
DT 01-M
DT 01-0
DT 01-0
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Buka musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae; Mus
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64.2%; Score 431.5; DB 11; Length
Best Local Similarity 66.4%; Pred. No. 1.2e-35;
Matches 83; Conservative 16; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                          Straubberg R.;
Straubberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 9E012207.13, 744112207.14.
InterPro; IPR007110; Ig-like.
InterPro; IPR00406; Ig-v.
Ffam; PF00047; 1912 2.
SNART; SM00406; IGV; 1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 27g AA; 29778 MW; F894F955DDCD948A CRC64;
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Gaps

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61 QGRVTITADKSTSTAYMELSSLRSEDTAVYYCA----SSNWGPYWYFDLWGRGTLVTVS 115
                                                                                                                                                                                                                                                                                                                                                                                                    65 QGRVTMTRDTSISTAYMELSSLRSEDTALYYCVRGFGYSYNYDYYYGMDVWGQGTTVTVS 124
                                                                                                                                                                                                                                                                                                                                           1 VQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPQQGLEWMGRIIPILGIANYAQKF
                                                                                                                                                                                                                                                                                                                  5 VOSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDYAQKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Bifinity Maturation of B Cell Antigen Receptors in Response to (4-
HVAPOXX-3-Nitroohenv1) Acetyl (NP).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                               63.9%; Score 429.5; DB 4; Length 116; 71.9%; Pred. No. 6.7e-36; rive 10; Mismatches 19; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067785; BAB63270.1; --
                                                                                                                                                                                      116 AA; 12605 MW; C8P9131DE13EA898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 AA
                      HSSP; PO1810, 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON TER 1 1 16
NON TER 116 AA; 12605 MW; 0
EMBL; AF035025; AAD56261.1; -. HSSP; P01810; 2FBJ.
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PIR; PH1152; PH1152.
PIR; PH1153; PH1153.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.9 Matches 87; Conservative
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PH1114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 NEKFKNKATLAVDKSSSTVYMQLSSLTSEDSAVYYCTRGYGYD---DVYF--DVWGAGTT 134
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Buka musoulus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98277139; PubMed-9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."; Clin. Immunol. Immunopathol. 87:184-192(1998).
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80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Straubberg R.;
Straubberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013490; ABL1349.11;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_V.
Pfam; PF00047; ig; 4.
SNART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 481 AA; 52105 MM; 97DF68D159463F65 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                             481 AA
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LTVSS 136
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                                               VIVSS 125
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Matches
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                                                                                                                                                                                                                                                                                                                                        1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDDNSGGTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 NEXFRGRATLSVDKSSSTAYMELTRLISEDSAVYFCARG-----DYYRRYFDLWGQGT
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Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
EMBL; AF240166; AAK43731.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.
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                                                                                                                                                                                                        Query Match
Best Local Similarity 64.8%; Pred. No. 2.2e-35;
Matches 81; Conservative 17; Mismatches 22; Indels
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PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;
                                                                                                                                    145 145
145 AA; 16081 MW; ECDBIA135E05B8AA CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
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PubMed=11819679;
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61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGY-SYNYDYYYGMDVWGQGT 119
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A DOX A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,

JOX A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,

Bohlan H., Diehl V., Wolf J.;

The sheen cof immunoglobulin in Hodgkin-Reed Sternberg cells of a sheet cofficient with mixed cellularity Hodgkin's disease is associated with somatic mutations within the untranslated regions of rearranged and class switch recombinated ig genes.";

Totals switch recombinated ig genes.";

EMBL; AJ005570, CAA06599.1;

REMBL; AJ005570, CAA06599.1;

RINE-PRO; IPR00710; Ig-like.

RINE-PRO; IPR00710; Ig-like.

RINE-PRO; IPR0047; igg.1.

REMBL; SM00440; igg.1.

REMBL; PS50835; IG_LIKE; 1.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 157;
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52.5%; Score 420; DB 4; Length 15'
Best Local Similarity 67.5%; Pred. No. 9e-35;
Matches 85; Conservative 13; Mismatches 22; Indels
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157 157
157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;
                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                               VH1 protein precursor (Fragment) VH1,
                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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120 TVTVSS 125
                                                    116 TVTVSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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Gencore version 5.1.6

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OM protein - protein search, using sw model

Run on:

April 21, 2004, 16:59:07; Search time 14.485 Seconds

(without alignments)

830.097 Million cell updates/sec

Title:

US-10-041-860-48

Sequence:

1 OVQLVQSGAEVKKPCASVKV.......YDYYYGMDVWGQGTTVTVSS 125

Scoring table:
BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 78:\*

seq length: 0 seq length: 2000000000

Minimum DB Maximum DB Database : PIR 78:\*
1: pirl:\*
2: pirz:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

No. Score Match Length DB ID

1 557 82.9 127 2 \$34014

1 557 82.9 127 2 \$34014

1 557 82.9 127 2 \$34014

1 9 heavy chain V r r glasses

2 537.5 76.9 118 2 \$335665

5 14 76.5 129 2 \$345330

1 10 heavy chain V r r glasses

5 15 76.9 118 2 \$335260

5 16 6 12 9 2 \$34539

6 514 76.5 129 2 \$34539

7 11 35 2 \$34530

1 10 heavy chain V r r glasses

8 500 74.4 131 2 \$256792

1 10 496.5 73.9 119 2 \$440561

1 11 496.5 73.9 119 2 \$440561

1 2 536792

1 3 495.5 73.7 171 2 \$23623

1 4 495.5 73.7 171 2 \$23623

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1 4 486 72.3 13 2 \$23623

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#### ALIGNMENTS

	1 140547 1 140147	
	Id heav	In heavy chain V region - human
	C;Speci	C.Species: Homo sapiens (man)
	C, Date:	C.Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
	C, Acces	sion: S34014; S30535
	R; Marie	R;Mariette, X.; Tsapis, A.; Brouet, J.C.
	Eur. J.	Immunol. 23, 846-851, 1993
	A, Title	domains or
	A; Refer	A;Reference number: S34001; MUID:93209281; PMID:/681398
	A; Acces	A, Accession: S34014
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	C;Super	C; Superfamily: immunoglobulin V region; immunoglobulin homology
	C, Keywe	C; Keywords: heteroterramer: immunoglobulin
	F; LD-7	/ DOMAIN: INMINUTED DOMAIN: IOMOTORY / FIFE./
	Query Ma Best Loc	Query Match  82.9%; Score 557; DB 2; Length 127; B8ct Local Similarity B2.7%; Pred. No. 1.5e-42; Marchae 10: Indels 2; Gaps 1; Marchae 10: Mismatches 10: Indels 2; Gaps 1;
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-	Ig hea	Ig heavy chain V region - human (fragment)
	C; Spec	C.Species: Homo Eaplans (man)
	C; Date	Cidades Zz-NOV-1995 #Bequesice_revisition to NOV-1995 #FOOV_Commod to Commod and Commod
	R, Cuis	nier, A.W.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
	submit	submitted to the EMBL Data Library, June 1992
	A; Desc	A;Description; Mechanisms that generate human immunoglobulin diversity operate from the
-	A, Acce	Alfaceseion: Salfoo
	A, Stat	A, Status: preliminary
	A, Mole	A;Molecule type: mrNA A:Regidues: 1-136 <cui></cui>
	A, Cros	A; Cross-references: EMBL: 214165; NID: 930994; PIDN: CAA78534.1; PID: 930995
-	C; Supe	framily: immunoglobulin v region; immunoglobulin nomology

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                                                                                                                                                                                                                                                                                 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                         Length 118;
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Best Local Similarity 78.6%; Pred. No. 7.6e-39;
Matches 99; Conservative 10; Mismatches 13; Indels
                                                                                                                                                                                       Indels
                                                                                                   DB 2;
                                                                                              Score 516.5; DB 2
Pred. No. 5.4e-39;
6; Mismatches 12
F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain V-1 region (WIL2) - human
                                                                                              Query Match 76.9%;
Best Local Similarity 80.0%;
Matches 1,00; Conservative
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C;Species: Homo sapiens (man)
C;Date: 03-Peb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.EMBO 1.2, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Deccies: Homo sapiens (man)
C;Deccies: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: 846393
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage b
A;Accession: 84639
A;Accession: 84639
A;Accession: 84639
A;Accession: 84639
A;Accession: 84639
A;Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 AQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYGAR------WRDAFDIWGQGTM 130
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A,Cross-references: EMBL:218846; NID:933121; PIDN:CAA79298.1; PID:9939900 C;Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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A, Status: preliminary, nucleic acid sequence not shown
A, Molecule type: mRNA
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6
                                                                                                                                                Score 537.5; DB 2
Pred. No. 8.6e-41;
6; Mismatches 7
                   C, Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                Query Match
Best Local Similarity 82.4%;
Matches 103; Conservative
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Secies: Homo sapiens (man)
C;Species: Homo Saf792
R;Accession: S26792
Bur. J Immunol. 22, 241-245, 1992
Bur. J Immunol. 22, 241-245, 1992
A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Reference number: S26792
A;Return: preliminary
A;Reference number: S26792
A;Return: preliminary
A;Residues: 1-131 < MOR>
A;Residues: 1-131 < MOR>
A;Residues: I-131 < MOR>
A;Residues: I-131 < MOR>
A;Cross-references: EMBL:X61012; NID:932804; PIDN:CAA43346.1; PID:91335131
C;Superfeanily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM'>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
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74.4%; Score 500; DB 2;
Best Local Similarity 72.5%; Pred. No. 1.7e-37;
Matches 95; Conservative 13; Mismatches 17,
        6; Mismatches
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            99; Conservative
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                     Matches
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antibody VH chain (VHI/DKI or DMI/JH4b) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: 849530
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Accession: 849530
A;Accession: 849530
A;Accession: 849530
A;Accession: 135 cMAH>
A;Residues: 1-135 cMAH>
A;Coss-references: EMBL:Z46348; NID:9550839; PIDN:CAA866467.1; PID:9550840
C;Superfemily: immunoglobulin v region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                     61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTALYYCVR-GFGYSYNYD---YYYGMDVWG 116
                                                                                                                                                                                                                                                                                                                                                                                61 AQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDSFGYCSSTSCPYYYYMDVWG 120
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                             Length 129;
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Pred. No. 2.1e-38;
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76.1%; Score 511.5; DB 2.
Best Local Similarity 79.4%; Pred. No. 1.7e-38;
Matches 100; Conservative 6; Mismatches 9.
                     Score 514; DB 2;
Pred. No. 9.8e-39;
8; Mismatches 16;
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79.2%;
                     tch 76.5%;
sal Similarity 78.3%;
101; Conservative
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121 KGTTVTVSS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 QGTTVTVSS 125
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Best Local Similarity
                             Query Match
Best Local S
Matches 101
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Figure 1909-8

Figure 2-1909-8

Figure 2-1909-8

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens

C.Species: Homo sapiens

C.Species: Homo sapiens

C.Species: Homo sapiens

C.Species: To April 1993

R.Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A.Fitle: Evidence for somatic selection of natural autoantibodies.

A.Reference number: PH0952; MUID:92202880; PMID:1552291

A.Reference number: PH0952; MUID:92202880; PMID:1552291

A.Reference number: PH0952; MUID:92202880; PMID:1552291

A.Reference number: PH0954

A.Reference number: PH0952; MUID:92202880; PMID:1552291

A.Reference number: PH0954

A.Reference number: PH0954

A.Reference number: PH0954

A.Reference number: immunoglobulin Nomology cIMM>

F.1-30/Region: framework 1

F.1-30/Region: framework 1

F.1-30/Region: framework 1

F.1-30/Region: framework 1

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                                                                                                                                                    61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVR
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P;51-67/Region: complementarity-determining 2
P;68-98/Region: framework 3
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nes 101; Conservative
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PH1670

19 heavy chain V region (clone 2A12) - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C;Accession: PH1670

R;Hilleon, O.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178 331-336, 1993

A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc

A;Reference number: PH1642; MUID:93301610; PMID:8315388

A;Accession: PH1670

A;Residues: 1-110 < HIL>
A;Residues: 1-110 < HIL>
A;Residues: 1-110 < HIL>
A;Residues: In-110 < HIL>
A;Experimental source: B cell

C;Superfamily: immunoglobulin v region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;7-90/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                          61 AQKFQGRVTITADESTSTAYAMELSSLRSEDTAVYYCARG-----YYYYYGMDVWGQGTT 114
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                                                                                     Length 119;
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                                                                                                                                                            14; Indels
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                                                                                  Score 499; DB 2;
Pred. No. 1.9e-37;
6; Mismatches 14;
           F;99-107/Region: complementarity-determining 3
                                                                                  Query Match
Best Local Similarity 79.2%;
Matches 99; Conservative
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RESULT 15
PH1666
Ig heavy chain V region (clone 6C9) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1666
A;Accession: PH1666
A;Accession: PH1666
A;Accession: PH1642; MUID:93301610; PMID:8315388
A;Accession: Inmunoglobulin V region; immunoglobulin homology
C;Keywords: hererotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology < NVM>
                                                                                                                         61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYG----- 111
                                                                                                                                                                80 GQKFQGRVTLTRDTSISTAYMELSRLISDDTAVYYCA-----IEYFYDGSDLKPSDV 131
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73.6%; Score 494.5; DB 2; Length 118;
Best Local Similarity 80.5%; Pred. No. 4.8e-37;
Matches 95; Conservative 6; Mismatches 16; Indels 1.
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132 FDIWGQGTMVTVSS 145
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April 21, 2004, 16:58:51; Search time 11.2661 Seconds (without alignments) 577.731 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-041-860-48 672 1 QVQLVQSGAEVKKPGASVKV......YDXYYGMDVWGQGTTVTVSS 125

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

141681 Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	4 homo	3 ношо	3 homo	ม สมาย (	6 mus	P01747 mus musculu	I mus	7 mus	e mns	9 mus m	2 homo	5 mus	Ξ	5 homo	enu s	mns /	L mus	homo	mus (	mus	Bun 8	. enm 0	8 mus	8 mus	33 mus	54 mus m	760 homo	749 mus m	18 mus m	33 homo	1 homo	11 homo	P01761 homo sapien
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dр	Query Match	7	L(C)	65.	9	61.	61.	.09		90.	58.	58.	57.	57.	56.	56.	55.	54.	54.	53.	52.	51	21	51		20	50.	49.	49.	49.	. 48.	5 48.	48.	5 48.
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P01768 homo sapien								
HV3G_HUMAN HV3E_HUMAN	HV01_RAT HV3T_HUMAN	HV3K_HUMAN	HV40 MOUSE	HV42_MOUSE	HV3 I_HUMAN	HV21_MOUSE	HV3H_HUMAN	HV32_MOUSE
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122	142	126	119	117	119	122	122	115
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# ALIGNMENTS

	HAVIC HUMAN STANDARD;  DYAGE HUMAN STANDARD;  DY 21-JUL-1986 (Rel. 01, Cz DI) 744;  DT 21-JUL-1986 (Rel. 01, Cz DI) 76-OCT-2001 (Rel. 42, Lab DE 10-OCT-2001 (Rel. 43, Lab DE 10-OCT-2001 (Rel. 43, Lab DE 10-OCT-2001 (Rel. 43, Lab DE 10-OCT-2001 (Rel. 43, Lab DE 10-OCT-2001 (Rel. 43, Lab DE 10-OCT-2001 (Rel. 43, Lab DE 10-OCT-2001 (Rel. 43, Lab DE 10-OCT-2001 (Rel. 43, Lab DE 10-OCT-2001 (Rel. 43, Lab DE 10-OCT-2001 (Rel. 43, Lab DE 10-OCT-2001 (Rel. 44) (Rel	DARD)  1, Cr  1, Cr  2, Lag  2, Lag  2, Lag  2, Lag  1, Cr	ed) annotation update) annotation update) by precureor (Fragmas, Caraniata, Verte ss; Catarrhini; Hom lisesed in a m lisesed i	Futeleosto e, Homo. e R.B., Vine r the human a cell line. velopments, velopmen	mi; "; "; OMA ,OMA
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EMBL; J00240; AAA52988.1; -.
PIR; A02024; HVHUHG.
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        STANDARD;
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Best Local Similarity
Matches 84; Conserv
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          HUMAN
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20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY 79
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                    AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRG----FGYSYNYDYYYGMDVWGQ
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01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-I region V35 precursor.
Ig heavy pain V-I region V35 precursor.
Exkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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85.7%; Pred. No. 3e-37;
ive 5; Mismatches 9; Indels
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PIR; S00476; HVHU35.
GSP; PO1772; ZFB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; F:antigen binding; NAS.
InterPro; IPR007110; Ig-like.
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AMRT; 800406; 1Gv; 1.
PROSITE; PSS0835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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                                                              118 GTTVTVSS 125
                                                                                140 GTTVTVSS 147
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P23083;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-83144028; PubMed=6298778;
Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-Mus musculus (Mouse)
Mus musculus (Mouse)
Mus musculus (Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 111
111 TaxID=10090;
                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy oblain V-1 region HG3 precursor.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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85.7%; Pred. No. 3.8e-37;
ive 5; Mismatches 9; Indels
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117 AA; 12946 MW; 2D3F92FCG0CD1FE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (VH) gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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GO, GO:0003823; F:antigen binding; NAS.
GO, GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_V.
PRT;
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SMART; SM00406; ig; 1.
PROSITE; PSS0835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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Heavy chain constant region domains.";

Elochemistry 21:415-544(1982).

HEACELLANBOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOWA PROTEIN HAS ALSO BEEN DETERMINED.

HEACELLANBOUS: THIS PROTEIN BINDS DEXTRAN.

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PROTEIN: A02039; MHMS4E.

PROSON MHMS4E.

INTERPO: IPRO047; 19.

REALLY: SMOUAGO, 109.

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REALLY: MHMS4E, PSS0835; 1G LIKE; 1.
MEDLINE=84182519; PubMed=6201362;
Didtop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
The Didtop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
The A V region determinant (idiotope) expressed at high frequency in B I ymphocytes is encoded by a large set of antibody structural genes.";
The EMBO J. 3:517-523(1984).
The EMBO J. 3:517-523(1984).
The PRO J. 3:517-523(1984).
The PRO J. 3:517-523(1984).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (COMPLEX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.3%; Score 418.5; DB 1; Length 118; 63.2%; Pred. No. 5.4e-35; ive 15; Mismatches 24; Indels 7
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nes 24; Indels
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118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
IIG heavy chain V region MOPC 104E.
Mus musculus (Mouse).
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D SEGMENT.
J SEGMENT.
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nes 79; Conservative
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P01756;
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62 OKFOGRVIMIRDISISTAYMELSSLRSEDTALYYCVRG--FGYSYNYDYYYGMDVWGQGT 119
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                                                                                                                                8; Gaps
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g heavy chain V region 36-65.
Ig heavy chain V region 36-65.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 711 TaxID=10090;
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                                     Length 117;
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                                                                        19; Indels
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-!-SIMILARITY: Contains 1 immunoglobulin-like domain.
HSSP; PO1789; 1MCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 120 120 120 AM; FF04E4A167B654AF CRC64;
117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
                                   Query Match
Best Local Similarity 63.2%; Pred. No. 1.5e-34;
Matches 79; Conservative 19; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma
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P01747;
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117 AA.

THAT ALSO MANY OF

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MEDLINE=80078170; PubMed=6765983; Schilling J., Clevinger B., Davie J.M., Hood L.,; Schilling J., Clevinger B., Davie J.M., Hood L.,; Schilling J., Clevinger B., Davie J.M., Hood L.,; Schilling J., Clevinger B., Davie J.M., Mainto acid sequence of homogeneous antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments."; Nature 28:35-40(1980).

-! MISCELLANGOUS: THE SEQUENCES OF 10 HYBRIDOWA PROTEINS THAT ALS BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.

-!- MISCELLANGOUS: THIS PROTEIN BINDS DEXTRAN.
-!- SIMILARITY: CONTAINS 1 immunoglobulin-like domain.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                         21-JUL,1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region J558.
Mus musculus (Mouse).
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BY SIMILARITY.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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SMART; SMO4066; IGv; 1.
ImmosITE; PS50835; IG LIKE; 1.
Immonoglobulin V region.
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P01746;
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                              MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AQKFQGRVTMTRDTSISTAYMBLSSLRSEDTALYYCVRGFGYSYNYDYYYG--MDVWGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOWA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL (NPB ANTIBODIES).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
                                          HW07 MOUSE STANDARD; PRT; 139 AA.
201751; 901752;
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain V region B1-8/186-2 precursor.
Eukary chain W region B1-8/186-2 precursor.
Sukary chain Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
11 TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V REGION B1-8/186-2.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, A90809; MRMS18.
PDB; 1A6U; 27-MAY-98.
PDB; 1A6U; 15-MAY-98.
INTERPROFILE 10 IG-11ke.
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IMMUNOGIODUIN V region; Signal; 3D-structure.
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D SEGMENT.
JH2 SEGMENT.
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                                      PRT;
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Best Local Similarity 63.0%
Matches 80; Conservative
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139 AA;
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61 AQKEQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                 Gapa
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-82152818; PubMed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.";
     Length 117;
                                                 22; Indels
/ Match 60.7%; Score 408; DB 1; Local Similarity 62.4%; Pred. No. 5.9e-34; nes 78; Conservative 17; Mismatches 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
IIG heavy chain V region 93G7 precursor.
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                        61 AQKFQGRVTMTRDISISTAYMELSSLRSEDTALYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
                                                                                                                                                                                                                                                                                                                                                          20 EVQLQQSGAELVRAGSSVKASCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
MEDLINE=84182519; PubMed=6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
The vegic determinant (idiocope) expressed at high frequency in B.
Thymbhocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
PIR: A02037; MHMS15.
                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                  Length 140;
                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION 93G7.
IG-LIKE,
                                                                                                                                                                                                                                                                                              Query Match
60.7%; Score 408; DB 1; Length 140
Best Local Similarity 60.8%; Pred. No. 7.3e-34;
Matches 76; Conservative 21; Mismatches 24; Indels
                                                                                                                                                                                                                                                              140 140 140 140 140 AM; 25A4CBBE31DA5CE8 CRC64;
Science 216:309-311(1982).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region AC38 15.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 120 AA.
                                                                                                                                              HSSP, PO1810, 2FBJ,
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; 1.
SMART; SMO0406; Ig.v, 1.
IMMUNOG10bulin V region; Hybridoma; Signal.
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SEGMENT.
SEGMENT.
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InterPro; IPRO07110, Ig-like.
InterPro; IPRO03596; Ig_v.
Pfam; PP00047; ig; 1.
SMART; SM04066; IG_v.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                       EMBL; J00493; AAA38128.1; -. PIR; A94264; HVMSG7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 LTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VTVSS 125
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SEQUENCE
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                                                                                                                                                         1 QVQLVQSGABVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino
acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
Biochemistry 9:3161-3170(1970).
                                                                                                                                        1 OVOLVOSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Gaps
                                                                                                      5; Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                    58.7%; Score 394.5; DB 1; Length 120; 60.0%; Pred. No. 1.4e-32; Indels 5; live 20; Mismatches 25; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.0%; Score 390; DB 1; Length 117; 67.2%; Pred. No. 3.7e-32; tive 9; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID.
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117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;
 22 96 BY SIMILARITY.
120 120
120 Aa; 13311 MM; 914453F426F09834 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00047; ig; 1.
SWART; SM0406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
119 heavy chain V-1 region EU.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 67.23
                                                                                                      75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                 121 VTVSS 125
                                                                                                                                                                                                                                                                                                                   116 VTVSS 120
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P01742;
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HV1A_HUMAN
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Matches
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61 AQKFQGRVTMTRDTSISTAYMELSSLRSEDTALYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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                                                              SO NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCAR----YRLGRYF--DYWGQGTT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWINPNSGNTDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=84248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Illegitimate recombination generates a class switch from C mu to C delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIN, A02031; PWST7.
InterPro; IPR007110; Ig-like.
InterPro; IPR005596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION TEPC 1017.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Indels
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59.2%; Pred. No. 2.2e-31;
ive 20; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                       138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-UT-1999 (Rel. 38, Last annotation update
1g heavy chain V region TEPC 1017 precursor.
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HVIF HUMAN STANDARD;
1D PAVIF HUMAN STANDARD;
1C 004326;
DT 01-JAN-1988 (Rel. 06, Created)
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Best Local Similarity 59.2.
The 74; Conservative
                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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133 LTVSS 137
                                                                                                                                                  121 VTVSS 125
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                                                                                                                                                                                                                                                                                                                                                       MOUSE
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NON TER
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HV48 MOU
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                                                                                       AQKFQGRVTMTRDTSISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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"Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24.625-637(1981).
-!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus. TaxID=10090;
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COMPLEMENTARITY-DETERMINING-1.
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FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION S43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.8%; Score 388.5; DB 1; Length 61.6%; Pred. No. 6.2e-32; ive 15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15200 MW; ADD5881BF44B8EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Abavy chain V region 543 precursor.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                  137 AA.
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JH2 SEGMENT.
BY SIMILARITY.
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InterPro; IPR007110, Ig-like.
InterPro; IPR003166; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM004066; IGv; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J00539; AAA38172.1; -.
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les 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NPB ANTIBODIES).
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VTVSS 117
                                                                                                                                                                                                          VTVSS 125
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P01755;
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Nucleic Acids Res. 8:4839-4840(1980).
-!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
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21-JJJ-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-ACT-2003 (Rel. 42, Last annotation update)
10-ACT-2003 (Rel. 42, Last annotation update)
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MEDLINE=86203277; PubMed=3084950;

A Kojima M., Koider T., Odani S., Ono T.;

Kojima M., Koider T., Odani S., Ono T.;

Minunoglobulin (Mot) having unusual papain cleavage sites.";

I immunoglobulin (Mot) having unusual papain cleavage sites.";

Mol. Immunol. 23:169-174(1986).

PIR; A02025; HYHUMO.

RISP; PO1772; 2FB4.

GO; GO:0003823; F: Pimmune response; NAS.

RO; GO:0003823; F: Pimmune response; NAS.

RICHEPPO; IPR007110; Ig-11ke.

RICHEPPO; IPR007110; Ig-11ke.

RICHEPPO; IPR00471; Ig; 1.

RARET; SM00440; Igy. 1.

SWART; SM00440; Igy. 1.

REMART; PRS50835; IG_LIKE; 1.

WINTURGIOBULIN V region.

V GROWNENT.
                                                                                                                                      Bukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=81053741; PubMed=6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
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58.4%; Pred. No. 6.3e-31;
ive 17; Mismatches 35; Indels
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125 125
125 AA; 13579 MW; F4C4285D6DF0C8EA CRC64;
   01-JAN-1988 (Rel. 06, Last sequence update) 15-WUL-1999 (Rel. 38, Last annotation update) 1dy heavy chain V-I region Mot. Homo sapiens (Human).
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Best Local Similarity 58...
Best Local 73; Conservative
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61 AQKFQGRVTMTRDISISTAYMELSSLRSEDTAIYYCVRGFGYSYNYDYYYGMDVWGQGTT 120
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                                                                                                                                                                                                                                                                                                           Length 121;
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56.0%; Score 376; DB 1; Length 12.

Best Local Similarity 58.4%; Pred. No. 9.6e-31;

Matches 73; Conservative 19; Mismatches 29; Indels
                                                                                                                                                                                                                        DOMAIN 1 112 IG-LIKE.
NON TER 121 121
SEQUENCE 121 AA; 13135 WW; 227AEF3EC56EDOBF CRC64;
                Contains 1 immunoglobulin-like domain.
FROM A MYELOMA THAT SECRETES IGG2B.
                -!- SIMILARITY: Contains 1 immu PIR; A93708; GVMS11. HSSP; P01810; 2FBJ. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig-V. Pfam; PF00047; ig; 1. PROSITE; PS50835; IG, LKE; 1. Immunoglobulin V region.
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Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 84, Appl
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Sequence 84, Appl
Sequence 129, Appl
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-652-816A-104
US-08-652-816A-104
US-08-652-816A-104
US-08-652-816A-104
US-08-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                        1 gfgysynydyyygmdv 16
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Maximum DB seq length: 200000000
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Score Match Length DB
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47.5
47.5
46
                                                                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
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Sequence 270, App Sequence 118, App Sequence 11, Appl Sequence 80, Appl Sequence 22, Appl Sequence 25, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 36,	Sequence 96, Appl Sequence 34, Appl Sequence 6014, Ap Sequence 5, Appli
US-09-042-353-270 US-08-758-417A-118 PCT-US-21-1083-73 US-09-472-087-80 US-09-472-087-70 US-09-376-594-282 US-09-240-274-25 US-09-240-274-153 US-09-240-274-153 US-09-240-274-153 US-08-08-11-492-35 US-08-08-11-492-35 US-08-10-478-35 US-08-10-478-35 US-08-08-623-3	US-08-476-349A-96 US-09-721-870-34 US-09-328-352-6014 US-09-147-236-5
<b>W 4 10 4 4 4 4 6 6 6 6 6 6 6</b>	444
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 9 .
444 11 12 12 444444 · · · · · 44444 00000000000000000000000000000000	44 44 45 3.5 44
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 4 U W 4 7

### ALIGNMENTS

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MOLECULE TYPE:
DESCRIPTION: peptide
FRAGMENT TYPE: synthetic peptide
FRATURE:
                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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RESULT 4
US-09-197-503-2
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Patent No. 6752045

GENUERAL INFORMATION:
APPLICANT: James M. Anderson
APPLICANT: Christina M. Van Itallie
TITLE OF INVENTION: Human Occludin, Its Uses and
TITLE OF INVENTION: Enhancement of Drug Absorption Using Occludin Inhibitors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yale University Medical School
ADDRESSEE: Section of Digestive Diseases
ADDRESSEE: Department of Internal Medicine
STREET: 333 Cedar Street, LCI 105
CITY: New Haven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                              Score 52; DB 3; Length 24;
Pred. No. 0.3;
1; Mismatches 4; Indels
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construct used in experi-
ments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTRY: New Aracus
CONTRY: On ted States of America
ZIP: 06520-08057
COMPUTER: EDABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM FC
COMPUTER: IBM FC
COMPUTER: IBM FC
COMPUTER: IBM FC
COMPUTER: IBM FC
COMPUTER: IBM FC
COMPUTER: ON THE PROCESSING
COMPUTER: WORD PROCESSING
COMPUTER: WORD PROCESSING
COMPUTER: WORD PROCESSING
COMPUTER: WORD PROCESSING
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/142,732
FILING DATE: MARCH 14, 1997
APPLICATION NUMBER: US. 60/013,625
ATTORNEY/AGENT INFORMATION:
NAME: MARY M. KRIBER;
NEGISTRATION NUMBER: 32423
REGISTRATION NUMBER: 32423
REGISTRATION NUMBER: 1751-P0016B.PCT
TELEPHONE: CONTENT NUMBER: 1751-P0016B.PCT
TELEPHONE: CONTENT NUMBER: 1751-P0016B.PCT
TELEPHONE: CONTENT NUMBER: 1751-P0016B.PCT
TELEPHONE: CONTENT NUMBER: 1751-P0016B.PCT
TELEPHONE: CONTENT NUMBER: 1751-P0016B.PCT
TELEPHONE: CONTENT NUMBER: 1751-P0016B.PCT
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53.6%; Score 52; DB
Best Local Similarity 61.5%; Pred. No. 7.9;
Matches 8; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION: polypeptide FRAGMENT TYPE: complete sequence
                                                                                                 Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , NAME/KEY: human occludin US-09-142-732-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELBFAX: 203-327-11096
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 522
                                                                                                                                                                                                       1 GFGYSYNYDYYYG 13
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
) OTHER INFORMATION:

) OTHER INFORMATION:

US-09-142-732-4
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Gaps
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APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
CORRESPONDENCES: 150
CORRESPONDENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSES: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
CONTY: USA
ZIP: 94111-318
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,641
FILING DATE: 20-VAY-1996
CLASSIFICATION NUMBER: US 07/904,068
FILING DATE: 33-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50.5; DB 1; Length 36; Pred. No. 0.75; 1; Mismatches 0; Indels
MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION NUMBER: US 07/990,860
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 10-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION NUMBER: US 07/853,408
FILING DATE: US 07/853,408
FILING DATE: US 07/853,408
FILING DATE: US 07/853,408
FILING DATE: US 07/853,408
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: SMICH, William M.
REGISTRATION NUMBER: 14643-9-3
TELEPHONE: 415-326-2402
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TVDE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-645-641-84; Sequence 84, Application US/08645641

Sequence 84, Application US/08645641

Patent No. 5719032; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S SYNYDYYYGMDV 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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TOPOLOGY: linear
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US-09-328-352-5599
US-09-328-352-5599
Sequence 5594, Application US/09328352
Rateat No. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUMBER US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 733
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US-06-053-131-84
; Sequence 84, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES:
; ADDRESSER: Townsend and Townsend Khourie and Crew
; STATE: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                  PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/945,826
FILING DATE: 05-NOV-1997
ATTORNEY APPROARTITOR ON TOWN DAME: PARACI, C. Joseph REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 0425-0660P
TELEPHONE: (703) 205-8060
TELEPHONE: (703) 205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACITERISTICS:
LENGTH: 522 antho acids
TYPE: antho acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ; ORGANISM: Acinetobacter baumannii US-09-328-352-5599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 53.6%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-09-197-503-2
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COMPUTER READABLE FORM:
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US-08-096-762-84
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Parent No. 5798650
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.1%; Score 50.5; DB 1; Length 36; 83.3%; Pred. No. 0.75; cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                            Score 50.5; DB 1; Length 36;
Pred. No. 0.75;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-000913
TELECOMMUICATION INFORMATION:
TELEPHONE: 415-326-2402
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 aming acids
                                                                                                                                                                                                                                52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 36 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYNYDYYYGMDV 16
                                                                                                                                                                                                                                                                                             5 SYNYDYYYGMDV 16
                                                                                                                                                                                                                                                                                                                  11 SYDY-YYYGMDV 21
                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-645-641-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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US-07-853-408B-84
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11 SYDY-YYYGMDV 21

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Gaps
Sequence 84, Application US/08096762
| Patent No. 5814318
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Lonberg, Nils
| APPLICANT: Kay, Robert M.
| TITLE OF INVENTION: Producing Heterologous Antibodies
| NUMBER OF SEQUENCES: 210
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 200
| CITY: San Francisco | STATE: California | COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.1%; Score 50.5; DB 2; Length 36; 83.3%; Pred. No. 0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC Compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLIG DATE: 22-JUL-1993
CLASSIPICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 22-ULI-1933
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-AR-1933
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/9163,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, Milliam M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECHONE: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-08-308-865-84
; Sequence 84, Application US/08308865
; Patent No. 5877397
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lonberg, Nils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: six
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5 SYNYDYYYGMDV 16
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; Sequence 281, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREE: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for TITLE OF INVENTION: Pransgenic No. 5877397-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies NUMBER OF SEQUENCES: 150 CORRESPONDER ADDRESS: Sinch STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco CITY: San Francisco CITY: Sur Francisco CITY: Sur Francisco COUNTRY: CUSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50.5; DB 2; Length 36;
Pred. No. 0.75;
1; Mismatches 0; Indels
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
FILING DATE: 23-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKT NUMBER: 14643-9-1-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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linear
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; STRANDEDNESS: single
; TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-865-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-042-353-281
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### CONTRING NUMBER: UN 00/104/10403

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### CONTRING NUMBER: UN 00/104/10403

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### CONTRING NUMBER: UN 00/104/10403

### CONTRING NUMBER: UN 00/104/1
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S SYNYDYYYGMDV 16

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Per-US92-1093-49

Per-US92-1093-109

Per-US92-1093-109

GENERAL INFORMATION:

PAPLICANT: Contered Nils

APPLICANT: Contered Nils

APPLICANT: Contered Nils

APPLICANT: Contered Nils

ADDRESSES: Allienia M. Smith

STREET: Contered ADDRESS:

COMPERS: California

STREET: Contered Nils

GENERAL STREET: Contered Nils

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Score 48; DB 3; Length 287; Pred. No. 15; 3; Mismatches 0; Indels
                                                                                          APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELEPHONE: (650) 813-5600
TELEPHONE: (650) 813-5600
TELEPHONE: (650) 494-0792
TELEPHONE: (650) 494-0792
TELEFAX: (650) 494-0792
TELEFAX: (650) 494-0792
TELEFX: 706141
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: April 21, 2004, 17:40:04 Job time : 20.2464 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear; MOLECULE TYPE: protein US-08-862-124-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 DYDHYYGLDV 256
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US-08-862-124-17
Sequence 17, Application US/08862124
Sequence 17, Application US/08862124
Sequence 17, Application US/08862124
Sequence 17, Application US/08862124
APPLICANT: Mait, Pradip K.
APPLICANT: Mait, Pradip K.
APPLICANT: Mait, Pradip K.
APPLICANT: Mait, Pradip K.
APPLICANT: Mait, Pradip K.
APPLICANT: Raplan, Howard A.
ITILE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE TITLE OF INVENTION: SPECIFICALLY DETECT CANCERS
ITILE OF INVENTION: DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESSONDENCESS:
ADDRESSEB: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIATE: CA
CONTRY: USA
ZIATE: CA
COMPUTER: READABLE FORM:
MEDIUM TYPE: BLOPPY disk
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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COMPUTER: IBM PC

OPERATING SYSTEM: MS DOS

SOFTWARE: Word Processing

CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/983,607

FILING DATE: April 27, 1998

CLASSIPICATION: 435

PRICK APPLICATION NUMBER: PCT/IB96/01032

PILING DATE: June 28, 1996

CLASSIPICATION NUMBER: PCT/IB96/01032

PILING DATE: WARMATION:
NAME: MARY M. KAILBAR:
APPLICATION NUMBER: 32423

REFERENCE/DOCKET NUMBER: 0CR-679

TELEPHONE: 203-773-9544

TELEPHONE: 203-773-1183

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARCTERISTICS:
LENGTH: 126 residues
TYPE: Amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: POLYPEPLIER

ORGANISM: Homo sapiens (melanoma patient
ORGANISM: Homo sapiens (melanoma patient
ORGANISM: Homo sapiens (melanoma patient
ORGANISM: immunized with autologous tumor cells)
INDIVIDUAL ISOLATE: OFTER
IMMEDIATE SOURCE:
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LIBRARY: fusion phage construct
CLONE: F2
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Best Local S
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Gaps

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version 5.1.6 - 2004 Compugen Ltd. GenCore Copyright (c) 1993

OM protein - protein search, using sw model

Run on:

April 21, 2004, 17:27:33; Search time 14.6087 Seconds (without alignments) 105.353 Million cell updates/sec

1 gfgysynydyyygmdv 16 Sequence:

SEQ3

Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	- 1			bable	chain	heavy chain	heavy	occludin - human	D.	Ig heavy chain V6	heavy chain	heavy chain	Ig heavy chain V r	lycosyltransfe	heavy	g heavy		heavy	heavy	chain	chai	otheti	chai			occludin - chicken		pothetical prot	Ig heavy chain V r
SUMMARIES	QI	S37456	F87623	PH1304	S64783	PH1307	PL0094	PH0954	G02533	T44825	S24686	PH1655	PH1328	831689	H97186	848797	S26792	PT0258	S24252	831106	GIHUHZ	PH1361	H81723	PH1364	C83831	823862	A49467	6339	644	S20776
	Length DB	1				19 2				9	വ	0	თ		4		_	₹#	97 2	_	ທ	<b>m</b>	ın	m				719 2		45 2
de	Query Match Le	62.9	59.8	57.2	56.7	φ	54.6	54.1	53.6	52.6	52.1	51.5	51.0	ın	'n	0	50.0	49.5	49.5	49.5	49.5	49.0	49.0	48.5	48.5	48.5	48.5	48.5	48.5	47.9
	Score	61	58	55.5	55	54.5	53	52.5	52	51	50.5	50	49.5	49	49	48.5		48	48	48	48	47.5	47.5	47	47	47	47	47	47	46.5
	Result No.	1 1	7	٣	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20

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E25114	PH0961	PH0955	AE1125	537847	C87305	E90159	T02673	PH1355	PH1371	830515	PH0960	A64961	PH1650	T05357	A49047	
N	η	N	~	N	~	N	N	7	~	N	0	0	~	0	7	
119	119	127	132	201	210	483	633	27	27	113	136	69	120	122	136	
47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	46.9	46.9	46.9	46.9	46.4	46.4	46.4	46.4	
46	46	46	46	46	46	46	46	45.5	45.5	45.5	45.5	45	45	45	45	
30	31	32	33	3.4	35	36	37	38	О	40	41	42	43	44	45	

# ALIGNMENTS

```
Sylvabor human (fragment)

CjSpecies: Homo sapiens (man)

CjSpecies: Homo sapiens (man)

CjSpecies: Homo sapiens (man)

CjAccession: S37456

RjMcIntcosh, R.S.; Tandon, N.; Weetman, A.P.

RjmcIntcosh, R.S.; Tandon, N.; Weetman, A.P.

RjmcIntcosh, R.S.; Tandon, N.; Weetman, A.P.

RjmcIntcosh, R.S.; Tandon, N.; Weetman, A.P.

Ajbecription: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from I AjReference number: S37453

AjAccession: S37456

AjReference number: S37456

AjReference number: S37456

AjReference number: S37456

AjReference number: S37456

AjReference number: S37456

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AjReference number: S37456

AjReference number: S37456

AjReference number: S37456

AjReference number: S37456

AjReference num
RESULT 1
S37456
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Gaps ö Query Match 62.9%; Score 61; DB 2; Length 116; Best Local Similarity 78.6%; Pred. No. 0.098; Matches 11; Conservative 0; Mismatches 3; Indels

. 0

92 GYSYGYYYYWDV 105 3 GYSYNYDYYYGMDV 16 ద ઠે

RESULT 2

hypotherical protein CC3024 [imported] - Caulobacter crescentus
C;Specession: Caulobacter crescentus
C;Accession: F87623
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolons
D, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136.4141, 2001
A;Hitle: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUD:21173698; PMID:11259647
A;Acterence preliminary
A;Molecule type: DNA
A;Residues: 1-205 <STO>
A;Coss-references: GB:AE005673; NID:g13424664; PIDN:AAKZ4986.1; GSPDB:GN00148
C;Ganetics:
A;Gene: CC3024

Gaps 4 Query Match
59.8%; Score 58; DB 2; Length 205;
Best Local Similarity 58.8%; Pred. No. 0.46;
Matches 10; Conservative 2; Mismatches 1; Indels

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Sobjected: Musucoulus (focts) - mouse (fragment)

Sispecies: Musucoulus (house mouse)

Sispecies: Musucoulus (house mouse)

Sispecies: Musucoulus (house mouse)

Siscession: PL0094

Six Maek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Cal

M. Exp. Med. 169, 519-533, 1889

A; Title: Structural characterization of antidiotypic antibodies; evidence that Ab2s are

A; Reference number: PL0080; MUID:89094248; PMID:2492056

A; Residues: 1-45 kMEB-

A; Molecule type: MRNA

A; Residues: 1-45 kMEB-

A; Note: the authors translated the codons AGC and AGU for residues 6 and 7 as Agp

A; Note: the sequence shown here is from the VH region of a syngeneic antibody to anti-3-1

C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                         Query Match 56.2%; Score 54.5; DB 2; Length 19; Best Local Similarity 78.6%; Pred. No. 0.12; Matches 11; Conservative 0; Mismatches 0; Indel8
                                  C;Superfamily: 'immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
54.6%; Score 53; DB 2; Length 45;
Best Local Similarity 81.8%; Pred. No. 0.47;
Matches 9; Conservative 0; Mismatches 2; Indels
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           A; Residues: 1-19 < WAS>
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                                                                                                                                                                                                                                     ig heavy chain DJ region (clone C439-111) - human (fragment)
C;Species: Homo sapiens (man)
C;Dactes: Homo sapiens (man)
C;Accession: PH1304
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1877-1881, 1992
A;Tells: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PH1302; MUID:93094761; PMID:1460419
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19 heavy chain DJ region (clone C96-119) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1307
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Accession: PH1302; MUID:93094761; PMID:1460419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residudes: 1-825 <DDD:
A;Cross-references: EMBL:Z73137; NID:g1360217; PID:e245752; PID:g1360218; GSPDB:GN00012;
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable membrane protein YLL032c - yeast (Saccharomyces cerevisiae)
NyAlexnate names: hypothetical protein L0926
C;Species Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002
C;Accession: S64783
**Subsestrathoeft, A,; Floeth, M,; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
Submitted to the Protein Sequence Database, May 1996
A;Reference number: S64775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1.19 kMAS.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 56.7%; Score 55; DB 2; Length 825; Best Local Similarity 66.7%; Pred. No. 5.2; Matches 9; Conservative 2; Mismatches 2; Indels
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C;Keywords: transmembrane protein
F;660-676/Domain: transmembrane #status predicted <TMM>
                                             165 GYGYGYDYDYAPRPYYG 181
       1 GFGYSYNYDY----YYG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: MIPS:YLL032c
A;Cross-references: SGD:S0003955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: PH1304
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Space: 1.7-Apr.1993 #sequence_revision 17-Apr.1993 #text_change 16-Aug-1996
C.Space: PH0954
R.Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
B.Kry. Med. 175, 983-991, 1992
A.Fitle: Evidence for somatic selection of natural autoantibodies.
A.Reference number: PH0952; MUID:92202880; PMID:1552291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 54.1%; Score 52.5; DB 2; Length 132; Local Similarity 78.6%; Pred. No. 1.7; nes 11; Conservative 0; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                            ;Molecule type: DNA;Residues: 1-132 <MAR>;Residues: 1-132 <MAR>;Superfamily: immunoglobulin V region; immunoglobulin homology;Keywords: heterotetramer; immunoglobulin
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-120/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-30/Region: framework 1
15-98/Domain: immunoglobulin homology <IMM>
31-35/Region: complementarity-determining 1
                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown
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"Ig heavy chain V region (clone 228) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Peb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C; Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C; Accession: PH1655
R; Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J; Exp. Med. 178, 331-336, 1993
A; Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A; Reference number: PH1642; MUID: 93301610; PMID: 8315388
A; Molecule type: mENA
A; Residues: 1-110 <HIL>
A; Residues: 1-110 <HIL>
A; Experimental source: B cell
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Seywords: heterotetramer; immunoglobulin
F; 7-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Id heavy chain DJ region (clone C113-148) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1328
R;Masserman. R.; Galii, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
B;Masserman. R.; Galii, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph:
A;Reference number: PH1328
A;Accession: PH1328
A;Molecule type: DNA
A;Residues: 1-29 - WAS>
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Ig heavy chain V region - human (fragment)

S.Species Homo sapiens (man)

C.Species Homo sapiens (man)

C.Species Homo sapiens (man)

C.Species Homo sapiens

C.Species Homo sapiens

C.Species Homo sapiens

C.Species Homo sapiens

C.Species Homo sapiens

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C.Species Homo sapiens

A.Species Homo sapiens

A.Species Homo sapiens

C.Species Homo sapiens

A.Species                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50; DB
Pred. No. 3.1;
71.4%; Pred. No. 3.1;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 51.5%; Score 50; DB Best Local Similarity 69.2%; Pred. No. 3.1; Matches 9; Conservative 0; Mismatches
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Local Similarity 71.4%;
Les 10; Conservative
                                                                                                                                                                                                                               104 GYDY---YYYGMDV 114
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Best Local Similarity 71.4<sup>§</sup>
Matches 10; Conservative
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NyAlternate names: protein tyrosine kinase
NyAlternate names: protein tyrosine kinase
Syspecies: Acinetobacter lwoffii
Cyspecies: Acinetobacter lwoffii
Cybate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
Cyacession: 144825
Ny Nakar, D; Guthick, D.L.
Submitted to the EMBL Data Library, July 1999
A;Description: Genomic organization of the wce region of Acinetobacter lwoffii RAG-1 req
A;Reference number: 22285
A;Reference number: 22285
A;Reference number: 22285
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residuas: 1-726 cNAK>
A;Residuas: 1-726 cNAK>
A;Residuas: 1-726 cNAK>
A;Residuas: lange RMBL:AJ243431; PIDN:CAB57193.1
C;Genetics:
A;Gene: wzc
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                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 29-Sep-1999
C;Datessabion: G0253
C;Accessabion: G0253
B;Van Itallie, C.M.
submitted to the EMBL Data Library, April 1996
A;Reference number: H01403
A;Reference number: H01403
A;Reference preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: mNNA
A;Molecule type: mNNA
A;Molecule type: mNNA
A;Residues: 1-522 < VVAN>
A;Cross-references: EMBL:U53823; NID:g1322281; PIDN:AAB00195.1; PID:g1322282
C;Superfamily: occludin
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Pred. No. 8.4;
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Matches 9; Conservative
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A,Residues: 1-128 cAMB.
A,Residues: 1-128 cAMB.
A,Residues: 1-128 cAMB.
A,CORS-TECTERCES: EMBL: 246379; NID:9587147; PIDN:CAA86512.1; PID:91340168
R,Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A,Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A,Reference number: $26885; MUID:93021117; PMID:1404388
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548797
19 heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Jana-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C;Accession: S48797; S26893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Submitted to the BME Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
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A; Cross-references: GB: AE001437; PIDN: AAK80283.1; PID: G15025335; GSPDB: GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics:
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A,Residues: 1-98 <TOM>
A,Cross-references: EMBL: Z12350, NID: 932922, PIDN: CAA78220.1; PID: 932923
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F,15-98/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-153 <CUI>.
A;Cross.references: EMBL:Z14187; NID:g31041; PIDN:CAA78556.1; PID:g31042
C;Superfamily: immunoploulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-121/Domain: immunoglobulin homology <IMM>
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50.0%; Score 48.5; DB 2; Length 128;
Best Local Similarity 71.4%; Pred. No. 5.9;
Matches 10; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                             Length 153;
                                                                                                                                                                                                                                                                                                             Query Match 50.5%; Score 49; DB 2; Best Local Similarity 56.2%; Pred. No. 6.1; Matches 9; Conservative 1; Mismatches t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 GIAVAGTSDYYYGMDV 142
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Arithes: Structural and idiotypic characterization of the L chains of human 19M autoantil Arithes: Structural and idiotypic characterization of the L chains of human 19M autoantil Aracession. 130601; MUDD:89215279; PMID:2496160  Aracession. 130607  Aracession. 130607  Aracidus pediannary  Aracidus pediannary  Aracidus and aracidus and aracidus and aracidus arac
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83757
12 kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: 537517
R;Klein, U.; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
                                                                                                                                                                                                                                                                                                                                                                                                                                     IG kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: 837513
R;Klein, U.; Kueppers, R.; Rajewsky, K.
R;Klein, U.; Kueppers, R.; Rajewsky, K.
A;Boesription: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood A;Reference number: 837501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: S37513
A;Accession: Draininary
A;Molecule type: mENA
A;Access: 1-92 <ALLS
A;Cross-references: EMBL:226598; NID:9405668; PIDN:CAA81352.1; PID:9405669
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Query Match 100.0%; Score 53; DB 2; Length 91; Best Local Similarity 100.0%; Pred. No. 0.0015; Matches 12; Conservative 0; Mismatches 0; Indels
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Matches 12; Conservative 0
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System Saper chain V region (V-kappa 3) - human (fragment)
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Cyspecipton: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: System
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A;Accession: System
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A;Accession: System
A;Corose-references: EMBL:Z26612; NID:g405682; PIDN:CAA81365.1; PID:g405683
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                        Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 534096
R;Wagner, S.D.; Luzzatto, L.
Bur. J. Immunol. 23, 331-337, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: 534076; MUID:93170387; PMID:8436174
A;Accession: 534096
A;Accession: 534096
A;Accession: S34096
A;Accession: S34096
A;Accession: S34096
C;Superiaminy: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin Nomology < IMM>
C;Keywords: heterotetramer; immunoglobulin
F;9-84/Domain: immunoglobulin homology < IMM>
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S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C;Species Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C;Accession: S67940
C;Accession: S67940
C;Accession: John; Purmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A;Title: Cloning of a human autoimmune response: preparation and sequencing of a human A;Reference number: S67940; MUID:92314301; PMID:1617110
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91
A;Residues: HEXA
A;Coss-references: EMBL:X73852
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Agobota chain V-III region (KV325) - human (fragment)
Ig kappa chain V-III region (KV325) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 29-Unn-1989 # Heequence_revision 29-Jun-1989 # text_change 21-Jan-2000
C;Accession: A30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soloni Tmmunol. 142, 3188-3163, 1989
A;Title: Structural and idiotypic of paracterization of the L chains of human IgM autoant: A;Reference number: A30601
A;Accession: A30601
A;Accession: A30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-96 cGON-
A;Residues: 1-96 cGON-
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
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337528
Ig Asapa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: O6-Jan-1995 #text_change 23-Jul-1999
C;Date: O6-Jan-1995 #text_change 23-Jul-1999
C;Accession: 837528
R;Klein, U: Kueppers, R: Rajewsky, K.
Rubmitted to the EMBL Data Library, September 1993
A,Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral bloom
A,Recreates number: 837528
A,Accession: 837528
A,Accession: 837528
A,Accession: S37528
A,Estaus: preliminary
A,Molecule type: mRNA
A,Residues: 1-93 «KLE>
A,Cross-references: EMBL:Z26616, NID:9405699; PIDN:CAA81369.1; PID:9405699
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin
    Is kappa chain V region (V-kappa 3) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: No. 2394 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C; Tatein, U.; Kueppers, R.; Rajewsky, K.
R; Klein, U.; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A; Description: Human 19M(+)19D(+) cells, the major B cell subset in the peripheral blooc
A; Recreated number: S37526
A; Accession: S37526
A; Accession: S37526
A; Accession: S37526
A; Residues: 1-93 < KLE>
A; Molecule type: mRNA
A; Residues: 1-93 < KLE>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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Pred. No. 0.0016;
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Best Local Similarity 100.
Matches 12; Conservative
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537514
19 Asapa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: 837514
R;Klein, U; Kueppers, R.; Rajewsky, K.
R;Klein, U; Kueppers, R.; Rajewsky, K.
R;Mesin, U; Kueppers, R.; Rajewsky, K.
R;Mesin, U; Kueppers, Rajewsky, K.
R;Accession: 837514
A;Accession: 837514
A;Accession: 837514
A;Accession: 837514
A;Residues: preliminary
A;Rocious: 1-92 < KLE>
A;Residues: 1-92 < KLE>
A;Cross-references: EMEL: 226597; NID:9405670; PIDN:CAA81351.1; PID:9405671
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 - KLES
A;Cross-references: EMBL:226615; NID:g405676; PIDN:CAA81368.1; PID:g405677
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Matches 12; Conservative 0; Mismatches 0; Indels
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A; Reference number: S37501
A; Accession: S37517
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Search completed: April 21, 2004, 17:38:28 Job time : 10.9565 secs
22 RASOSVSSSYLA 33
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IG kappa chain precursor V-III region (NG9) - human (fragment)
IG kappa chain precursor V-III region (NG9) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Use (man)
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C;Genetics:
GDB:136266
A;Crosplex: An immunoglobulin heterotetramer subunit consists of two identical light (ket of standard of stalfide bonds: In some cases, such as ISA and IGM, the subunits associate into lain disulfide bonds: In some cases, such as ISA and IGM, the subunits associate into ly Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;1-4/Domain: signal sequence (fragment) #status predicted <NAT>
F;20-95/Domain: immunoglobulin homology <IMM>
F;21-95/Domain: immunoglobulin homology <IMM>
F;27-93/Disulfide bonds: #status predicted
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Species: Homo sapiens (man)
Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
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Cyaccession: PH0964

Rymartin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med 175, 981-991, 1992

A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291

A;Rocession: PH0964

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Copyright (c) 1993 - 2004 Compugen Ltd.
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		LT 1 HUMAN KV3C_HUMAN	P01621; 21-JUL-1986 (Rel. 01, ( 21-JUL-1999 (Rel. 01, 1 15-JUL-1999 (Rel. 38, 1 19 kappa chain V-III re	Homo sapiens (Human Eukaryota, Metazoa, Mammalla, Eutheria, NCBI_TaxID=9606;	SEQUENCE FROM N.A MEDLINE=84093600;	Bentley D.L.; "Most kappa i a small famil	-!- MISCELLA PIR; A01894	HSSP; P80363 GO; GO:00056	GO, GO:0006: GO, GO:0006: InterPro; Il	Pfam; PF000 SMART; SM00	PROSITE; PS Immunoglobu NON TER	CHAIN DISULFID	SEQUENCE	Query Match Best Local Sim Matches 12;	1 RA         28 RA	RESULT 2 KV3L HUMAN ID KV3L HUMAN	P18135; 01-NOV-1990 (Rel. 16, 0 01-NOV-1990 (Rel. 16, 15, JE, JE, JE, JE, JE, JE, JE, JE, JE, JE
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group.";
Biochemistry 20:5816-5822(1981).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
PIR; A01892; K3HUSI.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                       IG KAPPA CHAIN V-III REGION HIC.
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COMPLEMENTARITY-DETERMINING-1.
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100.0%; Score 53; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels
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FRAMEWORK-3.
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1998 (Rel. 38, Last annotation update)
1G kappa chain V-III region SIE.
Homo sapiens (Human).
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
FRm; PR0047; ig; 1.
FRM; SM00406; IGv.
PROSITE; PS50835; IG_LIKE; 1.
GO; GO:0003823; F:antigen binding; NA GO; GO:0006955; P:immune response; NA InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 1.
PROSTTE; SMO465; IGv.
PROSTTE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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-i- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                              MEDLINE=88171307; PubMed=3127527;

Kipps T.J. Tomhave E., Chen P.P., Carson D.A.;

Kipps T.J. Tomhave E., Chen P.P., Carson D.A.;

Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";

J. Exp. Med. 167:840-852(1988).

-1- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KV3M HUMAN STANDARD; PRT; 129 AA.
P18136;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 Asppa chain V-III region HIC precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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PRAMENOKK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMENOKK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                             PIR; PLO022; K3HUHA.
HSSP, P80362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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HSSP; P80362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
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SMART; SM00406; ig; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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Les 12; Conservative
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129 AA;
        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                              SEQUENCE FROM N.A.
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A Klapper D.G., Capra J.D.;

Klapper D.G., Capra J.D.;

The amino acid sequence of the variable regions of the light chains

The amino acid sequence of the variable regions of the light chains

Trom two idiotypically cross reactive IgM anti-gamma globulins.";

Ann. Immunol. (Paris) 127C:261-271(1976).

L. MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

R PISP; PR015C2; IWTL.

R HSSP; P8015C2; IWTL.

R GO; GO:0005576; C:extracellular; NAS.

R GO; GO:0005576; C:extracellular; NAS.

R GO; GO:0005576; C:extracellular; NAS.

R GO; GO:0006555; P:immune response; NAS.

R GO; GO:0006555; P:immune response; NAS.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups are interdigitated
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Pred. No. 0.0036;
2; Mismatches 0; Indels
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13-AUG-1987 (Rel. 05, Last sequence update)
15-VUL-1999 (Rel. 38, Last annotation update)
16 Kappa chain V-lil region VH precursor (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Nucleic Acids Res. 12:9229-9236(1984).
                                                                                                                                                                                                                                                                                     Ig kappa chain V-III region POM.
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RASQSISNSYLA 35
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   24 RASQSVSNSYLA 35
                                                                                                                                               STANDARD;
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Suter L., Barnikol H.U., Matanabe S., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
II). IV. The complete amino acid sequence and its significance for
the mechanism of antibody production.";

Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).

-i- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-i- MISCELLANBOUS: This is a Bence-Jones protein.

PIR; A01895; K3HUTI.
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21-UTL-1986 (Rel. 01, Created)
21-UTL-1986 (Rel. 01, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region Ti.
Ig kappa chain V-III region Ti.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3.
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Pred. No. 0.0038;
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                                                                                                                              HSSP, P80362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:autigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00110; Ig-11ke.
InterPro; IPR00110; Ig-11ke.
Ffan; PF00047; ig; 1.
SWART; SW00406; IGV; 1.
FROSITE; PSS0355; IG LIKE; 1.
Immunoglobulin V region; Signal.
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
                                                                          EMBL; X02725; -; NOT_ANNOTATED_CDS
PIR; A01901; K3HUVH.
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NCBI_TaxID=10090;
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KV4A MOUSE
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Biochemistry 20:5816-5822 (1981).
-- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GANMA
GLOBULIN ACTIVITY.
PIR, A04896, X3HUML.
HSSP, P80362; 1NTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
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Milstein C.;
Winstein C.;
Whe basic sequences of immunoglobulin kappa chains: sequence studies of Bence Jones proteins Rad, Fr4 and B6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andrews D.W., Capra J.D.; "Amino acid sequence of the variable regions of light chains from two idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
                                                                                         Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 0.024;
0; Mismatches 1; Indels
                            Length 109;
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109 AA; 11746 MW; 566C115E6B9CBEEE CRC64;
                                Score 46; DB 1;
Pred. No. 0.015;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region B6.
                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-III region WoL.
Homo sapiens (Human).
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                         Query Match

86.8%; Score 46; DB

Best Local Similarity 83.3%; Pred. No. 0.01

Matches 10; Conservative 2; Mismatches
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SMART; SM00406; 1Gv; 1.
PROSITE; PS50835; 1G LIKE; 1.
Immunoglobulin V region.
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Best Local Similarity 90.9%;
Matches 10; Conservative
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P01619;
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KV3A_HUMAN
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MEDLINE=82115300; PubMed=6799208;

Kwan S.-P., Max B.E., Seidman J.G., Leder P., Scharff M.D.;

Kwan S.-P., Wax B.E., Seidman J.G., Leder P., Scharff M.D.;

Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.;

Cell 26:57-66(1981).

-I. MISCELLANGOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO

AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS

SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE

NORMAL KAPPA CHAIN S107.
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P01680;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1998 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-IV region S107B precursor.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        81.1%; Score 43; DB 1; Length 108; 75.0%; Pred. No. 0.063; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                  108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;
FEBS Lett. 2:301-304(1969).

-!- MISCELLANBOUS: This is a Bence-Jones protein.

PIR, A01891, KHUUBG.

HSSP, 80362; 1WTL.

InterPro; IPR00710; Ig-like.

InterPro; IPR00710; Ig-like.

Fam; PF00047; ig; 1.

SMART; SMO040; IG; 1.

SMART; ES50315; IG LIKE; 1.

Immunoglobulin V region; Bence-Jones protein.

DISULED 23 89 BY SIMILARITY.

NON TER 108 108

SEQÜENCE 108 AA; 11635 MM; 8BC14FF07A419B3D CRC6
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SMARY; 8M0406; iGv, 1.
PROSITE, PSSGB35; IG LIKE; 1.
Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0%
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Arch. Bio
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                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-AUG-1998 (Rel. 138, Last annotation update)
15 Sappa chain V-III region VG precursor (Fragment).
19 Homo sapiens (Human).
19 Ederyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-85087932; PubMed-6440122;
Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups are interdigitated within the VK locus.";
Nucleic Acids Res. 12:9229-9236(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAPPA CHAIN V-III REGION VG.
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
BY SIMILARITY.
                                                                                 'Match 73.6%; Score 39; DB 1; Length 129; Local Similarity 90.0%; Pred. No. 0.53; les 9; Conservative 0; Mismatches 1; Indels
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COMPLEMENTARITY-DETERMINING-
FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-
COMPLEMENTARITY-DETERMINING-
FRAMEWORK-3.

COMPLEMENTARITY-DETERMINING-
COMPLEMENTARITY-DETERMINING-
BY SIMILARITY.

115

Ny, 2DE47CDA3A17D555 CRC64;
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  45 111 BY SIMILARITY.
129 129
129 AA; 13833 MW; E4BB73072DCF6BE4 CRC64;
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PTR, A01900; K3HUVG.
HSSP; P80362; UWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00710; IG-11ke.
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PPE00047; ig; 1.
; SM00406; IGv; 1.
TE; PSS0835; IG LIKE; 1.
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nes 11; Conservative
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DR GO; GO:00059
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bolorin A., Wincker P., Mauger S., Jaillon O., Malaxme K., Weissenbach J., Ehrlich S.D., Sorokin A.; The complete genome sequence of the lactic acid bacterium Lactococcus lactis sep. lactis IL1403.", Genome Res. 11:731-753 (2001).
                                                                15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last sequence (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI).
PGI OR PGIA OR LIZIS (Bubsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-19.
MEDLINE-97312580; PubMed=9169021;
Nomura M., Nakajima I., Matsuzaki M., Kimoto H., Suzuki I., Aso H.;
Nomura M., Nakajima I., Matsuzaki M., Kimoto H., Suzuki I., Aso H.;
"The N-terminal sequence of Lactococcus lactis phosphoglucose
isomerase purified by affinity chromatography differs from the other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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--- PATHWAY: Involved in glycolysis and in gluconeogenesis.
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: Belongs to the GPI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arch. Biochem. Biophys. 341:315-320(1997).
-!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.7%; Score 38; DB 1; Length 447; 72.7%; Pred. No. 3.6; 2; Indels ive 1; Mismatches 2; Indels
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PROSITE; PRODOFS; P GLUCOSE ISOMERASE 1; 1.
PROSITE; PSO0174; P GLUCOSE ISOMERASE 2; 1.
ISOMERASE; Gluconeogenesis; Glycolysis; Complete proteome.
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447 AA
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HAMNE, MC 00473; -; 1.
InterPro; IPRO01672; G6P_Isomerase.
Pfam; PP00342; PGI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21235186; PubMed=11337471;
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1360;
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P01674;
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KV3V MOUSE
ID KV3V M
AC P01674
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IG KAPPA CHAIN V-III REGION IARC/BL41.

COMPLEMENTARITY-DETERMINING-1.

FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
JX1. SEGMENT.
BY SIMILARITY

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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003825; F:immune response; NAS.
InterPro; IPR003595; Ig.
InterPro; IPR003595; Ig.v.
Ffam; PF00047; ig; I.
SMART; SM00406; IGv; I.
PR051TE; PS50835; IG_LIKE; I.
Immuncglobulin V region; Signal.
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118
13
128
128 AA;
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HSSP; P01607;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                      SEQUENCE.
MEDILIPA 9073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
COMPLEMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 1; Length 108; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-III region IARC/BL41 precursor.
Homo sapiens (Human)
   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
115-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 AA
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BY SIMILARITY.
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                                                                                                                                                                                                                                                            Nature 276:785-790 (1978).
PIR; A01940; KVMS54.
HASP; P80362; IWTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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STRAIN=NEM316 / Serctype III;
MEDLINE=22245108; PubMed=12354221;
AGlaser P., Rusniok C., Buchrisser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
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STRAIN=2603 V/R / Serctype V;
MEDLINE=222988; PubMed=12200547;
MEDLINE=222988; PubMed=12200547;
Madoff D.C., Wolf A.M., Benan M.D., Eisen J.A., Peterson S., Madoff L.C., Wolf A.M., Benan M.D., Brinkac L.M., Daugherty S.C., Monoff D.C., Wolf A.M., Rolonay J.F., Madupu R., Lewis M.R., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M. Lacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D. Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
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Mol. Microbiol. 45:1499-1513(2002).
                                                                                                                                                                                                                                                                                                            "Complete genome sequence and comparative genomic analysis of ar emerging human pathogen, serotype V Streptococcus agalactiae.";
Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
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                                        66.0%; Score 35; DB 1; Length 128; 88.9%; Pred. No. 3.6; Live 1; Mismatches 0; Indels
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14070 MW; CC8957F0FE3B9012 CRC64;
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                                                                                                          Conservative
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Thu Apr 22 05:59:17 2004

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EMBL; AL766645; CAD46081.1; -

EMBL; AL76645; CAD46081.1; -

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EMBL; AL7664209; AMM99308.1; -

EMBL; AL7664209; AMM99308.1; -

EMBL; AL7664209; AMM99308.1; -

EMBL; AL7664209; AMM99308.1; -

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EMBL; PRO0174; PGLUCOSE ISOMERASE 1; 1.

EMBL; PRO0174; PGLUCOSE ISOMERASE 2; 1.

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Best Local Similarity 63.6%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 2; Indels
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Search completed: April 21, 2004, 17:33:59 Job time : 7.08696 secs

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Q3yfh8 aeropyrum p
065720 arabidopsis
09193 arabidopsis
08pzg7 methanosarc
08pzg7 methanosarc
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07uvg1 rhodopiral]
04238 aeccharomyc
03xm3 lactobacill
042436 notophthalm
09c2d7 neurospora
09144 arabidopsis
096889 homo sapien
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           April 21, 2004, 17:26:23 ; Search time 32 Seconds (without alignments) 118.319 Million cell updates/sec
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                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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1: SP_archea:*

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3: Sp_fungi:*

4: Sp_human:*

5: Sp_invertebrate:*

6: Sp_mammal:*

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Title: Perfect score: Sequence:

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Scoring table:

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Gapa Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. ö Query Match
100.0%; Score 53; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 12; Conservative 0; Mismatches 0; Indels 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
(Fragment).
Homo sapiens (Human). SEQUENCE 109 AA; 11928 NW; 243325F72C7DAC83 CRC64; PRT; 109 AA PRELIMINARY; NCBI\_TaxID=9606; 09ULB6 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q9ULB6 Q9UL78 Q8UL78 Q8QQP6 Q8QQP6 Q8QQP6 Q9UL83 Q9UL83 Q8C3A7 Q8G3A7 Q8C3A7 Q8A82 Q8A82 Q8A82 Q8A82 Q8A82 Q8A82 Q8A82 Q8A82 Q8A82 Q8A82 Q8A82 Q8A82

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Young D.C.;
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SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
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QBKIF1;
Q1-CCT-2002 (TrEMBLrel. 22, Created)
O1-CCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
                                                                                                                                                                                                                      Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035036; AAD56272.1; -.
PIR; A30601; A30608.
PIR; B30601; B30601.
PIR; B30607; B30607.
                                                      PRT; 109 AA.
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INTERPRO; IPR007110; IG-like.
InterPro; IPR003596; IG-V.
Pfan; PF00047; ig; 1.
SWART; SW00406; IGV; 1.
PROSITE; PSS0835; IG-LIKE; 1.
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24 RASQSVSSSYLA 35
                                                       PRELIMINARY;
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PIR; F30607; F30607.

PIR; G30601; G30601.

PIR; H30601; G30601.

PIR; H30607; H30607.

PIR; H30607; H30607.

PIR; PH0965; PH0963.

PIR; PH0965; PH0963.
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A zhou Y.-X., Taquchi H., Planque S., Karle S., Nishiyama Y., Paul S.;

Zhou Y.-X., Taquchi H., Planque S., Karle S., Nishiyama Y., Paul S.;

Innate proteolytic antibodies: Falled D-VIPase response to the D-
minate proteolytic antibodies: Falled D-VIPase V. Gonains.";

It submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

BEL, AFSI6284, AAM64202.1;

BEL, AFSI6284, AAM64202.1;

REL, ARSI6284, AAM64202.1;

REL, ARSI6284, AAM64202.1;

RICEPPO: IPRO03599; IG.

InterPro: IPRO03599; IG.

InterPro: IPRO03599; IG.

RART; SMO0409; IG. 1.

RARAT; SMO0406; IG. 1.

RARAT; SMO0406; IG. 1.

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RARAT; SMO0406; IG. 1.

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RARAT; SMO0406; IG. 1.
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SEQUENCE FROM N.A.

STRAIN=WEL/MpJ-lpr/lpr; TISSUE=Spleen;

A Takahashi S., Iroh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;

Takahashi S., Iroh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;

Takahashi S., Iroh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;

Takahashi S., Iroh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;

Takahashi S., Iroh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;

Takahashi S., Iroh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;

Mol. Immunol. 30:177-18(1933).

R. Mal. Immunol. 30:177-18(1933).

R. RhEL; D14629; BAA03482.1; -.

R. RhEL; D14629; BAA03482.1; -.

R. InterPro; IPR00359; Ig.

R. RhEL; D14629; BAA03482.1; -.

R. SMART; SM00406; Ig. I.

R. RAART; SM00406; IG. I.

R. RAART; SM00406; IG. II.

R. PROSITE; PS50835; IG_LIKE; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutherla, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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IMMUNOGLOBULIN GAMMA-3 KAPPA CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.0%; Score 44; DB 11; Length 114; 90.9%; Pred. No. 0.32; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ol-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Munoglobulin gamma-3 kappa chain precursor (Fragment).
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CHAIN 23 >131 IMMUNOGLOBULIN GAMMA-3 KAF
NON TER 131 131
SEQÜENCE 131 AA; 14083 MW; 558365695466659E CRC64;
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                              SEQUENCE FROM N.A
                                                                                       NCBI_TaxID=10090;
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SIGNAL
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46 RASSSVRSSYL 56

RESULT 5

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SEQUENCE FROM N.A.
Blank L.M., Hugehholtz P., Nielsen L.K.;
Blank L.M., Hugehholtz P., Nielsen L.K.;

"Cloning and characterization of the hyaluronic acid synthesis (has) operon from Streptococcus equi subsp. zooepidemicus.";

Submitteed (FBE-2011) to the EMBL/GenBank/DDBJ databases.

EMBL; AR347022; ARM65521; -.

GO; GO:0004347; F:glucose-6-phosphate isomerase activity; IEA.

GO; GO:0006094; F:glucose-6-phosphate isomerase activity; IEA.

GO; GO:0006094; F:glucose-genesis; IEA.

Interpro; IRRO0162; GP_ISOMERASE.

PEAM; PRO0342; PGI; 1.

PRINTS; PRO0342; PGI; 1.

PRINTS; PRO0342; GF_ISOMERASE.
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STRAIN=13 / Type A;

MEDLINE=21664373; PubMed=11792842;

Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,

Shimizu T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;

Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater.";

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).

Hypothetical protein; Complete protecome.

SEQUENCE 363 AA; 39379 MM; 791E04184ACBEDC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.8%; Score 37; DB 16; Length 363; Best Local Similarity 70.0%; Pred. No. 33; Matches 7; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.7%; Score 38; DB 2; Length 449; 72.7%; Pred. No. 26; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                           Streptococcus equi subsp. zooepidemicus.
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 AA; 49509 MW; FC23F8B6D404D96D CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Pypothetical protein CPE1546.
                                                                                      01-Mar-2003 (TrEMBLrel. 23, Created)
01-Mar-2003 (TrEMBLrel. 23, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Glucose-6-phosphate isomerase.
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PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
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les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AGNSISSSYLA 127
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                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=40041;
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NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isomerase.
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                         Q8GDP6
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Matches
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MEDLINE=20448942; PubMed=10992488;
MEDLINE=20448942; PubMed=10992488;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of streprococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
EMBL, AF206028; ARF69326.1; -.
BIRSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCDI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo gapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=98271139; PubMed=9614934;
ML X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.0%; Score 35; DB 11; Length 101; 70.0%; Pred. No. 21; ative 2; Mismatches 1; Indels
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01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sentencion update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 101
101 AA; 10778 MW; 0A7F65E6A7E6F14D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clin. Immunol. Immunopathol. 87:184-192 (1998)
EMBL, AP035031 AAD56267.1; -.
PIR, B30609, B30609.
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                                                                                                 101 AA
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                                                                                               PRT;
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InterPro; IPR003596; Ig.v.
Pfam: PR0047; ig. 1.
SMART: SM00406; IGv; 1.
PROSITE; PS50835; IG-LIKE; 1.
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Best Local Similarity 70...
Triconservative
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2 ASOSVSSSYL 11
                81 SSQSISSSYV 90
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09JL78;
01-OCT-2000
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MEDLINE-22265278; PubMed=12381468;
Sachse S., Seidel P., Gerlach D., Guenther E., Roedel J., Straube E.,
Schmidt K.H.;
                                                                 Tourier to the gene (s) in human pathogenic Streptococcus dysgalactiae, subsp. equisimilis: Genomic localization of the gene ancoding streptococcal pyrogenic exctoxin G (sped).";

I encoding streptococcal pyrogenic exctoxin G (sped).";

FEMS Immunol. Med. Microbiol. 34:159-167(2002).

R EMBL; Au489606; CAD33905.1; ...

R GO; GO:0006933; F::Somerase activity; IEA.

R GO; GO:0006094; P::Slucose-6-phosphate isomerase activity; IEA.

R GO; GO:0006094; P::Slucose-genesis; IEA.

R GO; GO:0006096; P::Slucose-genesis; IEA.

R GO; GO:0006096; P::Slucose-genesis; IEA.

R FAD; PPO0342; PGI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

1JAcl W.P.-J., van Strien E.A., Heldens J.G.M., Broer R., Zuidema Goldbach R.W., Vlak J.M.,
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDIINE=20036646; PubMed=10567663;
IJVEI W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.W.;
"Sequence and organization of the spodoptera exigua multicapsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.0%; Score 35; DB 12; Length 388; 75.0%; Pred. No. 94; 1:ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 2; Length 195;
Pred. No. 44;
2; Mismatches 2; Indels
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InterPro; IPR008562; DUF844.
Pfam; PF05815; DUF844; 1.
SEQUENCE 388 AA; 43654 MW; 9DDA0BCCBEFC9777 CRC64;
                                                                                                                                                                                                                                                                                                              195 AA; 21515 MW; 52C0182D022B1F45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses, dsDNA viruses, no RNA stage; Baculoviridae, Nucleopolyhedrovirus.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
0RF64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 AA
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J. Gen. Virol. 80:3289-3304(1999)
                                                                                                                                                                                                                                                                                                                                                                         63.68;
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                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 63.0
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Q8RP79
ID Q8RP7
AC Q8RP7
DT 01-JUD
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Q9J871
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MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium.
The FANTOM Consortium of the Riken Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Thanslysis of the mouse transcriptome based on functional annotation of 60,770 full-length counse.";
Mature 420:563-573 (2002).
EMBL; AKO86466; BAC39674.1; -.
EMBL; AKO86466; BAC39674.1; -.
EMBL; AKO86466; BAC39674.1; -.
EMBL; AKO86466; BAC39674.1; -.
EMBL; AKO86466; BAC39674.1; -.
EMBL; AKO86466; BAC39674.1; -.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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66.0%; Score 35; DB 4; Length 108;

Best Local Similarity 88.9%; Pred. No. 23;

Matches 8; Conservative 1; Mismatches 0; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Putative glucose-6-phospate isomerase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
D930030005RIK
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                                                    HSSP, P80362; IWTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; I.
SMART; SM00406; IGv; I.
PROSITE; PS50835; IG_LIKE; I.
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Best Local Similarity 66.77
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RGSQNSSSSWLA 81
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PIR; S34098; S34098.
PIR; S34099; S34099.
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Q8C3A7

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Created) Last sequence update)

01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,

PRELIMINARY;

Q8RP79 Q8RP79;

Streptococcus. NCBI\_TaxID=119602; [1] SEQUENCE FROM N.A.

RESULT 10
28G9K4
1D CORG9K
AC 08G9K
AC 08G9K
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TRP SEQUE

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1 RASQSVSSSYL 11
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Q96A82;
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2098VP0
2098VP0
AC 098VP
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DT 01-MA
DT 01-MA
DT 822D1
GN Arabi
OC Sarabi
COC Sperm
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AC 09648
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Read T.D., Pouts D.E., Myers G.S.A., Nelson K.E., Seshadri R.,

Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,

Tettelin H., Dodson R.T., Umxin S., Kolonay J., Madupu R., Nelson M.,

Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson M.,

Namathavan J., Fran B., Upton J., Hansen T., Shetty J., Knouri H.,

Namathavan J., Radune D., Ketchum K.A., Dougherty J., Fraser C.M.;

"Role of mobile DNA in the evolution of vancomycin-resistant

Enterococcus facealis.",

Science 299:2071-2074(2003)

EMBL; AE016951; AA081207.1; -.

RIGO, GO:0004447; F:glucose-6-phosphate isomerase activity; IEA.

GO; GO:0016853; F:isomerase activity; IEA.
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Infect. Immun. 70:1254-1259(2002).

-! CATLYTIC ACTIVITY: D-GLUGOSE 6-PHOSPHATE = D-FRUCTOSE 6-PHOSPHATE.

-!- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.

-!- SUBLILARITY: BELONGS TO THE GPI PAMILY.

-!- SIMILARITY: BELONGS TO THE GPI PAMILY.

--- SIMILARITY: BELONGS TO THE GPI PAMILY.

--- SIMILARITY: PROCATION: CYTOPLASMIC (BY SIMILARITY).

--- SIMILARITY: PELONGS TO THE GPI PAMILY.

--- SIMILARITY: PROCATION: CYTOPLASMIC (BY SIMILARITY).

--- SIMILARITY: PROCASO-6-phosphate isomerase activity; IEA.

--- GO; GO:000693; P:Gluconeogenesis; IEA.

--- R GO; GO:000693; P:Gluconeogenesis; IEA.

--- R GO; GO:000603; P:Glycolysis; IEA.

--- R PRINTS: PROO342; PGI; I.

--- PRINTS: PROO362; GGEISOMERASE.
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDILIA=21843113; PubMed=11854208;

MEDILIA=21843113; PubMed=11854208;

Younes Z.N., Moore J.C., Lane J.D., Wilson R., Pribul P.K.,

Younes Z.N., Dobson R.J., Everest P., Reason A.J., Redfern J.M.,

Greer F.M., Paxcon T., Panico M., Morris H.R., Feldman R.G.,

Santangelo J.D.;

"Identification of Major Outer Surface Proteins of Streptococcus
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Glucose-6-phosphate isomerase (BC 5.3.1.9) (GPI) (Phosphoglucose
isomerase) (PGI) (Phosphohexose isomerase) (PHI).
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                                                                                                      Streptococcus agalactiãe.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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PROSITE; PS00174; P GLUCOSE ISOMERASE 2; 1.
GLUCODEOGENESIS; GLYCOLYSIS; ISOMERASE.
SEQUENCE 449 AA; 49585 MW; 5199E72DEOCDCEIB CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Glucose-6-phosphate isomerase.
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117 AGNSISSTYLA 127
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NCBI_TaxID=1311;
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Nighi T., Nakagawa S., Sench A., Mizuguchi H., Inagaki H.,
Nishi T., Nakagawa S., Sench A., Mizuguchi H., Inagaki H.,
Nishi T., Inser, Otsuki T., Sato H., Ota T., Wakamatsu A.,
Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
Ishii S., Yamanoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
A Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
Rubo human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO54668; BAB70788.1;
InterPro; IPR007421; DUF467.
RHYPOTHORIASE; AAA div; 1.
KHYPOTHORIASE; AAA div; 1.
KHYPOTHORIASE; AAA div; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels
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Pred. No. 2e+02;
1; Mismatches 2; Indels
GO; GO:0006094; P:gluconeogenesis; IEA.

GO; GO:0006096; P:glycolysis; IEA.
Interpro; IPRO01672; G6P Isomerase.
PETAM; PRO01842; PGI: 1.
PRINTS; PRO0662; G6PISOMERASE.
PROSITE; PS00765; PGLUCOSE ISOMERASE 1; 1.
PROSITE; PS00714; PGLUCOSE_ISOMERASE 2; 1.
ISOMErase, Complete protecome.
SEQUENCE 449 AA; 49734 MM; IDFIA5BSD483D336 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DBC-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein FLJ30106 (Fragment).
Homo sapiens (Human)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
10-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
F22113.120 OR AT4G38350.
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Best Local Similarity 72.7%;
Matches 8; Conservative
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RP SEQUENCE FROM N.A.

RA Bevan M., Wedler H., Kutzner M., Wambutt R., Bancroft I., Mewes H.W.,
R. Bevan M., Schweller C.;
R. Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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R. Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
R. Mayer K.F.X.;
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R. Mayer K.F.X.;
R. Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
R. Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
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Search completed: April 21, 2004, 17:37:18 Job time : 34 secs

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GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  OM protein - protein search, using sw model  Run on: April 21, 2004, 17:25:18; search time 48 Seconds  (without alignments) 70.637 Million cell updates/sec	Title: Perfect score: 53 Sequence: 1 rasgsvsssyla 12	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 1586107 seqs, 282547505 residues	Total number of hits satisfying chosen parameters: 1586107
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

A\_Geneseq\_29Jan04:\*
1: geneseqp1980s:\*
2: geneseqp21990s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003s:\*
7: geneseqp2003bs:\*
8: geneseqp2003bs:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARIES

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	Description	Aar15375	Aau70331	Aau83718	Abb57480	Abb57475	Abb57469	Abb57472	Aae38096	Aae38067	Ada90302	Ada90308	Ada90317	Ada90323	Ada90324	Ada90641	Ada90751	Ada90867	Ada90869	Ada91097	Ada90322	Ada90487	Ada90497	Ada90871	Ada90953	Ada91010
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SUMMARIES	ΩI	AAR15375	AAU70331	AAU83718	ABB57480	ABB57475	ABB57469	ABB57472	AAE38096	AAE38067	ADA90302	ADA90308	ADA90317	ADA90323	ADA90324	ADA90641	ADA90751	ADA90867	ADA90869	ADA91097	ADA90322	ADA90487	ADA90497	ADA90871	ADA90953	ADA91010
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels

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56	27	28	50	30	31	32	33	3.4	3	36	3.7	80	66	40	41	2	43	4	45	

# ALIGNMENTS

RESULT AAR153	RESULT 1 AAR15375 TD AR815375 standard: protein: 12 AA.
XX.	
X	25-MAR-2003 (revised) 05-MAR-1992 (first entry)
X E	Igm-RF Glo.
ŽŽ:	Rheumatoid factor; RF; antigen; CDR; IgM.
X 8 :	Synthetic.
X Z	US5068177-A.
X & :	26-NOV-1991.
X E I	05-AUG-1985; 85US-00762698.
X E	05-AUG-1985; 85US-00762698.
X &	(SCRI ) SCRIPPS CLINIC & RES FOUND.
žE;	Carson DA, Fong S, Chen PP;
ž 8	WPI; 1991-368612/50.
X L L L	Synthetic polypeptide(s) for inducing anti-idiotype antibodies - useful for treating auto immune-, endocrine- and rheumatic-diseases and myasthenia gravis.
X 82	Claim 10; Page 42; 44pp; English.
%888888888%%	Three rabbits were incculated with two s.c. injections of PGL1 (synthetic peptide) conjugated to KLH as an immunogen, and their sera were analysed for anti-peptide antibody activity by BLISA. All three immunised rabbits produced anti-PGL1 antibody. Antisera drawn from a rabbit on two different days reacted significantly with the corresp. intact IgM-RF Glo. See also AAR15365-74 and AAR15375. (Updated on 25-MAR-2003 to correct PA field.)

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Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding protein polypeptides specific to ligand, selecting plant cells for
                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin; antibody; light chain; heavy chain; CDR; FR; complementarity determining region; framework region; IgBP; transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 14; 129pp; English.
                                                                                                                                                                                         AAU70331 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                        Human Kappa III light chain CDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAY-2001; 2001WO-US014349
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                                                                                                                                                                                                                                                                                                     (first entry)
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ANUB3718 standard, paptide, 12 AA.

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B. G. HAW-2002 (first entry)

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Gaps

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100.0%; Score 53; DB 5; Length 12; 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 12; Conserv

RESULT 3

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mechanisms are needed to cause or lead to the killing. The killing is dependent on the action of non-capsase proteases and/or cannot be inhibited by zVAD-fmk or zDEVD-fmk. The present sequence is a complementarity determining region (CDR) based on the human antigen binding polypeptides of the invention MS-GPC-1, 6, 8 and 10. The CDRs are either the native sequence or have been optimised/mutated to alter their antigen binding capabilities
                                                                                                                                                                                                                           Sequence 12 AA;
        88888888888
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100.0%; Score 53; DB 5; Length 12; 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels
    Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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ABB57480 standard; peptide; 12 AA.
                                                                                       18-MAR-2002 (first entry)
                                            ABB57480;
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HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-6.

Immunomodulatory human MHC class II antigen-binding protein; HLA; human leukocyte antigen; immune system; immunosuppression; antibody; major histocompartibility complex; antidiabetic; antiabritic; neuroprotective; antilifammatory; antidiabetic; antipsoriatic; immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis; thyronimetic; hepatotropic; immune response suppressor; narcologis; theumatoid arthritis; imvenile arthritis; multiple solerosis; insultis; Grave's disease; insulin-dependent diabetes; Hashimoto's disease; systemic lupus erythematosus; ankylosing spondylitis; masthenia gravis; transplant rejection; graft versus host disease; pemphigus vulgaris; glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirrhosis; irritable bowel disease; Sjogren's syndrome. 

Homo sabiens. Synthetic. WO200187338-A1.

22-NOV-2001.

14-MAY-2001; 2001WO-US015626.

12-MAY-2000; 2000EP-00110063. 06-OCT-2000; 2000US-0238762P.

GPCB-) GPC BIOTECH AG. (MORP-) MORPHOSYS AG. Thomassen-Wolf E; Tesar M, Nagy Z,

WPI; 2002-075289/10.

Composition for suppressing immune response, treating diseases of immune system, has polypeptide comprising antibody-based antigen-binding domain of human composition, which binds antigen expressed on a cell surface.

Example; Page 60; 139pp; English.

The present invention describes a composition (I), comprising a polypeptide comprising an antibody-based antigen-binding domain of human composition with binding specificity for an antigen expressed on the surface of a cell, where treating cells expressing the antigen with the polypeptides leads to suppression of an immune response, and the IC50 for the suppression of immune response is 1 microM or less. (I) has

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antirheumatic, antiarthritic, neuroprotective, antinflammatory,
antidabetic, antipsoriatic, immunosuppressive, dermatological,
can tidhyroid, nephrotropic, thyromimetic and hepatocropic activities, and
can be used as suppressor of immune response. (I) is useful for
can be used as suppressor of immune response. (I) is useful for
suppressing IL-2 secretion by a cell, the interaction of a cell of the
immune system with another cell, immunosuppressing a patient and for
ckilling a cell expressing an antigen, human leukocyte antigen (HiA)-DR on
the surface of the cell, where neither cytotoxic entities nor
ckilling a cell expressing an antigen, human leukocyte antigen (HiA)-DR on
the surface of the cell, where neither cytotoxic entities nor
cmannological mechanisms are needed to cause or lead to the killing. (I)
(optionally linked to cytotoxic or immunogenic agent) is useful for
cytotoxillis, juvenile arthritis, multiple solerosis, Grave's disease,
crathritis, juvenile arthritis, multiple solerosis, Grave's disease,
insulin-dependent diabetes, narcolopsy, psoriasis, systemic lupus
crathritis, lawingoto's disease, myashbania gravis, pemphigus vulgaris,
colomerulonephritis, thyroiditis, pancreatitis, insulitis, primary biliary
cirrhosis, irritable bowel disease and Sjogren's syndrome in humans.

CRABA22469 to ABA92474 and ABB57590 represent sequence used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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100.0%; Score 53; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
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HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-4. ABB57475 standard; peptide; 12 AA. 18-MAR-2002 (first entry) 

Immunomodulatory human MHC class II antigen-binding protein; HLA; human leukocyte antigen; immune system; immunosuppression; antibody; major histocompatibility complex; antithermatic; antiantifitition; introductive; antiminflammatory; antidiabetic; antiposoriatic; immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis; thyromimetic; hepatotropic; immune response suppressor; narcologis; rheumatoid arthritis; juvenile arthritis; multiple solerosis; insulitis; grave's disease; insulin-dependent diabetes; Hashimoto's disease; systemic lupus erythematosus; ankylosing spondylitis; mysathenia gravis; gransplant rejection; graft versus host disease; pemphigus vulgaris; glomerulonephritis; thyroiditis; panoreatitis; primary biliary cirrhosis; irritable bowel disease; Sjogren's syndrome.

Synthetic.

40200187338-A1 22-NOV-2001.

14-MAY-2001; 2001WO-US015626. 12-MAY-2000; 2000EP-00110063. 06-OCT-2000; 2000US-0238762P.

(GPCB-) GPC BIOTECH AG. (MORP-) MORPHOSYS AG. (MORP-)

Thomassen-Wolf E; Nagy Z, Tesar M,

WPI; 2002-075289/10

22-NOV-2001

Composition for suppressing immune response, treating diseases of immune system, has polypeptide comprising antibody-based antigen-binding domain of human composition, which binds antigen expressed on a cell surface.

Example, Page 60; 139pp; English.

The present invention describes a composition (I), comprising a composition with binding specificity for an antigen expressed on the camposition with binding specificity for an antigen expressed on the surface of a cell, where treating cells expressing the antigen with the cautient expressed on the suppression of immune response, and the ICSO for the suppression of immune response, and the ICSO for antidiabetic, antipsoriatic, immunosuppressive, dermatological, antidiabetic, antipsoriatic, immunosuppressive, dermatological, antidiabetic, antipsoriatic, immunosuppressive, dermatological, can be used as a suppressor of immune response. (I) is useful for can be used as a suppressor of immune response. (I) is useful for suppressing activation or proliferation of a cell of the immune system, compared to call, where cell, immunosuppressing a patient and for killing a cell expressing an antigen human leukocyte antigen (HLA)-DR on the surface of the cell, where neither cytotoxic entities not immunological mechanisms are needed to cause or lead to the killing. (I) (optionally linked to cytotoxic or immunogenic agent) is useful for preparing a pharmaceutical preparation for the treatment of rheumatoid arthritis, juvenile arthritis, multiple solerosis, Grave's disease, insulin-dependent diabetes, narcolepsy, psoriasis, systemic lupus corporation, grave disease, insulint corporation, grave and signame, corporation, grave and signame, corporation pharmaceutics, hyproidities, pancreatities, insulities, primary biliary corporation of the present invention corporation humans.

Sequence 12 AA;

Gaps ; 0 Query Match
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels

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ABB57469 standard; peptide; 12 AA

ABB57469;

18-MAR-2002 (first entry)

HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-2.

Immunomodulatory human MHC class II antigen-binding protein; HLA; human leukocyte antigen; immune system; immunosuppression; antibody; and partbrittic; netastrocmpartibility complex; antidiabetic; antistrbritic; immunosuppressive; dermatological; antidiabetic; antipsoriatic; immunosuppressive; dermatological; antidiabetic; nephrotropic; psoriasis; theumatoid arthritis; immunosuspressor; narcolepsy; rheumatoid arthritis; imvenie arthritis; multiple solerosis; insulitis; grave's disease; insulin-dependent diabetes; Hashimoto's disease; systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis; transplant rejection; graft versus host disease; pemphigus vulgaris; glomerulonephritis; thyroiditis; pancreatitis; primary biliary cirhosis; irritable bowel disease; Sjogren's syndrome. RESULT 6
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sapiens

WO200187338-A1

The present invention describes a composition (I), comprising a polypeptide comprising an antibody-based antigen-binding domain of human composition with binding specificity for an antigen expressed on the curface of a cell, where treating cells expressing the antigen with the curface of a cell, where treating cells expressing the antigen with the polypetides leads to suppression of immune response, and the IC50 for the suppression of immune response, and the IC50 for antidiabetic, antipeoriatic, neuroprotective, antidiahetic, antipeoriatic, immunosuppressive, dermatological, antidiabetic, antipeoriatic, immunosuppressive, dermatological, can be used as a suppressor of immune response. (I) is useful for cur be used as a suppressor of immune response. (I) is useful for suppressing activation or proliferation of a cell of the immune system, comparessing in the cell, where cell, immunosuppressing a patient and for killing a cell expressing an antigen, human leukocyte antigen (HiA)-DR on the surface of the cell, where neither cytocoxic entities nor immunological mechanisms are needed to cause or lead to the killing. (I) (optionally linked to cytotoxic or immunogenic agent) is useful for preparing a pharmaceutical preparation for the treatment of rheumatoid arthritis, juvanile arthritis, multiple sclerosis, Grave's disease, insuliary comparation to the treatment of rheumatoid carbinesses, ankylosing spondylitis, transplant rejection, graft versus comparation the dependent diabetes manacolessy, psoxiasis, systemic lumpus comparation; insuliary insuliaris, thyroiditis, pancreatitis, insuliaris, phanacoles, continosis, insuliaris, thymodialiases and 3902469 to Aba92469 position for suppressing immune response, treating diseases of immune system, has polypeptide comprising antibody-based antigen-binding domain of human composition, which binds antigen expressed on a cell surface. ö Thomassen-Wolf Example; Page 60; 139pp; English. 14-MAY-2001; 2001WO-US015626. 12-MAY-2000; 2000EP-00110063 06-OCT-2000; 2000US-0238762P (GPCB-) GPC BIOTECH AG. (MORP-) MORPHOSYS AG. WPI; 2002-075289/10. Tesar M, Sequence 12 AA; Nagy Z, 

Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels

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ABB57472 standard; peptide; 12 AA. 18-MAR-2002 (first entry) ABB57472; ABB57472 8X8X8X8X8X8X

RESULT 7

HLA-DR-specific protein VL-CDR1-Sequence MS-GPC-3.

Immunomodulatory human MHC class II antigen-binding protein, HLA; human leukocyte antigen; immune system; immunosuppression; antibody; major histocompatibility complex; antitheumatic; antiarthritic; neuroprotective; antithfammatory; antidabetic; antipsoriatic; immunosuppressive; dermatological; antithyroid; nephrotropic; psoriasis;

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Homo
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thyromimetic; hepatotropic; immune response suppressor; narcolepsy; hematoid arthritis; juvenile arthritis; multiple sclerosis; insulitis; Grave's disease; insulin-dependent diabetes; Hashimoto's disease; systemic lupus erythematosus; ankylosing spondylitis; myasthenia gravis; stransplant rejection; graft versus host disease; pemphigus vulgaris; glomerulonophritis; thyroiditis; panoreatitis; primary biliary cirrhosis; irritable bowel disease; Sjogren's syndrome.
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sapiens. Synthetic. WO200187338-A1

22-NOV-2001

14-MAY-2001; 2001WO-US015626.

12-MAY-2000; 2000EP-00110063. 06-OCT-2000; 2000US-0238762P

(GPCB-) GPC BIOTECH AG. (MORP-) MORPHOSYS AG.

Thomassen-Wolf E; Tesar M, Nagy Z,

WPI; 2002-075289/10.

Composition for suppressing immune response, treating diseases of immune system, has polypeptide comprising antibody-based antigen-binding domain of human composition, which binds antigen expressed on a cell surface.

Example; Page 60; 139pp; English.

The present invention describes a composition (I), comprising a composition with binding specificity for an antigen expressed on the cauface of a cell, where treating cells expressing the antigen with the surface of a cell, where treating cells expressing the antigen with the cautace of a cell, where treating cells expressing the antigen with the polypeptides leads to suppression of an immune response, and the ICSO for the suppression of immune presence, and the ICSO for antidabetic, antiarthritic, immunosuppressive, dermatological, antidathyroid, nephrotropic, thyromimetic and hepatocropic activities, and can be used as a suppressor of immune ersponse. (I) is useful for suppressing IL-2 secretion by a cell, the interaction of a cell of the immune system with another cell, immunosuppressing patient and for chilling a cell expressing an antigen, human leukocyte antigen (HLA)-DR on the surface of the cell, where neither cytotoxic entities nor continually linked to cytotoxic or immunogenic agent) is useful for or preparing a pharmaceutical preparation for the treatment of rheumatoid archingular jubetes, narcolepsy, psoriaais, systemic lupus carbritis, juvenile arthritis, multiple sclerosis, Grave's disease, insulin-dependent diabetes, narcolepsy, psoriaais, systemic lupus carbritis, irritable bowel disease, mysathenia gravis, pemphigus vulgaris, continual irritable bowel disease and Sjogren's syndrome in humans.

The properties of the call disease and Sjogren's syndrome in humans.

The properties of the call disease and Sjogren's syndrome in humans. the exemplification of the present invention

Sequence 12 AA;

Gaps ö 100.0%; Score 53; DB 5; Length 12; 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels 12; Conservative Query Match Best Local Similarity

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RASQSVSSSYLA 12

RASOSVSSSYLA 12 d

AAE38096 RESULT

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AAE38096 standard; peptide; 12 AA
                                       AAE38096;
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(first entry) 36-NOV-2003 Human COU-1 antibody VL CDR1 peptide #1.

Human, cancer-associated epitope, cytokeratin KB; cytokeratin K18; VL; adenocarcinoma, therapy; cancer; antibody; light chain variable region; complementarity determining region; CDR.

402003057168-A2

17-JUL-2003.

03-JAN-2003; 2003WO-US000297

03-JAN-2002; 2002US-0345208P.

(SCRI ) SCRIPPS RES INST.

Ditzel H, Jensenius JC;

WPI; 2003-598315/56

Novel isolated cancer-associated epitope comprising two separate polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18 polypeptide, useful as component of vaccine for preventing or treating adenocarcinoma.

Claim 15; Page 36; 155pp; English.

The invention provides a cancer-associated epitope comprising two separate polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18 polypeptide. Vaccine composition of the invention is useful for treating or preventing colon adenocarcinoma, ovarian adenocarcinoma, renal adenocarcinoma, mammary adenocarcinoma, lumg adenocarcinoma, pancreatic adenocarcinoma or non-seminomal testis carcinoma. The invention is also mammal. The present sequence is human COV-1 cancer-associated epitope antibody VL (light chain variable region) CDR (complementarity 

Sequence 12 AA;

Gaps ö 100.0%; Score 53; DB 6; Length 12; 100.0%; Pred. No. 0.0013; .ive 0, Mismatches 0; Indels Conservative Similarity 12, Conserv Query Match Best Local

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RESULT 9 AAE38067

AAE38067 standard; peptide; 12 AA. 

(first entry) 06-NOV-2003 Human 17G1 CD30 antibody VL CDR1 peptide.

Human; antibody; CD30; tumour; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; systemic sclerosis; Grave's disease; ALCL; atopic dermatitis; Hashimoto's thyroiditis; chronic renal failure; ALD; acute infectious mononucleosis; angioimmunoblastic lymphadesnopathy; HIV; Hodgkin's disease; Castleman's disease; Kaposi's sarcoma; lymphoma; ATL; adult T cell lymphoma; human immunodeficiency virus; carcinoma; therapy;

WO2003070760-A2 Homo sapiens.

Synthetic

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Wegner's granulomatosis; anaplastic large cell lymphoma; Omen's syndrome;
light chain variable domain; VL; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-598476/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MEDA-) MEDAREX INC.
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                                                                                                          Homo sapiens
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20-FEB-2002; 2002EP-00003844. 20-FEB-2003; 2003WO-EP001759 28-AUG-2003. (MORP-) ઠે 셤 The invention relates to human monoclonal antibody that binds to human CC CD30. The antibody is useful for treating or preventing tumour or autoimmune disease e.g. rheumacoid arthritis, systemic lupus carteimmune disease e.g. rheumacoid arthritis, systemic lupus cerythematosus, systemic sclerosis, atopic dermatitis, Grave's disease, CC chronic renal failure, acute infectious monouncleosis, herges or HIV (human immunodeficiency virus) virus-associated diseases. The antibody is also useful for treating Hodgkin's disease, anaplastic large cell lymphoma (ALCL), adult T cell lymphoma (ATL), angloimmunoblastic coll lymphadenopathy (ALLD)-like T cell lymphoma, HIV associated body cavity lymphomas, embryonal carcinomas, undifferentiated carcinomas of the chino-pharynx (e.g. Schmincke's tumour), Castleman's disease, Raposi's sarcoma and other T-cell or B-cell lymphomas. The present sequence is Sarcoma and other T-cell or B-cell lymphomas. The present sequence is human CD30 antibody VI (light chain variable domain) CDR (complementarity determining region) peptide ö antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; a disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging. Gaps New human monoclonal antibody that binds to human CD30, useful for treating or preventing tumor or autoimmune disease, e.g., rheumatoid ·. Query Match
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels MS-Roche #3.2 L-CDR1 amino acid sequence. Disclosure; Page 117; 122pp; English. ADA90302 standard; peptide; 12 AA. Treml J; 09-JAN-2002; 2002US-0347649P. 19-AUG-2002; 2002US-0404427P. 06-DEC-2002; 2002US-0431684P. 07-JAN-2003; 2003WO-US000440. (first entry) 1 RASOSVSSSYLA 12 RASOSVSSYLA 12 Keler T, Graziano R,

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The present invention describes an antibody molecule (I) capable of pecifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Gul-Phe-Arg-His-Asp-Good Comprises the amino acid sequence Ala-Gul-Phe-Arg-His-Arg-His-Abla-Gul-Lya-Lya-Dhagagge or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gul-Lya-Lya-Phe-Phe-Ala-Gul-App-Val-Composition (I) Appagger or its fragment. Also described: (I) a nucleic acid molecule calcomprising the vector comprising the nucleic acid of (I); (3) a vector comprising the nucleic acid of (I); (3) a nucleic acid of (I); (4) preparing (I), comprising (I) culturing the host cell of (3) under conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of (I); (8) testing the resulting Fab optimisation library by panning (I); (8) testing the resulting Fab optimisation library by panning (I); (8) testing the resulting Fab optimisation of (I); and formulating the composition, comprising optimisation of (I); and formulating the composition, comprising optimisation of (I); and formulating the composition prepared by method (8). (1) has a composition comprising optimisation of (I); and formulating the composition prepared by method (8). (1) has a composition for composition preparing a pharmaceutical composition for composition preparing a pharmaceutical composition for composition preparing a disposit composition for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease is capinity because is the disease mentioned above. The antibody is used for the disease is creatified Jacob disease, hereditary cerebral hammorrhage with amyloid-plaques or for passive immulsation of peacetion. In paramorphic lacera myloid plaques or leaves and paramorphic laceral sclerosts or neuropal described amyloid-place or neuropath, bown's synders anyloid-place or neuropath and paramorphic laceral sclerosts or neuropal
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                                                                                                                                                                                                                                                                                              New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                           Kretzschmar T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                Huber W,
Rothe C;
                                                                                                                Brockhaus M,
Nordstedt C,
(HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
ADA90308
ID ADA90308 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 64; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity lvv.
Local 2, Conservative
                                                                                                                    Bohrmann B,
Loetscher H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RASOSVSSSYLA 12
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                                             MORPHOSYS AG.
                                                                                                                                                                                                                                    MPI; 2003-663848/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (e.g. dementia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12 AA;
                                                                                                                    Bardroff M,
Loehning C,
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seq4.open.rag

28-AUG-2003. 

nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer's disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging. antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; MS-Roche #3.2.H2 L-CDR1 amino acid sequence. (first entry) 20-NOV-2003 ADA90308

Homo sapiens Synthetic.

WO2003070760-A2

20-FEB-2003; 2003WO-EP001759.

20-FEB-2002; 2002EP-00003844.

(HOFF ) HOFFMANN LA ROCHE & CO (MORP-) MORPHOSYS AG.

AG

Kretzschmar T; Huber W, Rothe C; Brockhaus M, Nordstedt C, Bohrmann B, Loetscher H, Bardroff M, Loehning C,

WPI; 2003-663848/62.

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation (e.g. dementia).

Example 5; Page 64; 312pp; English.

The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta. The first region comprises the amino acid sequence Ala-Gill-Re-Arg-His-Asp. (I first region comprises the amino acid sequence Ala-Gill-Rap-Arg-His-Asp. (C dity ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gill-Lys-Leu-Val-Phe-Phe-Ala-Gill-App-Val-C dity ADA89887 or its fragment. Also described; (I) a nucleic acid molecule conding (I); (2) a vector comprising the mucleic acid of (I); (3) a host cell comprising the host cell of (2); (4) preparing (I); comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or an antibody molecule produced by method (4); (6) a kit comprising (I) or nucleic acid of (I), vector of (2) or host cell of (3); (7) optimising (I), vector of (2) or host cell of (3); (7) optimising (I) or nucleic acid of (I), vector of (2) or host cell of (3); (7) optimising (I) or nucleic acid of (I), vector of (2) or host cell of (3); (3) a kit comprising (I) optimised clones; (II) preparing a pharmaceutical composition of (II), and formulating the coptimised antibody/antibody/antibody molecule with a carrier; and (I2) a pharmaceutical composition prepared by method (8). (I) has neuroprotective, notoropic and antibody molecule with a carrier; and can be used in preparing a disagnostic composition for the prevention and/or amyloid-plaque formation. The antibody molecule (C of the disasse mentioned above. The antibody is used for the detection daminish and antibody is used for the detection of the disasse mentioned above. The antibody is used for the dementia, Alzheimer's disease, hereditary cerebral hamorrhage with against better amyloid plaques or for passive immunisation. C cof the disasse mentioned above. The antibody is used for the dementia, Alzheimer's disease, hereditary cerebral hamorrhage with against better amyloid plaques or heuropathy. Down's syndrom, anyloidosis butch trye, parkins

The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Aspramino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Bap-Val-Cly-Aba89886 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Bap-Val-Cly Aba89887 or its fragment. Also described: (1) a nucleic acid molecule concoding (I); (2) a vector comprising the nucleic acid of (1); (3) a host coll of (3) under conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of (1) and recovering (1) from the culture; (5) a composition comprising (1) or an antibody molecule produced by method (4); (6) a kit comprising (1) concomprising (1); (8) testing the resulting Fab optimisation library by panning against Abeta4, (9) identifying optimised clones; (10) expressing composition, comprising optimisation of (1), and formulating the composition, comprising optimisation of (1), and formulating the composition, composition of (1), and comprising the composition of (1), and commissing the composition, composition of (1), and commissing the composition of (1), and formulating the composition of composition of (1), and composition of (1) a composition of (1) and composition of (1) and commission of (1) and

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New antibody molecule capable of specifically recognizing two regions the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation

WPI; 2003-663848/62.

Example 5; Page 64; 312pp; English.

(e.g. dementia).

ö antibody molecule; antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; heralitary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; Gaps Huber W, Kretzschmar T; Rothe C; ö 100.0%; Score 53; DB 6; Length 12 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels MS-Roche #3.4.H6 L-CDR1 amino acid sequence. Brockhaus M, Nordstedt C, (HOFF ) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG. ADA90317 standard; peptide; 12 AA. 20-FEB-2003; 2003WO-EP001759. 20-FEB-2002; 2002EP-00003844. (first entry) Bohrmann B, Loetscher H, neuronal disorder; aging 12; Conservative 1 RASOSVSSSYLA 12 RASQSVSSSYLA 12 Query Match Best Local Similarity Matches 12; Conserv WO2003070760-A2. Sequence 12 AA; Homo sapiens. Bardroff M, Loehning C, 20-NOV-2003 28-AUG-2003 ADA90317; Synthetic RESULT 12 ADA90317 X 8 ઠે 셤

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pharmaceutical composition prepared by method (8). (I) has

neuroprotective, nootropic and antiparkinsonian activities, and can be

used in gene therapy. The antibody molecule (I), nucleic acid molecule,

cused in gene therapy. The antibody molecule (I), nucleic acid molecule,

cused in gene therapy. The antibody molecule,

the prevention and/or recatment of a disease associated with

camploidogenesis and/or amyloid-plaque formation. The antibody molecule

may also be used in preparing a diagnostic composition for the detection

of the disease mentioned above. The antibody is used for the

disintegration of beta-amyloid plaques or for passive immunisation

claimtegration of beta-amyloid plaques or for passive immunisation

claimtegration of beta-amyloid plaques formation. In particular, the disease is

dementia, Alzheiner's disease, motor neuropathy, Down's syndrome,

creutzfeldt Jacob disease, hereditary cerebral haemorthage with

cmyloidosis butch type, Parkinson's disease, HIV-related dementia,

amyloidosis butch type, Parkinson's disease, HIV-related dementia,

amyloidosis lateral solezosis or neuronal disorders related to aging. The

present sequence is used in the exemplification of the present invention.
                85999999999999888
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Sequence 12 AA;

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Gaps
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y Match 100.0%; Score 53; DB 6; Length 12; Local Similarity 100.0%; Pred. No. 0.0013; nes 12; Conservative 0; Mismatches 0; Indels
                                                                      77
                                                                                                   1 RASOSVSSSYLA 12
                                                                     1 RASOSVSSSYLA
 Query Match
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RESULT 13

ADA90323 standard, peptide, 12 AA. ADA90323

20-NOV-2003 (first entry) ADA90323; 

MS-Roche #3.4.H12 L-CDR1 amino acid sequence.

antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer; s disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; herelitary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis; neuronal disorder; aging.

Synthetic

Homo sapiens.

WO2003070760-A2.

28-AUG-2003

20-FEB-2003; 2003WO-EP001759.

20-FEB-2002; 2002EP-00003844.

(HOFF ) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG.

Bohrmann B, Loetscher H, Bardroff M, Loehning C,

New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation WPI; 2003-663848/62.

Huber W, Kretzschmar T; Rothe C;

Brockhaus M, Nordstedt C,

Example 5; Page 64; 312pp; English.

(e.g. dementia).

The present invention describes an antibody molecule (I) capable of specifically recognising two regions of the beta-A4 peptide/Abeta4. The

tirst region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-CC Ser-Gly-Tyr ADA89886 or its fragment, and the second region comprises the amino acid sequence Val-His-Gla-Lys-Leu-Val-Phe-Ala-Glu-Asp-Val-Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule encoding (1); (2) a vector comprising the nucleic acid of (1); (3) a host cell of (3) under conditions that allow synthesis of cell comprising the vector of (2); (4) preparing (1); comprising the host cell of (3) under conditions that allow synthesis of (1) and recovering (1) from the culture; (5) a composition comprising (1) or an antibody molecule produced by method (4); (6) a kit comprising (1); (7) optimising (1); (8) testing the resulting Fab optimisation library by panning against Abeteaf Abetea, (9) identifying optimised clones; (10) expressing of selected, optimised clones; (11) preparing a pharmaceutical composition, comprising optimised clones; (11) and formulating the centribody/antibody molecule with a carrier; and (12) a pharmaceutical composition prepared by method (4); (1) had composition for neuroprotective, nootropic and antiparkinsonian activities, and can be used in gene therapy. The antibody molecule of (1), nucleic acid molecule, composition and/or readment of a disease associated with antibody molecule of the prevention and/or readment of a disease associated with antibody molecule of the prevention and/or antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the dementia, Alzheimer's disease, more receptarly hown's syndrome, against beta-amyloid plaque formation. In patricular, the disease is carriarial heamering dementia, alzheimer's disease, more receptarly hown's syndrome, amyloidesis Dutch type, Parkinson's disease, Hereditary cerebral heamers related to aging. The amyloidesis Dutch type, Parkinson's diseases, Hereditary cerebral heamers and in the exemplification of present in 

Sequence 12 AA;

Gaps ö 100.0%; Score 53; DB 6; Length 12; 100.0%; Pred. No. 0.0013; .ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 12; Conservative

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ADA90324

ADA90324;

ADA90324 standard; peptide; 12 AA.

MS-Roche #3.4.H13 L-CDR1 amino acid sequence.

20-NOV-2003 (first entry)

antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nnoercopic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer a disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; hereditary cerebral haemorrhage; amyloidosis; neuronal disorder; aging. 

Synthetic

WO2003070760-A2. Homo sapiens.

28-AUG-2003.

:0-FEB-2003; 2003WO-EP001759.

20-FEB-2002; 2002EP-00003844.

(HOFF ) HOFFMANN LA ROCHE & CO AG F. (MORP-) MORPHOSYS AG.

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New antibody molecule capable of specifically recognizing two regions of
the beta-A4 peptide, useful for diagnosing, preventing or treating
diseases associated with amyloidogenesis or amyloid-plaque formation
   Kretzschmar T;
    Huber W,
Rothe C;
   Brockhaus M,
Nordstedt C,
                                             Example 5; Page 64; 312pp; English.
    Bohrmann B,
Loetscher H,
                WPI; 2003-663848/62.
                                     (e.g. dementia).
                                                                                                                                                                                                Sequence 12 AA;
   Bardroff M,
Loehning C,
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ö 100.0%; Score 53; DB 6; Length 12; 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels 0.0013; hes 0; Indels 100.0%; ---Best Local Similarity 100. Matches 12; Conservative Query Match

1 RASOSVSSSYLA 12 RASOSVSSSYLA 12

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RESULT 15

ADA90641

ADA90641 standard; peptide; 12 AA. ADA90641;

MS-Roche #7.9.H1 L-CDR1 amino acid sequence. (first entry)

20-NOV-2003

antibody molecule, antibody; beta-A4 peptide; Abeta4; neuroprotective; nootropic; antiparkinsonian; gene therapy; amyloidogenesis; amyloid-plaque formation; beta-amyloid plaque; immunisation; dementia; Alzheimer: disease; motor neuropathy; Down's syndrome; Creutzfeldt Jacob disease; hereditary cerebral haemorrhage; amyloidosis; Parkinson's disease; HIV-related dementia; amyotrophic lateral sclerosis;

The present invention describes an antibody molecule (1) capable of specifically recognising two regions of the beta-A# optide/Abeta4. The first region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-Cflrst region comprises the amino acid sequence Ala-Glu-Phe-Arg-His-Asp-CC Ser-Gly-Tyr ADA8986 or its fragment, and the second region comprises the amino acid sequence Val-His-His-Gla-Liu-App-Val-CG Gly ADA89887 or its fragment. Also described: (1) a nucleic acid molecule conding (1); (2) a vector comprising the nucleic acid of (1); (3) a host cell comprising the vector of (2); (4) preparing (1), comprising (1) culturing the host cell of (3) index conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of culturing the host cell of (3) under conditions that allow synthesis of culturing the host cell of (3) index conditions that allow synthesis of (1) and recovering (1) from the culture; (5) a composition comprising (1), vector of (2) or host cell of (3); (7) optimising (1), comprising optimised clones; (11) preparing a pharmaceutical composition comprising optimised clones; (11) preparing a pharmaceutical composition prepared by method (8). (1) has a paramaceutical composition prepared by method (8). (1), nucleic acid molecule optimised antibody/antibody molecule with a carrier; and (12) and pharmaceutical composition prepared by method (8). (1) has a composition of the prevention and/or amyloid-plaque formation. The antibody molecule may also be used in preparing a pharmaceutical composition for the prevention and/or amyloid plaques or for passive immunisation of the disease mentioned above. The antibody is used for the disease mentioned above. The antibody is used for the disease is dementia, Alzheimer's disease, hereditary cerebral hemorrhage with amyloidopal plaque formation. In paramaceutical composition of beta-amyloid plaques or for passive immunisation.

Contextent sequence is used in the exemplification of the present invention. New antibody molecule capable of specifically recognizing two regions of the beta-A4 peptide, useful for diagnosing, preventing or treating diseases associated with amyloidogenesis or amyloid-plaque formation Kretzschmar T; 100.0%; Score 53; DB 6; Length 12; 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels Huber W, Rothe C; Brockhaus M, Nordstedt C, Example 5; Page 66; 312pp; English. ROCHE & CO AG 20-FEB-2002; 2002EP-00003844. 20-FEB-2003; 2003WO-EF001759. Bohrmann B, Loetscher H, neuronal disorder; aging Bohrmann (HOFF ) HOFFMANN LA F (MORP-) MORPHOSYS AG. WPI; 2003-663848/62. Local Similarity les 12; Conserv (e.g. dementia). WO2003070760-A2 Sequence 12 AA; Homo sapiens. Bardroff M, Loehning C, 28-AUG-2003 Synthetic Query Match Best Loca Matches 

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GENERAL INFORMATION:

APPLICANT: Blictte Pharmaceuticals, Inc.;
APPLICANT: Hiatt, Andrew C.

APPLICANT: Hein, Mich B.

ITLES OF INVENTION: BWRARYOTIC CELLS

TITLE OF INVENTION: BWRARYOTIC CELLS

TITLE OF INVENTION: BWRARYOTIC CELLS

FILE REFERENCE: 310098.406PC

CURRENT FILING DATE: 2001-05-02

NUMBER OF SEQ ID NOS: 197

SEQ ID NO 11

LENGTH: 12

LENGTH: 12

LENGTH: 12

CREANISM: Homo sapien

PCT-US01-14349-11
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100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels
ALIGNMENTS
       PCT-US01-14349-11
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20: (cgn2 6/ptodata/2/paa/USO9 COMB.pep:*
20: (cgn2 6
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                         6019581 seqs, 976053577 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 36163, Sequence 36683,

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Result No.

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Sequence 40, Application PC/TUS0210788

SEQUENCE 41 The Scripps Research Institute

APPLICANT: The Scripps Research Institute

APPLICANT: Burton, D.

APPLICANT: Schaller, M.

TITLE OF INVENTION: Attibodies inhibiting autoimmune disease

FILE REFERENCE: 1361.005w01

CURRENT FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: US 09/828,708

PROFINARE: PROFICATION NUMBER: US 09/828,708

PROFINARE: PROFICATION NUMBER: US 09/828,708

SPRIOR FILING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FasetSEQ for Windows Version 4.0

LENGTH: 12
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APPLICANT: Ditzel, H.
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
FILE REPRENCE: 1361.005W01
CURRENT APPLICATION WUMBER: PCT/US02/10788
CURRENT FILING DATE: 2002-04-05
FRIOR APPLICATION NUMBER: US 09/828,708
FRIOR PRILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 12
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100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels
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100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels
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PCT-10788-41
Sequence 41, Application PC/TUS0210788
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
                                                                                                                                  PCT-1802-10788-38; Sequence 38, Application PC/TUS0210788; GENERAL INFORMATION:
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                                 1 RASOSVSSSYLA 12
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1 RASOSVSSSYLA 12
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CORGANISM: Homo sapiena
PCT-US02-10788-38
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CRGANISM: Homo sapiens
PCT-US02-10788-40
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Sequence 42, Application PC/TUS0210788

SAPELICANT: The Scripps Research Institute

APPLICANT: Ditzel, H.

APPLICANT: Burton, D.

APPLICANT: Schaller, M.

TILE OF INVENTION: Antibodies inhibiting autoimmune disease
FILE REFERENCE: 136.1005W0.1

CURRENT APPLICATION NUMBER: PCT/US02/10788

CURRENT APPLICATION NUMBER: PCT/US02/10788

PRIOR PILING DATE: 2001-04.06

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 42

LENGTH: 12
APPLICANT: Ditzel, H.

APPLICANT: Burton, D.
APPLICANT: Burton, D.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Antibodies inhibiting autoimmune disease
FILE REPERENCE: 1361,005401
CURRENT APPLICATION NUMBER: DCT/US02/10788
CURRENT FILING DATE: 2002-04-05
PRIOR PAPLICATION NUMBER: US 09/828,708
PRIOR PELLING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 12
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100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indele
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Sequence 15, Application PC/TUS0300297

SEQUENCE 15, Application PC/TUS0300297

GENERAL INFORMATION:

APPLICANT: The Scripps Research Institute

APPLICANT: Jensenius, Jens

TITLE OF INVENTION: Cancer-Associated Epitope

FILE REFERENCE: 1361.017WO1

CURRENT APPLICATION NUMBER: PCT/US03/00297

CURRENT APPLICATION NUMBER: US 66/345.208

PRIOR FILING DATE: 2002-01-03

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
PCT-US02-10788-41
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ORGANISM: Homo sapiens
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APPLICANT: Angen, Inc.
APPLICANT: Angen, Inc.
APPLICANT: Melcher, Andrew
APPLICANT: Chute, Hilary
APPLICANT: Li, Luke
APPLICANT: Huang, Haichun
ITLE APPLICANT: Huang, Haichun
ITLE OF INVENTION: Human anti-IFN-gamma Neutralizing Antibodies as Selective IFN-gamm;
ITLE OF INVENTION: Pathway Inhibitors
ITLE OF INVENTION: Pathway Inhibitors
FILE REFERENCE: 01-1635-G
CURRENT PELING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: US 60/419,057
PRIOR APPLICATION NUMBER: US 60/419,057
PRIOR APPLICATION NUMBER: US 60/479,241
PRIOR FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 38
LENGTH: 12
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APPLICANT: Medarex, Inc.
APPLICANT: Medarex, Inc.
APPLICANT: Melcher, Andrew
APPLICANT: Chute, Hilary
APPLICANT: Li, Luke
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FILE REFERENCE: 01-163-G
CURRENT APPLICANTION NUMBER: US 60/419, 057
PRIOR APPLICANTON NUMBER: US 60/419, 057
PRIOR APPLICANTON NUMBER: US 60/479, 241
PRIOR FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 57
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100.0%; Score 53; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0
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PCT-US03-36126-38
; Sequence 38, Application PC/TUS0336126
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                         Application PC/TUS0332678
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; ORGANISM: Homo sapiens
PCT-US03-32871-38
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; ORGANISM: Homo sapiens
PCT-US03-32678-38
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Sequence 4, Application PC/TUS0306155
Sequence 4, Application PC/TUS0306155
Sequence 4, Application:
APPLICANT: Eli Lilly and Company
TITLE OF INVENTION: Antagonistic Anti-hFas Ligand Human Antibodies and Fragments TITLE OF INVENTION: NUMBER: PCT/US03/06155
CURRENT APPLICATION NUMBER: PCT/US03/06155
CURRENT FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 4
IRBOTH: 12
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Sequence 20, Application PC/TUS0300440
Sequence 20, Application PC/TUS0300440
GENERAL INFORMATION:
APPLICANT: Medarex, Inc. et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
FILE REFERENCE: MXI-180PC;
CURRENT APPLICATION NUMBER: PCT/US03/00440
CURRENT APPLICATION NUMBER: US 60/347649
FRIOR FILING DATE: 2002-01-09
FRIOR APPLICATION NUMBER: US 60/404427
FRIOR PILING DATE: 2002-01-09
FRIOR APPLICATION NUMBER: US 60/431684
FRIOR PILING DATE: 2002-01-06-19
FRIOR PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 20
SEQ ID NO 20
LENGTH: 12
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PCT-US03-06155-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-00297-15
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RESULT 14
US-09-191-817-124
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US-09-563-222-11
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APPLICANT: Xiao Feng

APPLICANT: Xiao Feng

APPLICANT: Mark R. Nocerini

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2 AND USES THEREOF

FILE REPRENDENTX. 072A

CURRENT APPLICATION NUMBER: PCT/US03/38234

CURRENT PILING DATE: 2003-12-02

PRIOR FILING DATE: 1003-12-02

PRIOR FILING DATE: NA

NUMBER OF SEQ ID NOS: 222

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 194

LENGTH: 12
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PCT-USS8-24303-124
PCT-USS8-24303-124
Sequence 124, Application PC/TUS9824303
GENERAL INPORMATION:
APPLICANT: Purdue Pharma L.P.
TITLE OF INVENTION: MODIFIED ANTIBODIES WITH ENHANCED ABILITY TO ELICIT AN TITLE OF INVENTION: ANTI-IDIOTYPE RESPONSE
FILE REFERENCE: 6750-015-228
CURRENT APPLICATION NUMBER: PCT/US98/24303
CURRENT PILING DATE: 1998-11-13
CURRENT APPLICATION NUMBER: 60/081,403
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
GENERAL INFORMATION:
APPLICANT: Genmab A/S
TITLE OF INVENTION: HOAM MONOCLONAL ANTIBODIES AGAINST CD25
FILE REFERENCE: GAM--059PC
CURRENT APPLICATION NUMBER: PCT/US03/36126
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: P00426690
PRIOR PILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PSECE FOR Windows Version 4.0
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abgenix, Inc.
APPLICANT: Lexicon Genetics Incorporated
APPLICANT: Gregory M. Landes
APPLICANT: Mary Haak-Frendscho
APPLICANT: Ling Chen
APPLICANT: Yen-Wah R. Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 194, Application PC/TUS0338234 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 12; Conservative
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Matches 12; Conservative
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CORGANISM: Homo sapiens
PCT-US03-38234-194
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ORGANISM: Homo sapiene
PCT-US03-36126-38
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PCT-US03-38234-194
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: ANTI-IDIOTYPE RESPONSE

TITLE OF INVENTION: ANTI-IDIOTYPE RESPONSE

TITLE OF INVENTION: ANTI-IDIOTYPE RESPONSE

TITLE OF INVENTION: ANTI-IDIOTYPE RESPONSE

TITLE REFERENCE: 6750-015

CURRENT APPLICATION NUMBER: 60/081,403

EARLIER PILING DATE: 1998-11-13

EARLIER PILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1997-11-14

SEQ ID NO: 124

LENGTH: 12

LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew
APPLICANT: Hiatt, Andrew
TITLE OF INVENTION: EUKARYOTIC CELLS
TITLE OF INVENTION: EUKARYOTIC CELLS
FILE REFERENCE: 310098.406
CURRENT APPLICATION WHERE: US/09/563,222
CURRENT FILLING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 12
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100.0%; Score 53; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 12; Conservative 0; Mismatches 0; Indels
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EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/065,716
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 153
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 124
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ORGANISM: Homo sapiens
US-09-191-817-124
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PCT-US98-24303-124
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CORGANISM: Homo sapien
US-09-563-222-11
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Thu Apr 22 05:59:17 2004

1 RASQSVSSSYLA 12 |||||||||||| 1 RASQSVSSSYLA 12

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Search completed: April 21, 2004, 17:57:23 Job time : 179.435 secs

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; Sequence 40, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
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APPLICANT: Ditzel, H. APPLICANT: Burton, D. APPLICANT: Schaller, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-09-828-708-38
RESULT 2
US-09-828-708-40
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Sequence 40, Appl
Sequence 41, Appl
Sequence 11, Appl
Sequence 8, Appl
Sequence 6, Appl
Sequence 20, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
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                                                                                April 21, 2004, 17:37:29; Search time 36.1739 Seconds (without alignments) 91.715 Million cell updates/sec
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| Cgn2 6/prodata/2/pubpaa/NSO7_PUBCOMB.pep:*
| Cgn2 6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
| Cgn2 6/prodata/2/pubpaa/USO6_NEW_PUB.pep:*
| Cgn2 6/prodata/2/pubpaa/USO6_NEW_PUB.pep:*
| Cgn2 6/prodata/2/pubpaa/USO6_NEW_PUB.pep:*
| Cgn2 6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-828-708-41
US-09-828-708-41
US-09-828-708-41
US-09-563-222-11
US-10-374-81
US-10-374-93
US-10-374-93
US-10-374-62
US-10-374-93
US-10-374-62
US-10-374-93
US-10-375-046-19
US-10-375-046-19
US-10-275-046-19
US-10-269-711-5-687-23
US-10-125-687-23
US-10-125-687-23
US-10-041-860-371
US-10-453-698-29
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                                                                                                                                                                                                                      1133595 seqs, 276475211 residues
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                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                    SEQ4
53.
1 rasgsvsssyla 12
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
                                                                                                                                                                                      Scoring table:
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                                                                                     Run on:
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        US-10-194-975-82
        Sequence 82, Appl Sequence 10, Appl 19

        17
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        US-10-153-382-22
        Sequence 10, Appl 10

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        US-10-041-860-370
        Sequence 370, Appl 20

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        US-10-041-860-376
        Sequence 37, Appl 20

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        Sequence 37, Appl 20

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        US-10-308-817-29
        Sequence 29, Appl 20

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        Sequence 29, Appl 30

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        US-10-308-762-35
        Sequence 37, Appl 30

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        Sequence 37, Appl 30

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        US-09-828-708-3
        Sequence 5, Appl 30

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Sequence 8, Application US/10379741

Sequence 8, Application US/10379741

Publication No. US20040071702A1

GENERAL INFORMATION:

APPLICANT: van de Winkel, Jan G.J.

APPLICANT: van Dijk, Marcus Antonius

APPLICANT: Schuuran, Janine

APPLICANT: Baadsgaard, Ole

APPLICANT: Betersen, Jorgen

APPLICANT: Betersen, Jorgen

APPLICANT: Badsgaard, Ole

APPLICANT: Badsgard, Ole

CURRENT APPLICANION NUMBER: US/10/379,741

CURRENT APPLICATION NUMBER: US 60/314,731

PRIOR PLING DATE: 2003-03-05

PRIOR PLING DATE: 2001-08-23

PRIOR PLING DATE: 2001-08-23

PRIOR FILING DATE: 2001-08-23

PRIOR FILING DATE: 2001-08-23

PRIOR FILING DATE: 2001-08-23

PRIOR FILING DATE: 2001-08-23

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Sequence 11, Application US/09563222
Sequence 11, Application US/09563222
Publication No. US20030079253A1
GENERAL INFORMATION:
APPLICANT: Hiatt, Andrew
TITLE OF INVENTION: INMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: INMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: BUKARYOTIC CELLS
FILE REFERENCE: 310098 406
CURRENT PILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 12
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Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels
Query Match

100.0%; Score 53; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0058;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 12, Conservative
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-11
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US-09-828-708-41
is Sequence 41, Application US/09828708
is Patent No. US20020146753A1
is General Information:
is Patent No. US20020146753A1
is APPLICANT:
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Fatent No. US2020146753A1

GENERAL INCRMATION:

APPLICANT: Ditzel, H.

APPLICANT: Burton, D.

TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil

TITLE OF INVENTION: autoimmune disease

TITLE OF INVENTION: autoimmune disease

TITLE OF INVENTION: autoimmune disease

TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil

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TITLE OF INVENTION
     TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici TITLE OF INVENTION: autoimmune disease FILE REFERENCE: 1361.005/SI autoimmune disease CURRENT APPLICATION NUMBER: US/09/828,708 CURRENT FILING DATE: 2001-09-24 NUMBER OF SEQ ID NOS: 123 SOFTWARE: FESTERED FOR SEQ FOR MINDOWS VERSION 1.00
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100.0%; Score 53; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 12; Conservative
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CRGANISM: Homo sapiens
US-09-828-708-42
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CORGANISM: Homo sapiens
US-09-828-708-40
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US-09-828-708-42
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LENGTH: 12
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; ORGANISM: Homo sapiens
US-10-338-366-20
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US-10-374-932-8

US-10-374-932-8

Sequence 8, Application US/10374932

Publication No. US20030235586A1

GENERAL INFORMATION:

APPLICANT: van de Winkel, Jan G.J.

APPLICANT: van Dijk, Marcus Antonius

APPLICANT: van Dijk, Marcus Antonius

APPLICANT: Schuurman, Janine

APPLICANT: Baadsgaard, Ole

APPLICANT: Betersen, Jorgen

TITLE OF INVENTION: HUMAN ANTIBODIES SPECIFIC FOR INTERLEUKIN 15 (IL-15)

FILE REFERENCE: GMI-024CP

CURRENT FILING DATE: 2001-02-26

FRIOR APPLICATION NUMBER: US 60/314,731

PRIOR FILING DATE: 2001-08-23

PRIOR FILING DATE: 2001-08-23

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSEQ for Windows Version 4.0
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Query Match

100.0%; Score 53; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0; Indels
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APPLICANT: Keler, Tibor APPLICANT: Treml, John
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ORGANISM: Homo sapiens
US-10-374-932-8
                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Homo sapiens
US-10-001-934-62
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LENGTH: 12
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TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
CURRENT APPLICATION NUMBER: US/10/338,366
CURRENT FILING DATE: 2003-01-07
FRIOR FILING DATE: 2003-01-07
FRIOR FILING DATE: 2002-01-09
FRIOR FILING DATE: 2002-01-09
FRIOR FILING DATE: 2002-01-09
FRIOR FILING DATE: 2002-01-09
FRIOR FILING DATE: 2002-01-09
FRIOR FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 53
SOFTWARE FASTESEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 53; DB 15; Length 12; Best Local Similarity 100.0%; Pred. No. 0.0058; Matches 12; Conservative 0; Mismatches 0; Indels
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US-10-269-711-57
Sequence 57, Application US/10269711
Publication No. US20040071694A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: DeVites, Peter J.
APPLICANT: Reilly, Edward B.
APPLICANT: Getrow, Dave
APPLICANT: Green, Lary
TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING;
TITLE OF INVENTION: ANTIBODIES
FILE REPRENCE: 6989.US.01
CURRENT APPLICATION NUMBER: US/10/269,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 53; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 12; Conservative 0; Mismatches 0;
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CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: HLA-DR specific polypeptide
US-10-275-046-19
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US-10-125-687-23

is Sequence 23, Application US/10125687

is Publication No. US20030054407A1

is GENERAL INFORMATION:

is TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY

is TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY

is CURRENT APPLICATION NUMBER: US/10/125,687

is CURRENT FILING DATE: 2002-04-17

is SOFTWARE: PALENTIN version 3.1

is SEQ ID NOS: 28

is LENGTH: 74
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OTHER INFORMATION: light chain variable region predicted sequence for corner INFORMATION: Vk A-27 germline
US-09-948-939-5
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Sequence 5, Application US/09948939

Publication No. US20020086014A1

GENERAL INFORMATION:

APPLICANT: Konnan, Alan J.

APPLICANT: Halk, Edward L.

APPLICANT: Lonberg, Nils

APPLICANT: Halk, Edward L.

APPLICANT: Halk, Edward L.

APPLICANT: Halk, Edward L.

APPLICANT: MUMBER: US/09/948,939

CURRENT APPLICATION NUMBER: US/09/948,939

CURRENT FILING DATE: 1099-08-24

PRIOR APPLICATION NUMBER: US/0/150,452

PRIOR FILING DATE: 1099-08-24

PRIOR FILING DATE: 1000-08-24

PRIOR FILING DATE: 2000-08-24

FRIOR FILING DATE: 2000-08-24
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100.0%; Score 53; DB 14; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 12; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 28
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ORGANISM: Homo sapiens
                                                                                                                                                 TYPE: PRT CAGANISM: Homo sapiens US-10-269-711-57
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100.0%; Score 53; DB 12; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 12; Conservative 0; Mismatches 0; Indels
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APPLICANT: Corvalan, Jose R.F.
APPLICANT: Tia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Feng, Xiao-Chi
APPLICANT: Weber, Radari
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APPLICANT: Weber, Radari
APPLICANT: Reserved
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 3772-01-07
SEQ ID NO 371
LENGTH: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 53; DB 14; Length 95; Best Local Similarity 100.0%; Pred. No. 0.05; Matches 12; Conservative 0; Mismatches 0; Indels
100.0%; Score 53; DB 12; Length 95; 100.0%; Pred. No. 0.05; tive 0; Mismatches 0; Indels
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US-10-453-688-29
Squence 29, Application US/10453698
Squence 29, Application US/10453698
Publication No. US20040038308A1
GENERAL INFORMATION:
APPLICANT: ROCHEY, Russell
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT TILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
TENGTH: 96
TENGTH: 96
TENGTH: 96
TYPE: RAT
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ORGANISM: homo sapiens
FEATURE:
NAME/KEX: VARIANT
LOCATION: 54
FORTURE:
NAME/KEX: VARIANT
LOCATURE INFORMATION: Xaa = Any Amino Acid
FEATURE:
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-371
                                                                                                                                                                                                                                                                        Sequence 371, Application US/10041860; Publication No. US20030157109A1; GENERAL INFORMATION:
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        Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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Thu Apr 22 05:59:16 2004

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Search completed: April 21, 2004, 18:02:06 Job time : 36.1739 secs

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100.0%; Score 53; DB 4; Length 96; 100.0%; Pred. No. 0.0064; ive 0; Mismatches 0; Indels
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Patent No. 5861155
GENERAL INFORMATION:
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-09-472-087-87
RESULT 2
US-08-652-558-49
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US-09-472-087-87
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Sequence 150, Appl
Sequence 150, Appl
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Sequence 16, Appl
Sequence 17, Appl
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                                                                           April 21, 2004, 17:28:28; Search time 14.4348 Seconds (without alignments) 42.918 Million cell updates/sec
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 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-652-558-49

US-08-645-113B-150

US-08-477-448-150

US-08-477-431-150

US-08-645-150

US-09-136-150

US-09-136-150

US-09-711-485-150

US-09-711-485-150

US-09-711-485-150

US-09-711-485-150

US-09-025-769B-16

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US-09-045-090A-40

US-09-456-090A-55

US-09-456-090A-75

US-09-456-090A-75

US-09-456-090A-75

US-09-456-090A-75

US-09-456-090A-75

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                                                                                                                                                                                                                        389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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53
1 rasqsvbsbyla 12
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US-09-240-178
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US-09-456-090A-44
US-09-456-090A-78
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US-08-899-575-151
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US-08-472-0844-151
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Sequence 150, Application US/06488113B

Sequence 150, Application US/06488113B

Sequence 150, Application US/06488113B

Settle No. 5744580

APPLICANT: Batter, Marc D.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Droteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCES: 169

CORRESPONDENCES: 169

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STREET: Ushaios

COUNTRY: Ushaios
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 53; DB 2; Length 107; 100.0%; Pred. No. 0.0072; Live 0; Mismatches 0; Indels
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inchartible
COMPUTER IN PC compatible
COMPUTER SYSTEM: PC COMPATIBLE
COMPUTER SYSTEM: PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: NOTHERER 21, 1994
ATPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOTHERER 21, 1994
ATPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOTHERER 30, 237
ATPLING DATE: MAMBER: 92, 910
ATPLING DATE: MAMBER: 92, 910
ATPLING DATE: MAMBER: 92, 910
ATPLING DATE: MAMBER: 93, DB 2;
ATPRANDENES: GIPGE
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPAGE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PROFING APPLICATION NUMBER: US 08/64,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 09-DEC-1992
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Best Local Similarity 100.
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PRIOR APPLICATION DATA;

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PRIOR APPLICATION NATH, 199

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PRICAR APPLICATION NATH, 199

PRESENTANDENT, 190

PRESENTANDENT, 190

PRESENTANT NATH 190

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100.0%; Score 53; DB 2; Length 108; 100.0%; Pred. No. 0.0073; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 53; DB 2; Length 108; Best Local Similarity 100.0%; Pred. No. 0.0073; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 312/707-8889
TELERAX: 312/707-9155
TELERAX: 650 388-1248
INFORMATION FOR SEC 1D NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEFERIOR: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TYPE: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: EVENSSON, LEONARD REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-
                   FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RASOSVSSSYLA 12
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                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-646-360-150
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-081B-42
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Patent No. 5837431

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studinks, Gary M.
TITLE OF INVENTION:
INMUNOLOSIS: TORGENION:
NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:
ADDRESSEE: MANDERSEE: MANDERSEE:
ADDRESSEE: ADDRESSEE: MANDERSEE:
ADDRESSEE:
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100.0%; Score 53; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC COMPATION:
COMPUTER: TEM PC COMPATION:
COMPUTER: TEM PC COMPATION:
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENI APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION NUMBER: DET/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION DATA: US 08/064,691
FILING DATE: US 07/988,430
FILING DATE: US 07/988,430
FILING DATE: US 07/988,730
FILING DATE: US 07/988,730
FILING DATE: US 07/988,730
FILING DATE: US 07/991
ATTORNEY/AGENT INFORMATION:
NAME: MCMICHAIN NUMBER: US 07/787,567
FILING DATE: US -UNIVER: US 07/787,567
FILING DATE: US -UNIVER: US 07/787,567
FILING DATE: US -UNIVER: US 07/787,567
FILING DATE: US -UNIVER: US 07/787,567
FILING DATE: US -UNIVER: US 07/787,567
FILING DATE: US -UNIVER: US 07/787,567
FILING DATE: US -UNIVER: US 07/787,567
FILING DATE: US -UNIVER: US 07/787,567
FILING DATE: US -UNIVER: US 07/787,567
FILING DATE: US -UNIVER: US 07/787,567
FILING DATE: US -UNIVER: US 07/787,567
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500 West Madison Street, 34th floor
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MONICHOLS, Janet M.
REGISTRATION NUMBER: 11022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-8889
TELEFAX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acids
TYPE: amino acids
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
STRANDEDMESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RASOSVSSSYLA 12
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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GENERAL INFORMATION
                                                                                                  Sequence 150, Application US/08839765
; Sequence 150, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
ITILE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS: 169
; CORRESPONDENCE ADDRESS: 169
; ADDRESSEE: MCAndrewa, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
; STATE: Illinois
; CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 53; DB 3; Length 108; Best Local Similarity 100.0%; Pred. No. 0.0073; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Flopyd disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyd disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APELICATION DATA:
APPLICATION NUMBER: US/08/039,765
FILING DATE: 15-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1991
ATTORNEY/AGBAT INFORMATION:
NAME: MCMAINCAPION: NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 312/707-9889
TELEPHONE: 312/707-9155
TELEPHONE: 312/707-9155
TELEPAX: 312/707-9155
TELEPAX: 312/707-9155
TELEPAX: 10-107
TELEX: 650 388-1248
INPORMATION FOR SEQ ID NO: 150:
FUNDAMATION FOR SEQ I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 108 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 RASOSVSSSYLA 35
                                                                                             US-08-839-765-150
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RESULT 8 US-09-136-389-150 ; Sequence 150, Application US/09136389 ; Patent No. 6146850

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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Procesins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            ALDERSOES:

ALDERSOES:

CITY:

CLICAGO
STREET:

SON West Madison Street, 34th Floor
CITY:

CLICAGO
STATE:

ALDINOIS

COMPUTER RADDALE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READALE FORM:

MEDIUM TYPE: FORM:

MEDIUM APPLICATION DATA:

APPLICATION NUMBER:

MEDIUM APPLICATION DATA:

MAPLICATION NUMBER:

MEDIUM APPLICATION DATA:

MAPLICATION NUMBER:

MEDIUM APPLICATION DATA:

MAPLICATION NUMBER:

MEDIUM APPLICATION NUMBER:

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MAPLICATION NUMBER:

MAPLICATION NUMBER:

MAPLICATION NUMBER:

MARCHERRACE MOMBER:

MARCHERRACE MOMBER:

MARCHERRACE MOMBER:

MARCHERRACE MOMBER:

MEDIUM APPLICATION NUMBER:

MEDIUM APP
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UG-09-610-838-150
; Sequence 150, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312///, TELEFAX: 112///, TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150: SEQUENCE CHARACTER.STICS: LENGTH: 108 amino acids TVPE: amino acid double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RASOSVSSSYLA 12
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Score 53; DB 4; Length 108;
Pred. No. 0.0073;
Mismatches 0; Indels
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PRILING LATE.

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRICH ALCATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRICH DATE: 09-DEC-1992

PRICH DATE: 19-UM-1992

PRICH DATE: 19-UM-1992

PRICH DATE: 19-UM-1992

PRICH DATE: 19-UM-1992

PRICH DATE: 19-UM-1991

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,918

REGISTRATION NUMBER: 32,918

REGISTRATION NUMBER: 31,018

REGISTRATION NUMBER: 31,018

REGISTRATION NUMBER: 31,018

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REGISTRATION NUMBER: 31,018
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Patent No. 6300064
GENERAL INFORMATION: Achim
APPLICANT: Rnappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Pleckthum, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pr
Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
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MOLECULE TYPE: protein
US-09-711-485-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-09-025-769B-16
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APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunoccains Comprising Ribosome-Inactivating TITLE OF INVENTION: Immunoccains Immunoccains CORRESPONDENCE ADDRESS:
ADDRESSEE MCANDERSS:
STREET: 500 West Madison Street, 34th floor STREET: 500 West Madison Street, 34th floor STREET: 1100.00
STREET: 1110.01
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STREET: 100 West Madison Street, 34th floor STREET: 100 West Madison Street, 34th floor STREET: 100.00
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US-09-711-485-150
Sequence 150, Application US/09711485
Factor No. 6649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Garroll, Stephen F.
APPLICANT: Studnika, Gary M.
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TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor CITY: Chicago STREET: 111nois
COUNTRY: USA
ZIP: 60661
COMPUTER: READABLE FORM:
MEDIUW TY: EM PC compatible COMPUTER: FIDOPY disk
COMPUTER: FIDOPY disk
COMPUTER: PEACOLINE READABLE FORM:
MEDIUW TY PE: Floopy disk
COMPUTER: PEACOLINE READABLE FORM:
APPLICATION DATA: APPLICATION NUMBER: US/09/711,485
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PILING DATE 18 -NOT-1995

ATTORNEY AGENT INFORMATION:
NAME: JOHNEY AGENT INFORMATION:
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Patent No. 5661016
GENERAL INFORMATION:
APPLICANT: Lomberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for INTLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
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CONTESPONDENCE ADDRESSE:
CONTEST: One Market Plaza, Steuart Tower, Suite 200 CITY: San Francisco STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER: EDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 16-DEC-1992
CLASSIFICATION: 800
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
FILING DATE: 16-DEC-1992
FILING DATE: 10-DEC-1991
FILING DATE: 10-DEC-1991
FILING DATE: 10-DEC-1991
FILING DATE: 10-DEC-1991
FILING DATE: 18-MAR-1992
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 0.0074; Matches 12; Conservative 0; Mismatches 0; Indels
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; Patent No. 5814318
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
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Best Local Similarity 100.
Matches 12; Conservative
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US-08-096-762-183
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US-08-053-131-183
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ADDITIONER, Key, Robert M.

TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SCHOWERS:
CORRESSONDERGE ADDRESS:
ADDRESSER Townsend and Townsend Khourie and Crew
CITY: San Francisco Compatible
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 21, 2004, 17:25:48; Search time 3.55072 Seconds (without alignments) 102.653 Million cell updates/sec Run on:

SEQ5 31 1 atssrat 7

Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			_			Q66814 ebola virus	ebola v	_					_	rattu		P23949 mus musculu			Q9zsm8 arabidopsis	P37935 schizophyll	P31999 1 genome po	PB9876 1 genome po	094686 schizosacch	rhizop		clarias m	_		~	01622	_	22757	_
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	Score	31	28	27	27	27	27	27	27	27	27	27	27	27	27	56	26	26	26	26	26	26	26	25	25	25	2.5	25	25	25	25	25	25	25
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### ALIGNMENTS

	ate) pdate) pyme (EC 2.7.1.40) (PK),	Probable pyruvate Aniase, cycesolic isolyme (ic. first), comparate Angelsago OR Miss.180. Arabidopsis thaliana (Mouse-ear cress). Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Murphy G., Volckaert G.,	LI L.A., Rieger M., aier B., Mache R., Mueller M., ater B., Mache R., Mueller M., ateron M., Schmidtheini T., o M., Boutry M., Bancroft I., ler H., Ridley P.,	Acobsen J. Vandenbussche F., aens I., Aert R., Defoor B., T., Hilbert H., Braun M., averen M., Koetter P.,	Lamberth S., Van den Daele H., Villarroel R., De Clercq R., Duail M.A., Bray-Allen S., Lennard N., McLay K., Mayes R., aenes V., Rechmann S., imm M., Loehnert TH.,	arath K., Dauner D., Herzl A., yuori R., Piravandi B., huendlein A., Felber R., arny A., Aubourg S., tt A., Casacuberta B., ct A., Terol J., Torres A.,	RA Heijnen L., Schwarz S., Scholler B., Weber S., Francs P., Bielke C., RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C., R. Frishman D., Haase D., Lemcke K., Mewes HW., Stocker S., RA Faccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., RA Sachon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., Rahchon M., Murray J., Graves T., Harmon G., Edwards J., RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., RA Latreille P., Couriney L., Cloud J., Abbott A., Scott K., Johnson D., RA Minx P., Benley D., Fulton B., Miller M., Remp K., Ramer J., Fulton L., Mardis B., Dante M., Pepin K., Hillier L.W., RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C.,
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E	ted) sequence annotati	cycosolic se-ear cre Streptoph ta; eudic Brassicac	10617198; Wambutt	Stlekema andt P., G none V., C gdomenech , Perez-P	3., Bilham Suprez B., Voet M., E , Ramsperg ers S., Ve rst R., Ro	Feldpausch C., Gieler Cronin J I S., Kay A., Lyne P Scharfe M	ann B., Garann B., Calabauld (Clabauld W., Ger C., Medenbol M.,	B., benc choller P macke K., 18on R.K. oj L., Sc er P., Co er P., Co on B., Mi on B., Mi dis E., D
. Gogging	(Rel. 37, Creat (Rel. 37, Last	Probable pytuvate Kindse, Cycosoff Isozoff to Erring Myd26590 OR Miss.180. Arabidopsis thaliana (Mouse-ear cress). Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eprosids II; Brassicales, Brassicaceae, Arabidopsis.	=3702; ROM N.A. Columbia; 083488; PubMed=1 K., Schueller C	desterhoeft A., Ansorge W., Bra rener M., de Sist Delseny M., Puis ., Portetelle D heisel J., Zimme	-A., McCullagh I hueren J., Gryme , Weltjens I., ' er T., Bothe G. Brandt A., Pett	S., Hempel S., A., Buysshaert u M., Rogers J. Doggett J., Hal , Rajandream M., Bloecker H.,	Fuchs M., Fartm. Argiriou A., Quigley F., Hiller R., Sc. Cooke R., Ber, Weber N., Van,	z A., Purnelle Schwarz S., S Chwarz S., Le Dedhia N. Wi Murray J., She T., Kalicki J., P., Courney L. Fulton L., Mar Spieth J., Rya Spieth J., Rya
	NEIC ARAIR 065595; 15-DEC-1998 15-DEC-1998 10-OCT-2003	Probable py AT4G26390 C Arabidopsis Eukaryota; Spermatophy eurosids II	NCEI_TaxID=3702; [1] SEQUENCE FROM N.A STRAIN=CV. COlumb MEDLINE=20083488; Mayer K.F.X., Sch	Pohl T., D. Harris B., Weichselgar Kreis M., I. Reichert B.	Langham S. Van der Scl Braeken M. Weitzenegge Holzer E., Mooijman P.	Berneiser  De Keyser  Van Montagr  Clark L.,  Pettett A.  Borkova A.	Gabel C., Neumann S. Massenet O Schnabl S. Chefdor F.	perez-Pere Heijnen L. Frishman D Zaccaria P Parnell L. Sekhon M., Stoneking Latrellle Minx P., B Kramer J., Nelson J.,
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Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Chen B., Marra M.A., Martienssen R., McCombie W.R., Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE OF 1-1594 FROM N.A. Chen Y., Di Y.P., Wu R.; Chen Y., Di Y.P., Wu R.; Mulecular cloning of the amino-terminal and 5'-flanking region of thuman MUCSB mucin gene."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              Nature 402:769-777 (1999).

-!- CATALYTIC ACTIVITY: ATP + pyruvate = ADP + phosphoenolpyruvate.

-!- COPACTOR: Requires magnesium and potassium.

-!- PATHWAY: Glycolysis; final step.

-!- PATHWAY: Homotetramer (By similarity).

-!- SUBUNIT: Homotetramer (By similarity).

-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: Belongs to the pyruvate kinase family.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Q9HCB4; 000447; 000573; 014985; 015494; 095291; 095451; Q14881;
Q99HCB4; 000047; 000573; 015494; 095291; 095451; Q14881;
Q99HCB2; Q9UED8;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Mucin SB precursor (Mucin S subtype B, tracheobronchial) (High molecular weight salivary mucin MG1) (Sublingual gland mucin).
MUCSB OR MUCS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Therefore IPRO01697, Pyruvate kinase.

Refam; PRO0244, PK, 1.

Pfam; PRO1050, PKC, 1.

READOM; PRO1050; PYRUVIKNASE.

RECOOM; PRO10604; Pyruvate kinase; 1.

RIGREAM6; TICRO1064; Pyruv kin; 1.

RIGREAM6; TICRO1064; Pyruv kin; 1.

RESOILE; PS00110; PYRUVATE KINASE; 1.

RETAL 229 229 MAGNESIUM (BY SIMILARITY).

METAL 250 229 MAGNESIUM (BY SIMILARITY).

METAL 250 250 MAGNESIUM (BY SIMILARITY).

METAL 250 250 MAGNESIUM (BY SIMILARITY).

METAL 250 250 MAGNESIUM (BY SIMILARITY).

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SEQUENCE 497 AA; 54319 MW; 45D43EF54A89FE62 CRC64;
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SEQUENCE OF 1-1325 FROM N.A.
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ATSSRAT 383
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MEDLINE-9747489; PubMed=9201995;

MEDLINE-9747489; PubMed=9201995;

Desseyn J.-L., Aubert J.-P., Porrhet N., Laine A.;

Desseyn J.-L., Aubert J.-P., Porrhet N., Laine A.;

Desseyn J.-L., Aubert J.-P., Porrhet N., Laine A.;

Genomic organization of the 3 region of the human MUCSB mucin.";

J. Biol. Chem. 272:16873-16883(1997).

-!-FUNCION: Salivary mucin that is thought to contribute to the lubricating and viscoelastic properties of whole saliva.

-!-FUNCION: Salivary mucin that is thought to contribute to the lubricating and viscoelastic properties of whole saliva.

-!- SUNCELULAR LOCATION: Secreted.

-!- STRICATION: Socreted.

-!- FTM: Highly glycosylated.

-!- FTM: Highly glycosylated.

-!- FTM: Highly glycosylated.

-!- STMILARITY: Contains 3 VWFC domains.

-!- SIMILARITY: Contains 4 VWFD domains.

-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 40-1324 FROM N.A.
MEDLINE-99023932; PubMed=9804771;
Desseyn J.-L., Buisine M.P., Porchet N., Aubert J.-P., Laine A.;
"Genomic organization of the human mucin gene MUC5B: cDNA and genomic sequences upstream of the large central exon.";
J. Biol. Chem. 273:30157-30164(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Salivary gland;
MEDLINE=97292540; PubMed=9147051;
Niebsen P.A., Bennett E.P., Wandall H.H., Therkildsen M.H.,
Hannibal J., Clausen H.;
"Identification of a major human high molecular weight salivary mucin (MGI) as tracheobronchial mucin MUC5B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human mucin gene MUCSB, the 10.7 kb large central exon encodes various alternate subdomains resulting in a super-repeat. Structural evidence for a 11p15.5 gene family.";
                                             Offner G.D., Nunes D.P., Keates A.C., Afdhal N.H., Troxler R.F., "The amino-terminal sequence of MUC5B contains conserved multifunctional D domains: implications for tissue-specific mucin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=57293229; PubMed=9164870; Keates A.C., Nunes D.P., Afchal N.H., Troxler R.F., Offner G.D.; Weates A.C., Nunes O.P., Afchal N.H., Troxler R.F., Offner G.D.; Molecular cloning of a major human gall bladder mucin: complete terminal sequence and genomic organization of MUCSB."; Biochem. J. 324:295-303(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Troxler R.F., Offner G.D., Zhang F., Iontcheva I., Oppenheim F.(
"Molecular cloning of a novel high molecular weight mucin (MGI)
from human sublingual gland.", 217:1112-1119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
MEDINE=97166151; PubMed=9013550;
Desseyn J.-L., Guyonnet-Duperat V., Porchet N., Aubert J.-P.,
Laine A.;
                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 251:350-355(1998)
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TISSUE-Sublingual gland;
MEDLINE-96125355; PubMed-8554565;
MEDLINE=99009274; PubMed=9790959;
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We light SEQUENCE FROM N.A.

TISSUB=Liver;

X MEDLINE=97228413; PubMed=9074491;

X MEDLINE=97228413; PubMed=9074491;

X Rawai T., Suzuki Y., Eda S., Ohtani K., Kase T., Fujinaga Y.,

Sakamoro T., Kurimura T., Wakamiya N.;

Toloning and characterization of a cDNA encoding bovine mannan-binding

Totoin.", Gene 186:161-165(1997).

C-1- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-
dependent manner. Is capable of host defense against pathogens, by
activating the classical complement pathway independently of the
continue of the classical complement complement pathway independently of the
continue of the classical complement pathway independently of the
continue of the classical complement complement complement complement complement complement complement complement.

C-1- SIMILARITY: Contains I collagenous domain.

C-1- SIMILARITY: Contains I C-type lectin family domain.
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002659;
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mannose-binding protein C precursor (MBP-C) (Mannan-binding protein)
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Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia, Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBL_TaxID=9913;
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                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=99087489; PubMed=9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
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DNA Res. 5:297-308(1998).
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10-0CT-2003 (Rel. 42, Last sequence update)
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Probable aquaporin NIP4.2 (NOD26-like intrinsic protein 4.2)
(Nodulin-26-like major intrinsic protein 5) (AtNLMS) (NLMS protein)
NIP4.2 OR NLMS OR ATSG37620 OR K22F20,60.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Wagnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS00615; C TYPE LECTIN 1; 1.

PROSITE; PS50041; C TYPE LECTIN 2; 1.

Complement pathway; Membrane; Mannose-binding; Calcium; Repeat; Signal; Collagan; Lectin; Glycoprotein; Hydroxylation.

Signal, Collagan; Lectin; Glycoprotein; Hydroxylation.
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InterPro; IPR008160; Collagen.
InterPro; IPR001304; Lectin_C.
Pfam; PF001391; Collagen. 1.
Pfam; PF001591; Collagen. 1.
ProDom; PD000007; Clg_helix; 1.
SWART; SW00034; CLECT; 1.
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Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.1%; Score 27; DB 1; Length 283; 85.7%; Pred. No. 21; 1. Indels ive 0; Mismatches 1; Indels
                                       aquaglyceroporins.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2C70900EBCC2AB3A CRC64;
feig A.R., Jakob C.U.;
Functional characterisation of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0cT-1989 (Rel. 12, Created)
01-0cT-1989 (Rel. 12, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Methylenomycin A resistance protein (MMR peptide)
AMR OS SCF1.237C.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0783; MINTRINSICP.
ProDom; PD000295; MIP family; 1.
TIGRFAMS; TIGR0861; MIP; 1.
PROSITE; PS0221; MIP; 1.
PROSITE; PS0221; MIP; 1.
TRANSPORT; Transmembrane; Repeat; Multigene i TRANSMEM 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30277 MW;
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283 AA;
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Best Local Similarity
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P11545;
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Huang C.-H., Kieser A., Glarke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2);
Brutcon C.J., Wietzorrek A., Hartley N., Woodburn L., Chater K.F.;
"Genes involved in methylenomycin biosynthesis from plasmid SCP1 of
Streptomyces coelicolor A3(2).";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                proteins
STRAIN=A3(2);
MEDLINE=88112873; PubMed=2828187;
MEDLINE=88112873; PubMed=2828187;
Nucleotide sequence analysis reveals similarities between precenting methylenomycin A resistance in Streptomyces and tetracycline resistance in eubacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 1; Length 475;
Pred. No. 37;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL27667; CAB82871.1; -.
EMBL; AL589148; CAC32711.1; -.
EMBL; AL590464; CAC36763.1; -.
EMBL; AL59060; B25060.
InterPro; IPR007114; MPS.
PROSITE; P550850; MFS; 1.
Complete protecome. Transmembrane; Transport; TRANSMEM 28 48 POTENTIAL.
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MEDLINE=96195018; PubMed=8622982;

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MEDLINE=96195018; PubMed=8622982;

MEDLINE=96195018; PubMed=8622982;

MEDLINE=96195018; PubMed=8622982;

Trames and are expressed through transcriptional editing.";

Proc. Natl. Acad. Sci. U.S.A. 93:3602-3607(1996;

Trames and are expressed through transcriptional editing.";

Trames and are expressed through transcriptional editing.";

Transcriptions: Structural protein that forms the virion spike and which is responsible for binding to target cells and subsequent fusion of the viral and host-cell membranes. In cell receptor recognition of the viral and host-cell membrane process.

C. -- SUBMIT: Homotriner; each monomer consist of a GP1 and a GP2 subunit linked by disulfide bonds (By similarity).

C. -- SUBMIT: CACATION: Type I membrane processing (By similarity).

C. -- PTM: N-GJYCOSYJARCG, could also be O-GJYCOSYJAtcd (By similarity).

C. -- PTM: N-GJYCOSYJARCG, could also be O-GJYCOSYJAtcd (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch)
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DR EMBI 708134 AAB37096.1;

DR HSSP; 005320; 2EBO.

DR HSSP; 005320; 2EBO.

DR HSSP; 005320; 2EBO.

DR HSSP; 005320; 2EBO.

DR HSSP; 005320; 2EBO.

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THYE 601 608 N.LINKED ("T")

THYE 208 208 N.LINKED ("T")

258 257 257

268 268

268 268

296
                                                                                                                                                                                                                                                                Ebola virus (strain Sudan Boniface) (3bo).
Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
Ebola-like viruses.
NCBI_TaxID=128948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA EDITING: Modified positions=285; Note=Partially edited. RNA editing at this position consists of an insertion of one adenine nucleotide. The sequence displayed here is the full-length transmembrane glycoprotein, derived from the edited RNA. The unedited RNA gives rise to the small secreted glycoprotein (AC
                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Structural glycoprotein precursor (Virion spike glycoprotein)
[Contains: GP1; GP2].
                                                                                                      676 AA
                                                                                                      STANDARD;
204 ATESRAT 210
                                                                                                    VGP_EBOSB
Q66814;
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Gaps

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Conservative

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RN SEQUENCE FROM N.A. AND RNA EDITING.

RX SEQUENCE FROM N.A. AND RNA EDITING.

RA SANCHES A., Trappier S.G., Mahy B.W.J., Peters C.J., Nichol S.T.;

RA Sanchez A., Trappier S.G., Mahy B.W.J., Peters C.J., Nichol S.T.;

RA Sanchez A., Trappier S.G., Mahy B.W.J., Peters C.J., Nichol S.T.;

RA The virion glycoproteins of Ebola viriuses are encoded in two reading for and are expressed through transcriptional editing.";

RI Trames and are expressed through transcriptional editing.";

C. - I-TWINTION'S tructural protein that forms the virion spike and which is responsible for binding to target cells and subsequent fusion of the viral and hest-cell membranes. In cell receptor recognition of the viral and hest-cell membranes. In cell receptor recognition combunit linked by disulfide bonds (By similarity).

C. - SUBURILIAR LOCATION: Type I membrane protein. GP1 can also be shed by the virus after protechytic processing (By similarity).

C. - PTM: N-Glycosylated, could also be O-glycosylated (By similarity).

C. - PTM: Processing into GP1 and GP2 is effected by the host furin (By similarity).

C. - RNA EDITING: Modified positions=295; Note=Partially edited. RNA editing at this sequence displayed here is the full-length transmembrane glycoprotein, derived from the edited RNA. The recognition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified anor-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ebola virus (strain Sudan Maleo-79) (Ebo).
Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
Ebola-like viruses.
                                                                                                                                                                                                                                                                                        Gaps
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HSSP; Q05320; ZEBO.
InterPro; IPR002561; Filo glycop.
InterPro; IPR002561; Filo glycop.
Transmembrane; Envelope protein; Glycoprotein; Signal; RNA editing.
SIGNAL 32 POTENTIAL.
33 676 STRUCTURAL GLYCOPROTEIN.
CHAIN 33 676 GP2.
CHAIN 502 676 GP2.
GLCNAC. .) (POTENTIAL).
GLCNAC. .) (POTENTIAL).
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30-MAY-2000 (Rel. 39, Last sequence update)
15-WAY-2004 (Rel. 43, Last annotation update)
Structural glycopotein precursor (Virion spike glycoprotein)
[Contains: GP1; GP2].
                                                                                                                                                                                                                  Score 27; DB 1; Length 676;
Pred. No. 55;
0; Mismatches 1; Indels
                                                                                                                                                            700029BFD67F5E9A CRC64;
   N-LINKED
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85.7%;
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                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Clancy C., Cheng S., Chekley M.A., Lewin A., Nguyen M.-H.;
"Cloning and charaterization of phospholipase B gene (PLB2) of Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i. FUNCTION: Catalyzes the release of fatty acids from
lysophospholipids. Phospholipase B may well contribute to
pathogenicity by abetting the fungus in damaging and traversing
pathogenicity by abetting the fungus in damaging and traversing
host cell membranes, processes which likely increase the rapidity
of disseminated infection (By similarity).
-!- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)0 =
glycerophosphocholine + a fatty acid anion.
-!- SUBCELLULAR LOCATION Secreted (Probable).
-!- SIMILARITY: Belongs to the lysophospholipase family.
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D (GLCUNC. ) (POTENTIAL)
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5478;
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POTENTIAL.
IN-LINGOPHOCHPASE 2.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | DEBZ_CANGA | STANDARD; | PRT; 695 AA. | AC. | OFFGGG | CANGA | STANDARD; | PRT; 695 AA. | AC. | OFFGGG | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CANGA | CAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.1%; Score 27; DB 1; Length 676; 85.7%; Pred. No. 55; 1; Indels :ive 0; Mismatches 1; Indels
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL)
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                                                                                                         BY SIMILARITY
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InterPro; IPR002642; PLAC.
Pfam; PF01735; PLAC B; 1.
SMART; SM00022; PLAC; 1.
Lipid degradation; Hydrolase; GI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event-alternative splicing; Named isoforms=2;
Name=RTN1-B; Synonyms=S-RexB;
Isold=064548-1; Sequence=15splayed;
Name=RTN1-S; Synonyms=S-RexS;
Isold=064548-2; Sequence=VSP 005647, VSP 005648;
Isold=064548-2; Sequence=VSP 005647, VSP 005648;
TISSUE SPECIFICITY: EXPRESSED PREDOMINATIVI IN CENTRAL AND PERIPHERAL NERVOUS SYSTEM OF NEWBOON AND ADULT RATS. LOW LEVELS HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
EXPRESSION OF ISOFORM RIN1-B IS RESTRICTED TO PARTICULAR NEURONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS RIN1-B AND RIN1-S).
STRAIN=Wistar; TISSUE=Brain cortex;
MEDLINE=96186034; PubMed=8793864;
MEDLINE=96186034; PubMed=8793864;
Baka I.D., Ninkina N.M., Pinon L.G.P., Adu J., Davies A.M.,
Georgiev G.P., Buchman V.L.;
"Intracellular compartmentalization of two differentially spliced s-
"Intracellular compartmentalization of two differentially spliced s-
"Intracellular compartmentalization of two differentially spliced s-
"ENVCTION: Nay be involved in neuroendocrine secretion or in
membrane trafficking in neuroendocrine cells.
-!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By
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-1- ALTERNATIVE PRODUCTS:
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695 AA;
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SEQUENCE STATE-SEGUE ( AB972;

A MEDLINE-97313267; Pubmed-9169871;

A Dohnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,

Benes V., Brueckner M., Delius H., Dubois B., DuesterPhocft A.,

Benes V., Brueckner M., Goffeau A., Hebling U., Heumann K.,

A Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,

Louis B.J., Messenguy F., Mewes H.-W., Miosga T., Moostl D.,

Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,

Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,

Schaffe M., Schorlers B., Scholler P., Schwager C., Schwarz S.,

Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt B.,

Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,

Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
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IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW
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MEDLINE=98044229; PubMed=9382872;
Mang P.J., Hiffaker T.C.
"Stuzp: A microtubule-binding protein that is an essential component of the yeast spindle pole body.";
J. Cell Biol. 139:1271-1280(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cervisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                      Or Senu ...

REMBL; U17664; AAC53046.1; -..

REMBL; U17603; AAC53046.1; -..

REMBL; U17603; AAC53045.1; -..

REMBL; U17603; AAC53045.1; -..

REMBL; U17603; AAC53045.1; -..

DR. PROSITE; PS50845; RETICULON; 1.

DR. PROSITE; PS50845; RETICULON; 1.

REMOSIZE; PS50845; RETICULON; 1.

FT. TRANSMEM 604 624 POTENTIAL.

TRANSMEM 604 624 POTENTIAL.

TRANSMEM 727 777 RETICULON.
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777 AA; 83001 MW; AF7479C50F28DOAC CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
STUZ OR YLR045C OR L2108.
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nes 6; Conserv
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RA Gouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Babokan D., Bowman S., Ra Brooks K., Brown D., Rown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., R. Collins M., Connor R., Cronin N., Harris D., Hidalo J., Hodgson G., Rahlin N., Harris D., Hidalo J., Hodgson G., Almorsby T., Howarth S., Huchel E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., Robert S., McDonald S., McDean J., Noney P., McDonay P., Murgall K., Murphy L., Niblett D., Odell C., R. All R., R., Rebbinowitsch E., Stevens K., Starte S., Stevens K., Starte S., Stevens K., Starte S., Revers R., Squares R., Squares R., Squares R., Squares R., Starten T., Whitehead S., Modward J., Volckaert G., Aert R., Robben J., Grymonprez B., Modward J., Volckaert G., Aert R., Robben J., Grymonprez B., Amblicher B., Raber R., Starten T., Whitehead S., Rabel C., Puchs M., Fritzc C., Holzer E., Mosell D., Hilbert H., Rabel C., Puchs M., Peritzc C., Holzer E., Mosell D., Hilbert H., Rabert B., Stante C., Mottier S., Sante S., Lehrach H., Reinhardt R., Pohl T.M., A Goffeu A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Ralbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S., McConbet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dagar R.R., Cruzado L., Jimene S., Sanchez M., Gelsen C., Gerutti L., Lowe T., Mocombie W.R., Paulsen I., Potashkin J., Rappacone sequence of Schizosaccharomyces pombe.", Nature 415:871-880(2002).

-I- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for the replication of hiromosome ends by copying a template C. Suggence within the RNA component of the enzyme.

-I- Suggence Within the RNA component of the enzyme.

-I- Suggence Within the RNA component of the enzyme.

-I- Suggence Within the RNA component of the enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=013339-2; Sequence=VSP_006395;
--- MISCELLANDOUS: DELETION CAUSES TELOWERE SHORTENING AND SENESCENCE.
--- SIMILARITY: Belongs to the reverse transcriptase family.
Telomerase subfamily.
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Transferase; RNA-directed DNA polymerase; Telomere; Nuclear protein;
DNA-binding; Alternative splicing.
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988 AA; 116328 MW; AB2DC7030228F443 CRC64;
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/FTId=VSP_006395.
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EMBL; AR015783; AAC49803.1; --
EMBL; AL022299; CAA18391.1; --
FIR; T03838; T03838.
GeneDB_SPombe; SFBC2933.14c; --
InterPro; IPR004077; RVIBe.
InterPro; IPR00345; Telomerase_RT.
Pfam; PF00078; IVt; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H., Lingner J., Harley C.B., Cech T.R.; "Telomerase catalytic subunit homologs from fission yeast and human."; Science 277:955-959(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Germonline; 142107; -. SGD; SO04035; STU2.
SGD; SO004035; STU2.
SGD; SO004035; STU2.
GO; GO:0005817; F:microtubule binding; IMP.
GO; GO:0005200; F:structural constituent of cytoskeleton; IPI.
GO; GO:0007020; F:microtubule nucleation; IPI.
GO; GO:000071; F:microtubule nucleation; IPI.
InterPro; IPR008938; ARM.
InterPro; IPR000357; HEAT.
                  FUNCTION: May play a role in the attachment, organization, and/or
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498 535 HEAT 2.
888 AA; 100918 MW; 7A49C3702E21C7BF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U35247; AAA79057.1; -.
EMBL; X94607; CAA64292.1; -.
EMBL; Z3217; CAA97574.1; -.
BPIR; S61619; S61619.
GermOnline; 142107; -.
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es 6; Conservative
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TISSUE-Airway epithelium;
MEDLINE-95372368; PubMed=7544004;
Guo F.H., de Raeve R.H., Rice T.W., Stuehr D.J., Thunnissen F.B.J.M.,
Erzurum S.C.;
"Continuous nitric oxide synthesis by inducible nitric oxide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-COLORECTCAL Adenocarcinoma;
MEDLINE-94032282; PubMeds7692964;
Sherman P.A., Laubach V.E., Reep B.R., Wood E.R.;
"Purification and CDNA sequence of an inducible nitric oxide synthase from a human tumor call line.";
Biochemistry 32:11600-11605(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and expression of inducible nitric oxide synthase from human hepatocytes.";
Proc. Natl. Acad. Sci. U.S.A. 90:3491-3495(1993).
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MEDLIKE=95091827; PubMed=7528017;
Park C.S., Pardhasaradhi K., Gianotti C., Villegas E., Krishna G.;
Park C.S., Pardhasaradhi K., Gianotti C., Villegas E., Krishna G.;
Human retina expresses both constitutive and inducible isoforms of
nitric oxide synthase mRNA.";
Biochem. Biophys. Res. Commun. 205:85-91(1994).
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TISSUE_Articular Chondrocytes;

MEDLINE_34160116; PubMed=7522054;

Maier R., Bilbe G., Rediske J., Lotz M.;

Maier R., Bilbe G., Rediske J., Lotz M.;

Tinducible nitric oxide synthase From human articular chondrocytes:

CDNA cloring and analysis of mRNA expression.";

Bjochim. Biophys. Acta 1208:145-150(1994).
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MEDLINE=95155267; PubMed=7531687;
Hokari A., Zeniya M., Esumi H.;
Toloning and functional expression of human inducible nitric oxide synthase (NOS) cDNA from a glioblastoma cell line A-172.";
J. Biochem. 116:575-581(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Liver;
MEDLINE=93234523; PubMed=7682706;
MEDLINE=93234523; PubMed=7682706;
MEDLINE=93234523; PubMed=7682706;
MEDLINE=93234523; PubMed=7682706;
MEDLINE=93234523; PubMed=7682706;
MEDLINE A., Nument A.K., Simmons R.L., Snyder S.H., di Silvio M., Wang S.C., Nakayama D.K., Simmons R.L., Snyder S.H., Billiar T.R.;
                                                                                                                                                                                                                                                                                                                                                                   Eukaryora, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;
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                                                                                                                                                                                                                                          (NOS, type II)
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MEDINE-94066614, PubMed=7504305;
MEDINE-94066614, PubMed=7504305;
Charles I.G., Palla V.S., Moss D.W., Moncada S.;
Chubb A.P., Hall V.S., Moss D.W., Moncada S.;
"Cloning, characterization, and expression of a cDNA encoding inducible nitric oxide synthase from the human chondrocyte.";
Proc. Natl. Acad. Sci. U.S.A. 90:11419-11423(1993).
                                                                 NS2A HUMAN STANDARD; PRT; 1153 AA. P3528; 060757; 094994; 016263; 016692; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1996 (Rel. 23, Last sequence update) 01-FEB-1996 (Rel. 31, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Nitric oxide synthase, inducible (EC 1.14.13.39) (Inducible NOS) (Hep-NOS) NOS2A OR NOS2
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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reveals striking active-site conservation.";

Nat. Struct. Biol. 6:233-242(1999).

-! FUNCTION: Produces nitric oxide (NO) which is a messenger molecule with diverse functions throughout the body. In macrophages, NO mediates tumoricidal and bactericidal actions.

-!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+).

-! COPACTOR: Heme. Binds now mole each of FAD and FAM. Also requires tetrahydrobiopterin (BH4) which may stabilize the dimeric form of the enzyme (By similarity).

-!- ENZYME REGULATION: Regulated by calcium/calmodulin (in contrast with mouse NOS2). Aspirin inhibits expression and function of this enzyme and effects may be exerted at the level of
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MEDLÎNE-99340067; PubMed=10409685;
Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., Parkinson J.F.,
Whitlow M., Poulos T.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Crystal structures of zinc-free and -bound heme domain of human inducible nitric-oxide synthase. Implications for dimer stability and comparison with endothelial nitric-oxide synthase."; J. Biol. Chem. 274:21276-21284(1999).
                                                                                                                                 F.X., Yoneyama T., R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION.

BIDLINES-6647340, PubMed=7558036;
Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,
Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Zapol D.G.,
Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;
Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;
Three members of the nitric oxide synthase II gene family (NOS2A, NOS2B, and NOS2C) colocalize to human chromosome 17.";
Genomics 27:526-530(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 82-528.
MEDLINE=99173237, PubMed=10074942;
Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,
Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,
Weber P.C.;
"Structural characterization of nitric oxide synthase isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney,
MEDLINE=95165725; PubMed=7532248;
MCLAY JS., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G.
Raleton S.H., Grabowski P., Hattes N.E., Macleod A.M.,
Hawksworth G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nitric oxide production by human proximal tubular cells: a novel immunomodulatory mechanism?"; Kidney Int. 46:1043-1049(1994).
                                                                                                                                                                                                   "Dedifferentiated human ventricular cardiac myocytes express inducible nitric oxide synthase mRNA but not protein in response IL-1, TNF, IFNgamma, and LPS,";
J. Wol. Cell. Cardiol. 29:1153-1165 (1997).
                                                                                                                                                                                                                                                                                                                                Ogawa Y., Nishijima S., Goto M., Ida M.; Coning and characterization of a novel splice valiant of human inducible nitric oxide synthase."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
MEDLINE-99389665; PubMed-9721329;
TAYLOR B.S., Alarcon L.H., Billiar T.R.;
"Inducible nitric oxide synthase in the liver: regulation and
                                                                                           TISSUE-Cardiac myocytes;
MEDLINE-97304504; PubMed=9160867;
MEDLINE-97304504; PubMed=9160867;
MCGowan Luse H., Li R.-K., Shapiro R.A., Tzeng E., McGowan Hacakayama K., Geller D.A., Mickle D.A.G., Simmons Billiar T.R.;
in normal human airway epithelium in vivo.";
Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813(1995).
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 380-473 FROM N.A.
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Biokhimiia 63:766-781(1998)
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EMBL; 124553; AAA59171.1; -

EMBL; 124553; AAA59171.1; -

EMBL; 102450; AAA59171.1; -

EMBL; 10310; AAA5666.1; -

EMBL; 10311; AAA5666.1; -

EMBL; 102014; AAA5666.1; -

EMBL; 102014; AAA5666.1; -

EMBL; 102014; AAA5666.1; -

EMBL; ABA05231; BAA37123.1; -

EMBL; ABA05231; BAA37123.1; -

EMBL; ABA05218; BAA37123.1; -

EMBL; AF06326; AAD14179.1; -

EMBL; AF06326; AAD14179.1; -

EMBL; ABO05218; AAD14179.1; -

EMBL; ABO0531; FABD binding

EMBL; AAB676; EMBC, CYCOPOLORY

EMBL; AMOS; OG-FEB-00.

EMBL; AAB676; FABD binding Ilke.

EMBL; ABO05737; C:cytoplasm; TAS.

EGO-WORD STATE FINITIC-OXIGE SYNTC.

EMBL; ABOO05737; C:cytoplasm; TAS.

EMBL; ABOO05737; C:cytoplasm; TAS.

EMBL; ABOO05737; C:cytoplasm; TAS.

EMBL; ABOO05737; C:cytoplasm; TAS.

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IsoId=p328-2; Sequence=VSP 003582, VSP 003583;
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translational/posttranslational modification and directly on the catalytic activity (By similarity).
SUBUNIT: Homodimes
ALTERNATIVE PRODUCTS:
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100.0%; Pred. No. 1e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                          Event=Alternative splicing, Named isoforms=2;
Name=1;
IsoId=P35228-1; Sequence=Displayed;
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ID NME1_MOUSE STANDARD; PRT; 1464 AA

AC P34316; Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)
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nes 6; Conservative
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                                                                                                                                                                                                                                                                                              MEDILINE-92244361; PubMed=1374164;
MEDILINE-92243161; PubMed=1374164;
MEDILINE-92243161; PubMed=1374164;
Meduro H., Mori H., Araki K., Kushiya E., Kutsuwada T., Mishina M.;
Manzaki M., Kumanishi T., Arakawa M., Sakimura K., Mishina M.;
Marucional characterization of a heteromeric NWDA receptor channel
T. expressed from cloned cDNAs.";
Mature 357:70-74(1992).
I. Nature 257:70-74(1992).
I. SUBUNIT: Heterodimer of an epsilon subunit and a zeta subunit.
I. SUBCELLULAR LOCATION: Integral membrane protein.
I. SUMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Calcium; Magnesium.
1 22 POTENTIAL.
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613 2 (POTENTIAL).
614 3 (POTENTIAL).
614 (POTENTIAL).
614 (POTENTIAL).
615 A (POTENTIAL).
616 A (POTENTIAL).
617 PUNCTIONAL DEPERMINANT OF NWDA.
75 N-LINKED (GLCNAC. .) (POTENTIAL).
618 N-LINKED (GLCNAC. .) (POTENTIAL).
619 N-LINKED (GLCNAC. .) (POTENTIAL).
610 N-LINKED (GLCNAC. .) (POTENTIAL).
611 N-LINKED (GLCNAC. .) (POTENTIAL).
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611 N-LINKED (GLCNAC. .) (POTENTIAL).
612 N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
10-OCT-2003 (Rel. 42, Last annotation update)
Glutamate [NMDA] receptor subunit epsilon 1 precursor (N-methyl
D-aspartate receptor subtype 2A) (NR2A) (NMDAR2A).
GRINZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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GLUTAMATE [NMDA] RECEPTOR SUBUNIT
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PIR; S29159; 829159.
HSSP, P19491; 1GR2.
MGD, MGI:95820; Grin2a.
MGD, MGI:95820; Grin2a.
GO; GO:00452211; C:poetsynaptic membrane; IDA.
InterPro; IPR001320; Ion glu receptor.
InterPro; IPR001310; SBP/glu_receptor.
Pfam; PF00060; 1ig_chan; I.
PRINTS, PR00177; NMDARECEPTOR.
SMART; SM00079; PBPe; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75
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1464 AA;
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14 RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BRBL; M91561; AAC03565.1; --
BRBL; M91561; AAC03565.1; --
HSSP; P19431; 1GR2.
HICEPPO; IPRO01320; Ion glu_receptor.
InterPro; IPRO01320; Ion glu_receptor.
InterPro; IPRO01311; SBP/Glu_receptor.
InterPro; IPRO01508; NUMA_receptor.
PFfam; PF00060; 11g_Ghan; 1.
PRINTS; PR00177; NUMDARECEPTOR.
SMART; SM00079; PBPe; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
INTERACTION WITH AIP!
INTERACTION WITH AIP!
MEDLINE=98361985; PubMed=9694864;
Hirao K., Hata Y., Ide N., Takeuchi M., Irie M., Yao I., Deguchi M.,
Toyoda A., Sudhof T.C., Takai Y.;
Toyoda A., Sudhof T.C., Takai Y.;
A novel multiple PZ domain-containing molecule interacting with
N-methyl-d-asparate Exceptors and neuronal cell adhesion proteins.";
J. Biol. Chem. 273:21105-21110(1998).
-I-FUNCTION: MNDA receptor subtype of glutamate-gated ion channels
possesses high calcium permeability and voltage-dependent
sensitivity to magnesium and is mediated by glycine.
-I-SUBUNIT: Heterodimer of an epsilon subunit and a zeta subunit.
                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
MEDILTE=292157; PubMed=1350383;
MEDILTE=29215757; PubMed=1350383;
MONYET H., Sprengel R., Schoepfer R., Herb A., Higuchi M., Lomeli H., Burnashev N., Sakmann B., Seeburg P.H.;
Heteromeric NWDA receptors: molecular and functional distinction of
                                                                                                                                                                                                            Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monyer H., Sprengel R., Schoepfer R., Herb A., Higuchi M., Lomeli Burnashev N., Sakmann B., Seeburg P.H.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interacts with AIP1.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTIONAL DETERMINANT OF NMDA RECEPTORS (BY SIMILARITY). N-LINKED (GLCNAC. . .) (POTENTIAL)
                                             01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glutamate [NMDA] receptor subunit epsilon 1 precursor (N-methyl D-aspartate receptor subtype 2A) (NR2A) (NMDAR2A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.

POTENTIAL.

GLUTANATE [NMDA] RECEPTOR SUBUNIT

EPSILON 1.

EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
                         PRT; 1464 AA.
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SIGNAL 1 22 POTEN
CHAIN 23 1464 GLUTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS TO 595 AND 597-598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 256:1217-1221(1992).
                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 555
613
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                                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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556
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                      NME1 RAT
Q00959;
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REAL SEQUENCE FROM N.A.

REAL TISSUE=Kidney;

RA TISSUE=Kidney;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

R. Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

R. Altechul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhata N.K.,

R. Altechul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhata N.K.,

R. Altechul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhata N.K.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Bragheton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,

R. Brownstein M.J., Ubdin T.B., Tonchiyuki S., Carninci P., Prange C.,

R. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Antialon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R. Whiting M., Madan A., Young A.C., Sherchenko Y., Bouffard G.G.,

R. Altesled Y.S.N., Krzywinski W.I., Skalska U., Smailus D.E.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Butterfield Y.S.N., Krzywinski W.I., Skalska U., Smailus D.E.,

R. Schnerch A., Schehu J.B., Jones S.J.M., Marra M.A.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Schnerch A., Schehu J.B., J., Worles S.J.M., Marra M.A.,

R. Schnerch A., Schehu J.B., J., Spalska U., Smailus D.E.,

R. Schnerch A. Schehu J.B., Shalska U., Smailus D.E.,

R. Schnerch A. Schehu J.B., Shalska U., Smailus D.E.,

R. C. -- FUNCTION: Component of ribonuclease P, a protein complex that

C. -- CATALTYIT ACTIVITY: Endonuclease P, a protein complex that

C. -- Subunit: RNase P consists of a RNA moiety and at least 8 protein

C. -- Subunit: RNase P consists of a RNA moiety and at least 8 protein

C. C. Subunit S. RNA W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECTION N.A., AND SEQUENCE OF 21-30; 140-148 AND 185-198.
MEDLINE=97188428; PubMed=9037013;
Eder P.S., Kekuda R., Stolc V., Altman S.;
"Characterization of two scleroderma autoimmune antigens that copurify with human ribonuclease P.";
Proc. Natl. Acad. Sci. U.S.A. 94:1101-1106(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Kibomuclease P procein subunit p30 (EC 3.1.26.5) (RNaseP protein p30)
(RNase P subunit 2).
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
40 N-LINKED (GLCNAC. ..) (POTENTIAL)
43 N-LINKED (GLCNAC. ..) (POTENTIAL)
44 N-LINKED (GLCNAC. ..) (POTENTIAL)
165468 MW; DC1528E1898DECA4 CRC64;
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SUBCELLULAR LOCATION: Nuclear; nucleolar (Potential).
DISEASE: SERA FROM SCLERODERMA PATIENTS RECOGNIZE RPP38.
                                                                                                                                                                                                                      Score 27; DB 1; Length 1464;
                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tracey A.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                       1.3e+02;
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                                                                                                                                                                                                                                                    100.0%; Pred. No. 1.3
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                                                                                                                                                                                                                      87.1%;
                                                                                                                                                                                                                                                                                             6; Conservative
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           340
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       340 34
443 44;
444 44;
541 541
1464 AA;
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Best Local Similarity
Matches 6; Conserv
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P78346;
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SEQUENCE
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                                                                                                                                                                                                                                         EMBL; U77665; AAC51143.1; -.

R EMBL; U77665; AAC51143.1; -.

R EMBL; G006991; AAH06991.1; -.

R GX; P78346; -.

R MIM; 606115; -.

R GO; GO:0005655; C:nucleolar ribonuclease P complex; TAS.

R GO; GO:0005626; F:ribonuclease P activity; TAS.

R GO; GO:0004526; F:ribonuclease P activity; TAS.

R GO; GO:0004526; F:ribonuclease P activity; TAS.

R InterPro; IPR002738; RNase P p30.

R Fam; PF01876; RNase P p30.

R Hydrolase; Nuclear protein; tRNA processing; Antigen.

W HYdrolase; Nuclear protein; tRNA processing; Antigen.

CONFLICT 189 189 29321 MW; 2AB492D98ACDCCBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

83.9%; Score 26; DB 1; Length 268;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels
-!- SIMILARITY: BELONGS TO THE RPP1/RNASEP2 FAMILY.
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Gaps

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Search completed: April 21, 2004, 17:34:01 Job time : 5.55072 secs

|||||| | 92 ATSSRA 97 1 ATSSRA 6

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seq5.open.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 21, 2004, 17:27:33 ; Search time 6.3913 Seconds (without alignments) 105.353 Million cell updates/sec Run on:

SEQ5 31 1 atssrat 7 Title: Perfect score: Sequence: Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

283366 segs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	inase (	O	ribosomal protein	- 7JDS	5B, tr	Ig kappa chain V r	Ig kappa chain - h		anti		aromatic dioxygena		probable cytochrom	glycerol-3-phospha	potassium transpor	STU2 protein - yea		nitric-oxide synth	lutamate	as			hypothetical prote	mucin 6, gastric (	hypothetical prote	ornithine cyclodea	e cyclode	cal	conserved hypothet
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	Score	31	28	28	28	28	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	26	26	26	26	26	26	56	26	36
Result	No.		7	ო	4	u	w	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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Gaps

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Query Match

90.3%; Score 28; DB 2; Length 91;
Best Local Similarity 85.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 0; Indels

TPA-induced protei O-acetylhomoserine	E. 5	gumB protein - Syn probable DNA ligas	hypothetical prote	hypothetical prote	polycomb protein E	hypothetical prote	A-alpha Y 4 protei	hypothetical prote	hypothetical prote	hypothetical prote	ribosomal protein	hypothetical prote
C39590 T40463	S31436 D90211	S75310 G70649	T33170	T04980	T52415	T01503	C37271	T16759	T32552	T32550	T40691	H72486
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367	433 459	504 507	719	750	856	868	928	928	1966	2848	94	126
83.9 83.9	83.9 83.9	933	83.9	83.9	83.9	83.9	83.9	83.9	83.9	83.9	80.6	80.6
7 7 8 8 8	26 26	56 26	5 7 8	56	56	26	56	26	26	56	25	25
30 31	332	ይ c 4 ገ	900	37	38	39	40	41	42	43	4	45

## ALIGNMENTS

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Is year, and the region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Momo sapiens (man)
C;Species: Momo sapiens (man)
C;Accession: S37501
R;Kiein, U; Kuappers, R; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood A;Reference number: 837501
A;Accession: S37501
A;Cossar-references: EMBL:226611; NID:9405643; PIDN:CAA81364.1; PID:9405644
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jakapsa chain - human (fragment)
CySpecies: Homo sapiens (man)
CySpecies: Homo sapiens (man)
CySpecies: Homo sapiens (man)
CySpecies: Homo sapiens (man)
CySpecies: Homo sapiens (man)
CyAccession: S20633
Rylee, S.K.; Bridges, L.S.; Koopman, W.J.; Schroeder, H.W.
Submitted to the EMBL Data Library, April 1992
AyAccession: S20633
AyAccession: S20633
AyStatus: preliminary
AyMolecule type: mRNA
AyResidues: 1-124 < LEE>
AyEsidues: L-124 < LEE>
AyEsidues: L-124 < LEE>
AyCross-references: EMBL: Z11891; NID: G33185; PIDN: CAA77945.1; PID: G33186
CySuperfamily: immunoglobulin V region; immunoglobulin homology
CyReywords: heterotetramer; immunoglobulin
F;32-107/Domain: immunoglobulin homology < INM>
A; Accession: T45025
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-3570 <DES>
A; Rross-references: EMBL: Z72496; NID: g1834502; PIDN: CAA96577.1; PID: g1834503
A; Experimental source: placenta
A; Experimental source: placenta
A; Genetics:
A; Genetics:
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Pred. No. 3.9e+02;
1; Mismatches 0; Indels
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S35047

much out - human

c;Species: Homo sapiens (man)

c;Accession: S35047

R;Dutosee, J; Porchet, N.; Audie, J.P.; Guyonnet Duperat, V.; Laine, A.; van-Seuningen, B;Ochem. J. 293, 329-337, 1993

A;Aitle: Degenerate 87-base-pair tandem repeats create hydrophilic/hydrophobic alternation A;Reference number: S35047

A;Accession: S35047

A;Accession: S35047

A;Residues: pre-liminary

A;Residues: 1-543 < DUF>
A;Residues: 1-543 < DUF>
A;Residues: 1-543 < DUF>
A;Accession: S35047

A;Residues: 1-543 < DUF>
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A;Accession: S
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C.Species: Mycobacterium leprae
C.Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 13-Aug-1999
C.Accession: S77660; S49523
R.Psihi, H., Cole, S.T., Cole, S.T., Cole, S.T., Cole, S.T., Cole, S.T., Cole, S.T., Cole, S.T., Cole, S.T., Cole, S.T., Cole, S.T., MID: 96059637; PMID: 7476188
A.Title: The Mycobacterium leprae genome: systematic sequence analysis identifies key ca A.Title: The Mycobacterium leprae genome: systematic sequence analysis identifies key ca A.Accession: S77660
A.Accession: S7766
A.Molecule type: DNA
A.Molecule type: DNA
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A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule the nucleotide sequence was submitted to the EMBL Data Library, October 1994
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85.7%; Pred. No. 50;
iive 1; Mismatches 0; Indels
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85.7%; Pred. No. 57;
ive 1; Mismatches 0; Indels
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A;Gene: rps:
C;Superfamily: Escherichia coli ribosomal protein S1
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribosomal protein S1 - Mycobacterium leprae
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ATSSKAT 79
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C;Species: Pseudomonas sp.
C;Species: Pseudomonas sp.
C;Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 20-Jun-2000
C;Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 20-Jun-2000
C;Accession. B55523
R;Kikuchi, Y.; Nagata, Y.; Hinata, M.; Kimbara, K.; Fukuda, M.; Yano, K.; Takagi, M.
B;Acteriol. 176, 1689-1694, 1994
A;Title: Identification of the bphA4 gene encoding ferredoxin reductase involved in biph.
A;Reference number: A55523, MUID:94179104; PMID:8132464
A;Accession: B55523
A;Accession: B55523
A;Accession: B55523
A;Residues: 1-410 cKIK>
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C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 20-Sep-1999
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 20-Sep-1999
C;Accession: B29606
A;Accession: Application resistance protein
C;Accession: Accession: Accession resistance, transmembrane protein
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probable cytochrome P450 At2g44890 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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100.0%; Pred. No. 74;
cive 0; Mismatches
                                                                                                                                                             87.1%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
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C,Genetics:
A,Map position: 3
A,Introns: 53/1; 147/3
A,Note: T22K7.30
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                    hypothetical protein APE2398 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: E72469
R;Rawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kudoh, Y.; Yamazaki, J.; Kaference number: A;Reference of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A,Reference number: A72450; MUD:99310339; PMID:10382966
A,Scatus: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-131 <KAW>
A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81413.1; PID:d1045199; PID:g510
B;Experimental source: strain K1
C;Genetics:
A;Gene: APE2398
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C;Species: Orf virus
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
R;FAccession: B37473
Virology 195, 175-184, 1993
A;Title: Conservation of gene structure and arrangement between vaccinia virus and orf A;Reference number: A37473; MUD:93303916; PMID:8317094
A;Accession: B37473
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T5.Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000
T47426
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A,Molecule type: nucleic acid
A,Molecule type: nucleic acid
A,Molecule type: nucleic acid
A,Mossidues: 1-27, <FILE>
A,Mores: Generate and GB:S62819; NID:g386384; FIDN:AAB27258.1; FID:g386386
A,Note: sequence inconsistent with nucleotide translation
A,Note: sequence extracted from NCBI backbone (NCBIN:134136, NCBIP:134138)
A,Note: strain NZ2
C,Superfamily: vaccinia virus H6 protein
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100.0%; Pred. No. 23;
iive 0; Mismatches 0; Indels
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87.1%; Score 27; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-228 **RIE>
A;Experimental source: cultivar Columbia; BAC clone T22K7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           envelope antigen homolog F3R - Orf virus
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Matches 6; Conserv
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B37473
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Search completed: April 21, 2004, 17:38:30 Job time : 8.3913 secs
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Matches 6; Conservative
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AG3470
glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) [imported] - Brucella melitensis (strai
C;Species: Brucella melitensis
C;Decies: Brucella melitensis
C;Decies: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AG3470
C;Accession: AG3470
C;Accession: AG3470
C;Accession: AG3470
C;Accession: AG3470
C;Accession: AG3470
C;Accession: AG3470
C;Accession: AG3470
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Title: The genome sequence of the facultation intracellular pathogen Brucella melitens
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Keywords: oxidoreductase
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 02-Feb-2001
C;Accession: T00404; A84884
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Bxandon, R.C.; Sykes, S.M.; Masc submitted to the EMBL Data Library, July 1997
A;Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.
A;Reference number: Z14146
A;Accession: T00404
                                                                                                                                                                                                                                                                                                                                      A,Cross-references: EMBL:AC002388; NID:g3420042; PID:g2344895
A,Cross-references: EMBL:AC002388; NID:g3420042; PID:g2344895
A;Experimental source: cultivar Columbia
R;Ein, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Noffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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Similarity 100.0%; Pred. No. 93;
6; Conservative 0; Mismatches 0; Indels
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87.1%; Score 27; DB 2; Length 490;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 1; Indels
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A;Introns: 33/2, 248/3; 361/3; 428/3
C;Superfamily: Candida cytochrome P450 52A3; cyto
F;281-456/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                                                                              A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Best Local Similarity
Matches 6; Conserv
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A, Molecule type: DNA
A, Residues: 1-490 <STO>
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RESULT 15 AG0001

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potássium transport protein kup [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001
Species: Yersinia pestis
C;Date: 02-Nov-2001
S;Recession: AG0001
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
A;Parkhill, J.; Wren, B.W.; Simmonds, M.; Skelton, J.; Stevens, K.; Mnitchead, S.; Barrell, I.M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Mnitchead, S.; Barrell, I.M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Mnitchead, S.; Barrell, I.M.; Reference number: AB0001; MUD:21470413; PMID:11586360
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protein kup [imported] - Yersinia pestis (strain CO92)
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 21, 2004, 17:26:23; Search time 18.6667 Seconds (without alignments) 118.319 Million cell updates/sec Run on:

Title: SEQ5 Perfect score; 31 Sequence: 1 atssrat 7

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL 25:\*
1: Sp\_archea:\*
2: Sp\_bacteria:\*
3: Sp\_fungi:\*
4: Sp\_human:\*
5: Sp\_invertebrate:\*
6: Sp\_mammal:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Q87ct2 xylella fas	Q48277 haemophilus	Q7t298 brachydanio	Q14879 homo sapien	Q50471 mycobacteri	Q9nye4 homo sapien	Q9u225 caenorhabdi	Q9u0i6 plasmodium	Q9v8b7 drosophila	Q9ul86 homo sapien	Q9y987 aeropyrum p	Q9ud42 homo sapien	Q8p3g0 xanthomonas	Q86620 orf virus (	Q9m290 arabidopsis	Q8lpa9 hordeum vul
OCT TABLE OC	QI	Q87CT2	Q48277	Q7T298	Q14879	Q50471	Q9NYE4	Q9U225	910060	Q9V8B7	Q9UL86	Q9Y987	Q9UD42	Q8P3G0	086620	Q9M290	Q8LPA9
	DB	19	N	13	4	N	4	'n	S	Ŋ	4	17	4	16	12	10	10
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MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Oyprinidae; Danio.
NCBL_TaxID=7955;
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Pasteurellaceae; Haemophilus.
NCBI_TaxID=731;
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Score 28; DB 16; Length 281;
Pred. No. 1.1e+02;
1; Mismatches 0; Indels
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90.3%; Score 28; DB 2; Length 350;
Best Local Similarity 85.7%; Pred. No. 1.46+02;
Matches 6; Conservative 1; Mismatches 0; Indels
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Thesis (1996), V. I. D. O., University of Saskatchewan.
EMBL; U28154; AAC45158.1; -.
Inter: U28154; DARC0644; Major capsid_P2.
Pfan; PP05125; Phage cap_P2; 1.
TIGREAMS; TIGRO1551; major capsid P2; 1.
SEQUENCE 350 AA; 38973 WW; 07B47EC8F2C86116 CRC64;
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Putative major capsid protein.
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MEDLINE=97221585; PubMed=9068631;
   90.3%;
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MEDLINE-93443858; Pubmed=7916618;
Dufosse J., Porche N., Audie J.P., Guyonnet Duperat V., Laine A.,
Dufosse J., Porche N., Audie J.P., Guyonnet Duperat J.P.;
Van-Seuningen I., Marrakchi S., Degand P., Aubert J.P.;
Van-Seuningen I., Marrakchi S., Degand P., Aubert J.P.;
Van-Seuningen I., Marrakchi S., Degand P., Aubert J.P.;
Van-Seuningen I., Marrakchi S., Degand P., Aubert J.P.;
Incernating domains in human mucin peptides mapped to 11p15.";
Biochem. J. 293:329-337 (1993)
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettenan M., Madan A., Rodrígues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Gones J.J., Marza M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903 (2002).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1.8e+02;
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Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO54634; AAH54634.1; ..
Hypothetical protein.
SEQUENCE 440 AA; 49158 MW; 2480B79309437752 CRC64;
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Last annotation update)
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85.7%; Pred. No. 2.3e+02;
iive 1; Mismatches 0;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6, Conserv
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
X56A3A.6 protein.
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MEDLINE=99069613; PubMed=9851916;
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659 ATSSKAT 665
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
MEDLINE 29131752; PubMed=7830574;
MEDLINE 29131752; PubMed=7830574;
Zhang Y., Young D.;
Strain variation in the katG region of Mycobacterium tuberculosis.";
Mol. Microbiol. 14:301-308(1994).
EMBL; S77045; AAG60402.1;
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IRR00183; Decarbxy1862.
InterPro; IRR00183; Decarbxy1862.
InterPro; IRR00183; Decarbxy1662.
InterPro; PR00219; Mycobac_pentapep.
Pfam; PF01469; Pentapeptide_2; 8.
PROSITE; PS00879; ODR_DC_2_2; 3.
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SEQUENCE FROM N.A.

Ho 6.1a., Toribara N.W., Anway R.E., Spurr-Michaud S.J., Shekels L.L.,

Kettmann H.T., Hill J.A., Gipson I.K.,

"Expression cloning of human cervical proteins using an antibody to

cervical mucus.";

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF253321; AAF64523.1; -.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 10, Last sequence update)
01-NOT-2003 (TrEMBLrel. 25, Last annotation update)
01-St of katG (Species-specific fragment) (Fragment).
Mycobacterium tuberculosis.
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriacee; Mycobacterium.
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85.7%; Pred. No. 2.98+02;
tive 1; Mismatches 0; Indels
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716 AA; 71194 MW; 6F3F20E7512289F3 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Cervical mucin MUCSB (Fragment)
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                                 693 AA
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683 ATSTRAT 689
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SEQUENCE
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Q9U225
ID Q9U2:
AC Q9U2:
DT 01-M
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Q9NYE4
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Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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EMBL, AL035475; CAB62877.2; -.
Hypothetical protein.
SEQUENCE 833 AA; 100542 MW; DD231B04831DFD74 CRC64;
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Jabamodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
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                                                                                                                                                                                                                                                                                                                          Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
90.3%; Score 28; DB 5; Length 798;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                 Mattnews L.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
EMBL, AL132860, CAB6015.1; -.
WormPep; Y56A3A.6; CE22577.
SEQUENCE 798 AA; 85950 WW; 172FEB04895A9EEB CRC64;
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Last sequence update)
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09V8B7
1D 09V8B
AC 09V8B
DT 01-M
DT 01-M
DT 01-M
ON 0557!
GN CG57!
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Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                               "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
                                                                                                                 SEQUENCE FROM N.A.
BEDLINE-98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

87.1%; Score 27; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels
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EMBL; AF035028; AAD56264.1; -.
PIR, B03607; B13601.
PIR, B0362; UNTL.
INCEPTO; IPR00110; Ig-like.
INCEPTO; IPR00110; Ig-like.
INCEPTO; IPR00110; Ig-like.
PROSITE; PS50835; IG_LIKE; 1.
SWART; SMO0407; Agy 1.
SWART; SMO0407; Agy 1.
SWART; B00407; Agy 1.
SWART; B00407; Agy 1.
SWART; B00407; Agy 1.
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SEQÜENCE 109 AA; 11928 MW; 243325F72C7DAC83 C
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RADALINE-201806; PubMed=10731132;

RADALINE-201806; PubMed=10731132;

RADALINE-201806; PubMed=10731132;

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RADALINE-201806; PubMed=10731132;

RADALINE-201806; PubMed=10731132;

RADALINE-201806; PubMed=10731132;

RADALINE-201806; PubMed=107; Bayeng O., Champe N., Pfeiffer B.D., RADALINE N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Bouck N., Golbart W., Gleibart W., Gleibart W., Gleibart W., Gleibart W., Gleibart W., Gleibart W., M., Gleibart W., Harvey N., Harvey N., Houck J., Harvey N., Harvey N., Houck J., Harvey N., Harvey N., Molanson N., Rechum N., Lin X., Mallen N., Mallen N., Mallen N., Misch N., Misch N., Misch N., Misch N., Misch N., Misch N., Misch N., Misch N., Misch N., Misch N., Misch N., Misch N., Misch N., Misch N., Willer S., Will N., Misch N., Willer B., Sanders N., Misch N., Willer S., Willer S., Willer S., Willer S., Willer S., Willer S., Willer S., Willer S., Willer S., Willer S., Willer S., Willer S., Willer S., Willer S., Willer S., Standers N., Shupski M., Schelet F., Sheng N., Misch N., Willer S., Willer S., Standers N., Willer S., Willer S., Willer S., Standers N., Willer S., Willer S., Standers N., Willer S., Willer S., Willer S., Standers N., Willer S., Willer S., Standers N., Willer S., Willer S., Willer S., Standers N., Willer S., Willer S., Standers N., Willer S., Willer S., Standers N., Willer S., Willer S., St
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.3%; Score 28; DB 5; Length 1205; 85.7%; Pred. No. 5.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494; ChTBD2; 1.
1205 AA; 132314 MW; C18E2F0E0491AF62 CRC64;
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tes 6; Conservative
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Gaps

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2 TSSRAT 7

109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococacaeae; Aeropyrum.
NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BMBL; AP000064; BAA81413.1; -.
PIR; B72469; B72469.
Hypothetical protein; Complete proteome.
SEQUENCE 131 AA; 13019 MW; 0DA7559BA655BAA1 CRC64;
                                                                                                                                                                          097987;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE2398.
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Best Local Similarity 100.
                                                                                                                            PRELIMINARY;
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RESULT 11
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Q9UL86,
Q9UL86;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT--2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region

RESULT 10
Q9UL8
ID Q9UL8
AC Q9UL8
DT 01-MADT 01-MADT 01-MC

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Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W., Rudd S., Lencke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                            Complete proteome.
SEQUENCE 201 AA; 21267 MW; 08239FA3067863A2 CRC64;
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EMBL; AE012535; AAM43332.1; -.
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                                                                                                                                                                                                                                                                                                                                                                               108 ATSKRAT 114
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=22022145; PubMed=12024217;

MEDLINE=22022145; PubMed=12024217;

A a Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A loeg L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A loeg L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., Elborry H.,

Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

A cicarelli R.M.B., Coutinho L.L., Leite R.C.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.G.M., Lemos M.V.F.,

A corali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins B.C., Machado M.A., Machala A.M.B.N., Martinez-Rossi N.M.,

Martins B.C., Meddanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Martins B.C., Meddanis J., Menck C.F.M., Miyaki C.Y., Oliveira W.R.,

A pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M.Y., Sena J.A.D., Salva C., de Souza R.F.,

Trindade dos Santos W.Y., Sena J.A.D., Tesai S.M., White F.F.,

Tomparison of the genomes of two Xanthomonas pathogens with differing

H. Mast specificities ","

Martine S.C., Martines ","

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J. Neurochem. 64:85-91(1995).
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR003097; FAD binding.
Pfam; PF00667; PAD binding.1; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 13, Last annotation update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Nitric oxide synthase, NOS (Fragment).
Nitric oxide synthase, NOS (Fragment).
Eukaryosapiens (Human).
Eukaryosapiens (Homan).
Mammalia; Rutheria; Primates; Catarrhini; Hominidae; Homo.
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Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xanthomonas.
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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165 AA; 18466 MW; 99626E5FD04C2C3D CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Histone.
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Arabidopsis thallana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Supermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                     Orf virus (strain NZ2) (OV NZ-2). Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Parapoxvirus. NOSI_TaxID=10259;
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    Length 201;
/ Match
Local Similarity 85.7%; Pred. No. 1.46+02;
les 6; Conservative 0; Mismatches 1; Indels
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
NAC domain-like protein.
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Q86620;
Q1-NOV-1996 (TXEMBLrel. 01, Created)
Q1-NOV-1996 (TXEMBLrel. 01, Last sequence update)
Q1-OCT-2003 (TXEMBLrel. 25, Last annotation update)
Envelope antigen homolog.
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0
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EMBL; AL138641; CAB86913.1; -.
PIR; T47425; T47425.
Interpro; IPR003441; NAM.
PFan; PF02365; NAM.; L.
SEQUENCE 228 AA; 25304 MW; B5D67E70E96D2F44 CRC64;
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Search completed: April 21, 2004, 17:37:21 Job time : 21.6667 secs

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April 21, 2004, 17:25:18 ; Search time 28 Seconds (without alignments) 70.637 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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BLOSUM62 Gapop 10.0 , Gapext 0.5 SEQ5 31 1 atssrat 7 Scoring table: score: Sequence: Title: Perfect

1586107 segs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003as:\* A Geneseq 29Jan04:\* 1: geneseqp1980s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

# SUMMARIES

Abm66094 Propionib Abp73474 Candida a Abp73478 Candida a Abp43908 MUCSB par Abp62365 Human imm Aag87027 Saccharom Aau54148 Propionib Abm80667 Propionib Abm89514 Human imm Aae38332 Human ant Abb62768 Human ant Abg8286 Human imm Aac29549 Human ant Abg871911 Human ant Ada89184 Human ant Abg8184 Human ant Abg8184 Human ant Abg8184 Human ant Abg81891 Human ant Ada89184 Human ant Ada89184 Human ant Ada89184 Human ant Ada89184 Human ant	Peptid
ABM66094 ABP73474 ABP6734778 ABP62365 AAG87027 AAG87029 AAM59114 AAE38332 AAM59514 AAE32885 AAG922885 AAG922885 AAG929885 AAG929885 AAG929885 AAG929885 AAG929885 AAG929885	AAY29862 AAR47336
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77777777777777777777777777777777777777	4 4 5 5

## ALIGNMENTS

RESULT 1

```
Propionibacterium acnes immunogenic protein #2512.
  AAU41616 standard; protein; 88 AA.
            (first entry)
            13-FEB-2002
       AAU41616;
AAU41616
```

SAPHO syndrome, synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant. Propionibacterium acnes. WO200181581-A2

20-APR-2001; 2001WO-US012865. 01-NOV-2001.

Mitcham JL, Wang SS, , Jen S, Carter D; 21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P. Skeiky YAW, Persing DH, M. L'maisonneuve J, Zhang Y, (CORI-) CORIXA CORP.

Bhatia A;

Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris. WPI; 2001-616774/71. N-PSDB; AAS59515.

Example 1; SEQ ID NO 2811; 1069pp; English.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by p. acnes. The disorders include SAPHO synovicis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory

seq5.open.rag

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lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a mample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used a diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 88 AA;
            88888888888888888888
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100.0%; Score 31; DB 4; Length 88; 100.0%; Pred. No. 19; 0; Indels ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity luv...
7, Conservative
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ABM38135 standard; protein; 88 AA.
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RESULT 2
ABM38138
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Propionibacterium acnes predicted ORF-encoded polypeptide #2811.

Acne vulgaris, antiseborrhoeic, dermatological; antibacterial; immunostimulant; immune response; vaccine.

Propionibacterium acnes

WO2003033515-A1.

24-APR-2003.

11-OCT-2002; 2002WO-US032727

15-OCT-2001; 2001US-00978825

(CORI-) CORIXA CORP.

Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL; Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D; Barth B, Vallieve-Douglass J;

WPI; 2003-381789/36. N-PSDB; ACF64444. New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. Example 1; SEQ ID NO 2811; 1481pp; English. The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (BBM35634-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention, antibodies against polypeptides of the invention, antibodies against polypeptides of the invention, comprising a polypeptide of the invention, an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method of a vaccine composition (comprising P. acnes polypeptides,

polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne volgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the reading frame) contained within the P. acnes polynucleotides of the reading frame) but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/bublished\_pot\_gequences %

Sequence 88 AA;

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Arabidopsis thaliana protein fragment SEQ ID NO: 36783.

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thaliana.

06-SEP-2000.

EP1033405-A2

25-FEB-2000; 2000EP-00301439

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PR 23-AUG-1999; 99US-015329P.
PR 23-AUG-1999; 99US-015329P.
PR 23-AUG-1999; 99US-015329P.
PR 23-AUG-1999; 99US-015329P.
PR 23-AUG-1999; 99US-015329P.
PR 23-AUG-1999; 99US-015329P.
PR 23-AUG-1999; 99US-015329P.
PR 23-AUG-1999; 99US-015329P.
PR 23-AUG-1999; 99US-015329P.
PR 23-AUG-1999; 99US-015332P.
PR 23-AUG-1999; 99US-015332P.
PR 23-AUG-1999; 99US-015332P.
PR 23-AUG-1999; 99US-016334P.
PR 23-AUG-1999; 99US-016334P.
PR 23-AUG-1999; 99US-016334P.
PR 23-AUG-1999; 99US-016334P.
PR 23-AUG-1999; 99US-016334P.
PR 23-AUG-1999; 99US-016334P.
PR 23-AUG-1999; 99US-016334P.
PR 23-AUG-1999; 99US-016334P.
PR 23-AUG-1999; 99US-016334P.
PR 23-AUG-1999; 99US-016334P.
PR

Length 497;

DB 3;

Score 31;

100.08;

Query Match

7

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by per acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acnes ulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used a diagnostic agents for determining P. acnes presence, for example, by chis patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthalmitis; bone; joint, central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes predicted ORF-encoded polypeptide #2404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 4; Length 59;
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mitcham JL, Wang SS,
Jen S, Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 2404; 1069pp; English.
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                                                                                                                                                                                                                                                                                       21-AFR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                      20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
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Best Local Similarity 85.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-616774/71.
N-PSDB; AAS59514.
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                                                                                                                                                                    WO200181581-A2
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ABM37728
ID ABM3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence encoding a polypeptide comprising a sequence not given in the specification. A polynucleotide of the invention has fungicide activity, and may have a use in gene therapy. The nucleic acid is useful for preparing a composition for treating an infection caused by Cryptococcus neoformans. The present sequence represents a C. neoformans sequence of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.
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                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid, useful for preparing a composition for treating an infection caused by Cryptococcus neoformans.
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100.0%; Pred. No. 1.30+02; Pred. No. 1.30+02
                        Indels
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    Pred. No. 1.3e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                      C. neoformans amino acid sequence SEQ ID NO:3218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; SEQ ID NO 3218; 136pp; English
                                                                                                                                                                                                                                                                                                                                                                                fungicide; gene therapy; infection.
                                                                                                                                                                                                            ADB70174 standard; protein; 501 AA
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      100.08;
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                                                                                                                                                                                                                                                                                           04-DEC-2003 (first entry)
Best Local Similarity 100. Matches 7; Conservative
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                                                                                                        377 ATSSRAT 383
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                                                              1 ATSSRAT 7
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es 7; Conser
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Matches
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Bhatia A;

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Gaps

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RESULT 7
AAU41209
ID AAU4
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AC AAU4
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DT 13-F
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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                  Propionibacterium acnes immunogenic protein #27041
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                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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                     27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky YAW, Persing DH,
L'maisonneuve J, Zhang
                                                                                                                                                                                                                                            Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
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N-PSDB; AASS9715.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polynuclectide (ACF64435-ACF64733)

encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynuclectides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a division proteins comprising a polypeptide of the invention; a polymerlectide and an isolated T cell population comprising T cells prepared to the method, a vaccine composition (comprising P. acnes polypeptides, polymerlectides, antibodies, fusion proteins, T cell populations, or artigen-presenting cells that express the polypeptide); a method and an isolated T cell population or comprising P. acnes polypeptides, polymuclectides, and an express the polypeptide); a method and kit for detecting or determining the presence of P. acnes in a consideration. The populations or antigen-presenting cells that express the polypeptides in a patient, and a method for inhibiting the development of P. acnes in a patient, and a method for inhibiting the development of P. acnes in a patient, and a method for inhibiting the gevelopment of P. acnes in contraining the presenting cells that express the polymeric acid hybridisation. The polymerlectides are useful for diagnosing, preventing or treating acnes protein. The polymuclectides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulating a frame) contained within the P. acnes polymeric assay. The present cand the kit is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present cand the kit is useful to performing a diagnostic assay. The present cand the kit is assumented by an office the printed specification, but was obtained in electronic format directly contained by contained in electronic format directly contained aperior and th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                   Maisonneuve JL;
Jones R, Carter D;
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                       Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                   Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 2404; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Mitcham JL, Skeiky YAW, Persing DH,
Zhang Y, Wang S, Jen S, Lodes MJ,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                       11-OCT-2002; 2002WO-US032727.
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                                                                                                       Propionibacterium acnes
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Best Local Similarity
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N-PSDB; ACF64443.
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27 ATASRAT 33
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Bhatia A;

Mitcham JL, Wang SS, Jen S, Carter D;

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by cares. The disorders include SAPHO syndrome (syndritis, acne, pustulosis, hypertosis and osteomyealitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acnes in a patient comprises contacting to resence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention of polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to charged the expression and activity of P. acnes proteins. The antibodies may also be used as diagnosic agents for determining P. acnes proteins. The antibodies may also be used as diagnosic agents for determining P. acnes proteins. The antibodies may also be used as diagnosic agents for determining P. acnes proteins the acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnosic agents for determining P. acnes proteins for expression and activity of P. acnes polypeptides and the antibodies may also be used as diagnosic agents for determining P. acnes proteins the sequence data for this patent did not form part of Labrined specification, but was contactined in the account directly from MIPO at
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Best Local Similarity
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AAU66145 standard; protein; 70 AA.

RESULT 9
AAUG6145
ID AAUG
XX
AC AAUG

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AAU66145;

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant. Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris. Propionibacterium acnes immunogenic protein #11316 Skeiky YAW, Persing DH, Mitcham JL, Wang L'maisonneuve J, Zhang Y, Jen S, Carter 21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P. 20-APR-2001; 2001WO-US012865 27-FEB-2002 (first entry) Propionibacterium acnes WPI; 2001-616774/71. N-PSDB; AAS59548. (CORI-) CORIXA CORP. WO200181581-A2. 01-NOV-2001 

Example 1; SEQ ID NO 11615; 1069pp; English

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by practices. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyellite), uvertis and endophthalmitis. The acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes proper acnes proteins. The autibodies and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by chis patent did not form part of the printed specification, but was chis patent did not form part of the printed specification, but was ftp.wipo.int/pub/published\_pct\_sequences

Sequence 70 AA;

; 0 Score 28; DB 4; Length 70; Pred. No. 72; 1; Mismatches 0; Indels 90.3%; 6; Conservative Query Match Best Local Similarity

ATSSRAT 7 

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ABP03196 standard; protein; 70

ABP03196; RESULT 11
ABP03196
ID ABP03:
XX
AC ABP03:

Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardicvascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis. Human ORFX protein sequence SEQ ID NO:6374. 24-JUN-2002 (first entry) 

Homo sapiens

WO200192523-A2.

06-DEC-2001.

29-MAY-2001, 2001WO-US010836.

30-MAY-2000; 2000US-0206132P. 29-AUG-2000; 2000US-0228716P.

CURA-) CURAGEN CORP

Wang SS, Bhatia A;

Shimkets RA, Leach MD;

WPI; 2002-106308/14. N-PSDB; ABN18948.

Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

Disclosure; SEQ ID NO 6374; 1037pp; English.

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABNIST62 to ABNIST25 encode the human ORFX proteins given in ABP00010 to ABPI1500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a squances can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, proteins in the carding a treatment of cancer, hyperproliferative disorders, infrhosis of liver, proteins in the carding a treatment of cancer, hyperproliferative disorders, info in the carding burntation, cardiovascular diseases, disorders related to organ carding anterior, aradiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders infectious closus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also cuseful for treating burns, incisions, ulcers, for treating observation and treatment of lung or liver fibrosis, protection or regeneration and treatment of lung or liver fibrosis, corpection or regeneration and treatment of lung or liver fibrosis, ergemic cytokine damage. NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic corpused form part of the printed specification, but was obtained in electronic corpus of the printed specification, the propertion of the printed specification, but was obtained and electronic corpus of the printed specification, the very sequence of the printed specification of the printed specification intropublished pot electronic corp

Sequence 70 AA;

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Gaps ö 90.3%; Score 28; DB 5; Length 70; 85.7%; Pred. No. 72; 0; Indels ive 1; Mismatches 0; Indels Query Match
Best Local Similarity 85.7
Matches 6; Conservative

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ATSSRST 1 ATSSRAT

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ABM46939 standard; protein; 70 AA.

RESULT 12 ABM46939

(first entry)

20-OCT-2003

ABM46939;

The invention relates to an isolated polymucleotide (ACF64435-ACF64733)

encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (BABM5624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a distribution in the invention; additionally encompasses expression vectors and host cells comprising a polypeptide of the invention; and encoding a minute response specific for a . acnes constituted and an isolated T cell population comprising T cells prepared via this method, a vaccine composition (Comprising P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations, or antigner-presenting cells that express the polypeptide); a method and activate and an expense the polypeptide, a method and kit cfor detecting or determining the presence of P. acnes in a consider that present an expectation or antigner-presenting cells that express the polypeptides, polymuclations or antigen-presenting cells that express the polypeptides, polymuclation or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne to protein. The polymuclations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne controlled an immune response against P. acnes, or for treating acnes the protein. The polymuclacides can also be used as probes or primers for candito frame of an immune response against P. acnes, or for treating acnes and the kit is useful for performing a diagnostic assay. The present content of the printed specification, but was obtained in electronic format directly from without the polymuclacides and all across polymented in electronic format directly from particular and electronic format directly from with an electronic format directly and an electronic formation. ô New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. Gaps Maisonneuve JL; Jones R, Carter D; Propionibacterium acnes predicted ORF-encoded polypeptide #11615. ö Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine. Query Match 90.3%; Score 28; DB 6; Length 70; Best Local Similarity 85.7%; Pred. No. 72; Matches 6; Conservative 1; Mismatches 0; Indels Persing DH, Bhatia A, Lodes MJ, Benson DR, Example 1; SEQ ID NO 11615; 1481pp; English. Mitcham JL, Skeiky YAW, Pers Zhang Y, Wang S, Jen S, Lod Barth B, Vallieve-Douglass J; 11-OCT-2002; 2002WO-US032727 15-OCT-2001; 2001US-00978825 Propionibacterium acnes WPI; 2003-381789/36. N-PSDB; ACF64477. (CORI-) CORIXA CORP. Sequence 70 AA; WO2003033515-A1 24-APR-2003

The invention relates to an isolated polymucleotide (ACF64435-ACF64733)

cenceding a Propionibacterium acnes protein. The invention also relates to polymeptides encoded by the polymucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polymeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a convention; fusion proteins comprising a polymeptide of the invention; a comprising an immune response specific for a P. acnes for invention; fusion proteins comprising p. polymeptides of the invention; a composition (comprising T. cells prepared to invention; a method a vaccine composition (comprising T. cells prepared to polymeptides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polymeptide; a method and kit conferential cells that express the polymeptide; and method for inhibiting the development of P. acnes in a conference of patient, and a method for inhibiting the development of P. acnes in a proteins; T cell populations or antigen-presenting cells that express the colymeptides are useful for diagnosing, preventing or treating acnes to polymeptides are useful for diagnosing, preventing or treating acnes to polymeptides are useful for diagnosing, preventing or treating acnes to protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the performing a diagnostic assay. The present or sequence represents a polymeptide predicted to be encoded by an ORF (open the printed specification, but was obtained in electronic format directly to the printed specification, but was obtained in electronic format directly contained in the polymention. New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. Propionibacterium acnes predicted ORF-encoded polypeptide #27340. Acne vulgaris, antiseborrhoeic, dermatological, antibacterial; immunostimulant, immune response; vaccine. Persing DH, Bhatia A, Lodes MJ, Benson DR, Example 1; SEQ ID NO 27340; 1481pp; English. Mitcham JL, Skeiky YAW, Persi Zhang Y, Wang S, Jen S, Lodé Barth B, Vallieve-Douglass J; 11-OCT-2002; 2002WO-US032727. 15-OCT-2001; 2001US-00978825. (first entry) Propionibacterium acnes. WPI; 2003-381789/36. (CORI-) CORIXA CORP. N-PSDB; ACF64644. WO2003033515-A1. 20-0CT-2003 24-APR-2003 ABM62664; 

seq5.open.rag

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RESULT 1.

ABM62664 standard; protein; 70 AA.

Maisonneuve JL; Jones R, Carter D;

Sequence 70 AA

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The invention relates to a secretory polynucleotide (designated sptm) comprising any of 567 polynucleotide sequences (AB255837-AB236403), a naturally occurring polynucleotide sequence at least 90 % identical to the polynucleotide sequence, a polynucleotide complementary to them or an KNA equivalent of them. The polypeptide or polynucleotide are useful for treating, preventing or diagnosing a disease or condition associated with the expression of functional SPTM. These are particularly useful for the expression of functional SPTM. These are particularly useful for diagnosing, treating or preventing autoimmune/Ainfammatory disorders (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's disease), neurological disorders (e.g. epilepsy, Huntington's disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia; asthma; Crohn's disease; neurological disorder; epilepsy; cancer; thuntington's disease; Alzheimer's disease; Creutzfelder-Jakob disease; multiple sclerosis; Parkinson's disease; cell proliferative disorder; anti-inflammatory; immunosuppressive; neuroprotective; nootropic; anteropic antipsordatic; antiennulsant; oryestatic; antiparkinsonian; anxiolytic; secretory polynucleotide; secretory protein.
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Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PB, Amshey SR,
Daughtery SC, Dam TC, Liu TF, Ngyryen DA, Kleefeld Y, Gerstin EH;
Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
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                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secretory polypeptide SPTM SEQ ID NO 1015.
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                                Score 28; DB
Pred. No. 72;
1; Mismatches
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29-MAR-2001; 2001US-0280068P.
17-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291849P.
17-MAY-2001; 2001US-0299428P.
20-JUN-2001; 2001US-0299428P.
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Query Match
Best Local Similarity B5...
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N-PSDB; ABZ36273.
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                                                                                                                                                                       1 ATSSRAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP75831;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPNO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uvaitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
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dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease, multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety, schizophrenia or amnesia), or cell proliferative disorders (e.g. psoriasis, polycythemia vera or cancers including adenocarinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain, breast, cerrix or prostate). The present sequence is one of the SpTM proteins of the invention (ABP75384-ABP75962). Note: The sequence data for this patent did not form part of the printed specfication, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bhatia A;
                                                                                                                                                                                                                                                     6; Length 82;
                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes immunogenic protein #17485.
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, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 17784; 1069pp; English.
                                                                                                                                                                                                                                                   Score 28; DB
Pred. No. 85;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU56589 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW, Persing DH, M.
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                      74 ATSSKAT 80
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                                                                                                                                                                                                                     Sequence 82 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU56589;
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
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and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to down-regulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
           88888888888888
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Sequence 104 AA;

ö Gaps ö Query Match

90.3%; Score 28; DB 4; Length 104;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels

||||:|| 45 ATSSKAT 51 1 ATSSRAT 7

ઇ g Search completed: April 21, 2004, 17:33:15 Job time : 31 secs

Sequence

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APPLICANT: Corvaland, Jose R.F.
APPLICANT: Corvaland, Jose R.F.
APPLICANT: Gradual, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
ITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
ITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels
ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-10-041-860-49
; Sequence 49, Application US/10041860
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                            TYPE: PRT
CRGANISM: homo sapiens
US-10-041-860-377
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                                                                  RESULT 1
US-10-041-860-377
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LENGTH: 96
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7311, Ap
148739,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                               April 21, 2004, 17:37:29 ; Search time 21:1014 Seconds (without alignments) 91.715 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 225
Sequence 255
Sequence 375
Sequence 234
Sequence 234
Sequence 414
Sequence 731
Sequence 376
Sequence 376
Sequence 376
Sequence 28,
Sequence 28,
Sequence 62,
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-041-860-49
US-10-041-860-25
US-10-041-860-255
US-10-041-860-375
US-10-244-850-176884
US-10-320-797-3218
US-10-320-797-3218
US-10-425-114-41459
US-10-425-114-41459
US-10-425-114-41459
US-10-424-599-148739
US-10-424-599-148739
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US-10-067-800-62
US-10-292-486-47
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                                                                                                                                                                                                                                                1133595 segs, 276475211 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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1088
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Perfect score:
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Gaps

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Sequence 112, App Sequence 112, App Sequence 2, Appli Sequence 2, Appli Sequence 13, Appli Sequence 15, Appli Sequence 15, Appli

Sequence 15, Appl Sequence 255, App Sequence 158367,

Sequence 3428, Ap Sequence 3216, Ap Sequence 14, Appl 1 Sequence 2, Appl 1 Sequence 192945, Sequence 192945, Sequence 19710, Ap Sequence 1977, Ap Sequence 93, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl Sequence 69, Appl

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Gaps
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Pred. No. 34;
Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Corvalan, JOSE R.F.
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Peng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 375
LENGTH: 108
                                                                     APPLICANT: Gazir, Gadi
APPLICANT: Gazir, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
ITILE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
ITILE OF INVENTION: THEREOF
FILE REFREENCE: ABGRNIX.051A
CURRENT APPLICATION WUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 259
LENGTH: 108
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovallc David K
APPLICANT: Stou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
               Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
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Best Local Similarity 100.
----hes 7; Conservative
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CRGANISM: homo sapiens
US-10-041-860-375
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: homo sapiens
US-10-041-860-259
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Corvalian, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Cazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
FILE REPRENCE: AGGNIX.051A
CURRENT APPLICATION UNHER: US/10/041,860
CURRENT APPLICATION UNHER: US/200-01-07
NUMBER OF SEQ ID NOS: 377
NUMBER OF SEQ ID NOS: 377

NUMBER OF SEQ IO Windows Version 4.0
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                                                                                                                                                                                                  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES TITLE OF INVENTION: THEREOF FILE REPERRANCE: ABGENIX.031A CURRENT APPLICATION NUMBER: US/10/041,860 CURRENT FILING DATE: 2002-01-07 NUMBER OF SEQ ID NOS: 377 SOFTWARE: PASLSEQ for Windows Version 4.0 SEQ ID NO 49 LENGTH: 108
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100.0%; Pred. No. 3
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US-10-041-860-259
; Sequence 259, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 225, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
Publication No. US20030157109A1
                                   Corvalan, Jose R.F.
Jia, Xiao-Chi
                                                                           Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
Gazit, Gadi
Weber, Richard
Bezabeh, Binyam
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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CRGANISM: homo sapiens
US-10-041-860-225
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT,
CRGANISM: homo sapiens
US-10-041-860-49
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LENGTH: 108
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Sequence 41459, Application US/10425114

Sequence 41459, Application No. US20040034888A1

Sequence 41459, Application No. US2004003488BA1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FIR REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DAIE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 41459

LENTH: 340
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US-10-032-585-7311
US-10-032-585-7311
Sequence 7311, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Howard, Bussey
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery;
TITLE OF INVENTION: US2-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
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Pred. No. 4.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 31; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                           FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (435)..(435)
OTHER INFORMATION: Xaa = any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (437)..(438)
OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                              FEATURE:

NAME/KEY: MISC FEATURE

COCATION: (429)

OTHER INFORMATION: Xaa = any amino acid
US-10-320-797-3218
                        LENGTH: 501
TYPE: PRT
ORGANISM: Cryptococcus neoformans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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ORGANISM: Zea mays
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         SEQ ID NO 3218
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 176884
LENGTH: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2341, Application US/10389566

Publication No. US20040025202A1

GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Monsanto Technology, LLC
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cath V.
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(5290)D
CURRENT PILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/395,301
PRIOR PILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
NUMBER OF SEQ ID NOS: 2459
SEOTWARE: PREACTION VANDER: US 60/392,018
PRIOR APPLICATION VANDER: US 60/392,018
PRIOR APPLICATION VANDER: US 60/392,018
PRIOR APPLICATION VANDER: 202-06-26
SOFTWARE: PARCENTING DATE: 2002-06-26
SOFTWARE: PARCENTING DATE: 2002-06-26
SOFTWARE: PARCENTING DATE: 2002-06-26
SOFTWARE: PARCENTING DATE: 2002-06-26
SEQ ID NO 2341
LENGTH: 497
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Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_130743C.1.pep
US-10-424-599-176884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 31; DB 16;
100.0%; Pred. No. 1.5e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Arabidopsis thaliana US-10-389-566-2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
7; Conserva
                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ATSSRAT 27
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US-10-389-566-2341
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US-10-067-800-62

US-10-067-800-62

Sequence 62, Application US/10067800

Publication No. US20030100058A1

GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

TITLE OF INVENTION: Human G-protein Chemokine Receptor
CURRENT FILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: US/10/067,800

CURRENT FILING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/297,257

PRIOR PILING DATE: 2001-06-12

PRIOR PILING DATE: 2001-06-12

PRIOR PLING DATE: 2001-06-12

PRIOR PLING DATE: 2001-10-12

PRIOR FILING DATE: 2001-10-12

PRIOR FILING DATE: 2001-12-21

NUMBER: 60/310,458

PRIOR FILING DATE: 2001-12-21

NUMBER: PATENTING DATE: 2001-12-21

NUMBER: PATENTING DATE: 2001-12-21

NUMBER: PATENTING DATE: 2001-12-21

NUMBER: PATENTING DATE: 2001-12-21

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                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Application US/10371942
; Sequence 28, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION;
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVERTION: MAC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PSESEQ for Windows Version 4.0
; SEQ ID NO. 28
                                                                                    87.1%; Score 27; DB 14; Length 96; 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                     Best Local Similarity 100.
Matches 6; Conservative
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; ORGANISM: Homo sapiens
US-10-067-800-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
   ; ORGANISM: homo sapiens
US-10-041-860-376
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                                                                                              Query Match
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US-10-424-599-148739
j Sequence 148739, Application US/10424599
j Sequence 148739, Application No. US20040031072A1
j Sequence 148739, Application No. US20040031072A1
j Sequence 148739, Application No. US20040031072A1
j SPELICANT: La Rosa Thomas J
j APPLICANT: La Coa Yongwillon Soy Nucleic Acid Molecules and Other Molecules Associated With
j TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
j TITLE OF INVENTION: 182223
j CURRENT APPLICATION NUMBER: US/10/424,599
j CURRENT FILING DATE: 2003-04-28
j SEQ ID NOS: 285684
j SEQ ID NO 148739
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GENERAL INCOCRAMILON:
APPLICANT: Corrallan, Jose R.F.
APPLICANT: Vang, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Tang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NOWBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOCTANRE: FastSRQ for Windows Version 4.0
SEQ ID NO 376
LENGTH: 96
                                                                                                                                                                                                                                                                       Score 28; DB 14; Length 842;
Pred. No. 1.1e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.1%; Score 27; DB 12; Length 79;
100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_105333C.1.pep
US-10-424-599-148739
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             2001-12-20
CURRENT FILING DATE: 2001-12-2
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7311
LENGTH: 842
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Glycine max
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US-10-041-860-376
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RESULT 15

US-10-292-486.47

Sequence 47, Application US/10292486

Publication No. US20030228309A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors

TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors

CURRENT FILING DATE: 2002-10-13

FILE REPERBNCE: PF532P1

CURRENT FILING DATE: 2002-10-13

PRIOR FILING DATE: 2002-10-13

PRIOR PLILOR DATE: 2002-10-14

PRIOR PLILOR DATE: 2001-10-14

PRIOR PLILOR DATE: 2001-10-14

PRIOR PLILOR DATE: 2001-10-17

PRIOR APPLICATION NUMBER: 60/33/359

PRIOR PLILOR DATE: 2001-10-17

PRIOR PRILOR DATE: 2001-10-17

PRIOR PLILOR DATE: 2001-10-17

PRIOR PRILOR DATE: 2001-10-17

PRIOR PLILOR DATE: 2001-10-17

PRIOR PLILOR DATE: 2001-10-17

PRIOR PLILOR DATE: 2001-10-16

PRIOR PLILOR DATE: 2001-10-16

PRIOR PLILOR DATE: 2001-10-16

PRIOR PLILOR DATE: 2001-11-16

PRIOR PLILOR DATE: 2001-11-16

PRIOR PLILOR DATE: 2001-11-16

PRIOR PLILOR DATE: 2001-10-16

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PRIOR PLILOR DATE: 2000-
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Query Match 87.1%; Score 27; DB 14; Length 109; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
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Search completed: April 21, 2004, 18:02:07 Job time : 22.1014 secs

52 TSSRAT 57

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

April 21, 2004, 17:37:29 ; Search time 27.1304 Seconds (without alignments) 91.715 Million cell updates/sec Run on:

SEQ6 Title: Perfect score: Sequence:

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1133595 segs, 276475211 residues Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/pcodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_MBW\_PUB\_pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NBW\_PUB\_pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_NBW\_PUB\_pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NBW\_PUB\_pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/US08\_NBW\_PUB\_pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NBW\_PUB\_pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US09\_NBW\_PUB\_pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

19: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

19: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB\_pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB\_pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Sequence 49, Appl	Sequence 225, App	Sequence 259, App	Sequence 375, App	Seguence 3475, Ap	Sequence 3, Appli	Seguence 5, Appli	Seguence 5, Appli	Sequence 1, Appli	Sequence 10, Appl					
ΙD	US-10-041-860-49	US-10-041-860-225	US-10-041-860-259	US-10-041-860-375	US-10-104-047-3475	US-10-013-310-3	US-09-903-248-5	US-09-859-604-5	US-09-903-063-5	US-09-903-216-5	US-09-903-199-5	US-09-903-023-5	US-09-436-184-5	US-10-085-027-1	US-10-334-143-10
DB	14	74	14	14	15	13	σ	თ	ው	σ	σ	σ	70	13	15
% Query Match Length DB	108	108	108	108	412	695	1242	1242	1242	1242	1242	1242	1242	1242	1316
% Query Match	100.0	100.0	100.0	100.0	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5
Score	51	51	51	51	98	39	39	39	ტ ტ	99	ზ	39	99	39	39
Result No.		7	m	4	Ŋ	φ	7	80	σ	10	11	12	13	14	15

52,	Sequence 56, Appl	e 32,	35	19.	19.	9.19	13	equence 24	13	equence 57	equence 29	30	equence 82	83	equence 22	equence 10	equence 37	37	e 37	29	e 30	35	13	m	7, A	e 163	10	e 14,	-
-60-	US-09-828-708-56	0 US-09-972-656-	2 US-09-948-939-3	2 US-10-029-9	5 US-10-032-037B-19	5 US-10-029-9	5 US-10-032-423A-19	5 US-10-338-366-2	0 US-09-5	US-10-269-711-5	US-10-453-698-	US-10-453-698-3	194-975-8	194-975-8	153-382-2	041-860-1	US-10-041-860-3	-10-041-8	.4 US-10-041-860-377	US-10-308-817-	-817-3	5 US-10-309-7	.0 US-09-972-656-135	US-09-828-70	US-09-828-70	'n	US-08-844-215-1	0-340-18	Þ
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38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38	38
16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 US-10-041-860-49

		Ö
		0
equence 49, Application US/10041860 ublication No. US2003015710941 APPLICANT: Ocrvalan, Jose R.F. APPLICANT: Corvalan, Jose R.F. APPLICANT: Fend, Xiao-Chi APPLICANT: Fend, Xiao-Chi APPLICANT: Yang, Xiao-Dong APPLICANT: Yang, Xiao-Dong APPLICANT: Gazi, Gadi APPLICANT: Bezabeh, Binyam APPLICANT: Meber, Richard APPLICANT: Meber, Richard APPLICANT: Meber, Richard APPLICANT: Meber, Richard APPLICANT: Meber, Richard APPLICANT: ABCABCH, Binyam TITLE OF INVENTION: THEREOF FILE REFRENCE: ABGENTS, 051A TITLE OF INVENTION: THEREOF FILE REFRENCE: ABGENTS, 051A NUMBER OF SEQ ID NOS: 377 NUMBER OF SEQ ID NOS: 377 NUMBER OF SEQ ID NOS: 377 EQ ID NO 49 LENGTH: 108 TYPE: PRI ORGANISM: homo sapiens	Score 51; DB 14; Length 108; Pred. No. 0.25;	Indels
O ANI	14;	; 0
> PDGE	Score 51; DB 1 Pred. No. 0.25;	sec
TED TC	. 51; No.	Mismatches
1860 DIRECT 7 Presion	Scor	0; Mi
/1004; 09A1 R.F. B DIES 1 10A 1 US/: -01-0	100.0%;	
Application US/10 o. US20030157109) MATTON: orvalan, Jose R Jia, Xiao-Chi Feng, Xiao-Chi Feng, Xiao-Chorg Carg, Xiao-Dong Gazit, Gadi Weber, Richard Bezabeh, Birpyam ENTION: THEREOF CE: ABGENIX. OSIA ENTION: THEREOF CE: ABGENIX. OSIA OLD NOS: 377 stSEQ for Window omo sapiens		ä
Application U o. US20030157 warucol orvalan, Jose Jia, Xiao-Chi Freng, Xiao-Chi Freng, Xiao-Co Caren, Francin Gazit, Francin Bezabeh, Biny Bezabeh, Biny ENTION: THER ICATION: THER ICATION: ANTIB OG DATE: 200 OG ID NOS: 377 stSEQ for Winn	rity	nserv
Sequence 49, Application US/10041860 Sublication No. US20030157109A1 GENERAL INFORMATION: APPLICANT: Jia, Xiao-Chi APPLICANT: Feng, Xiao-Chi APPLICANT: Feng, Xiao-Chi APPLICANT: Carvalan, Jose R.F. APPLICANT: Carvalan, Jose R.F. APPLICANT: Gazit, Gadi APPLICANT: Chen, Francine APPLICANT: Gazit, Richard APPLICANT: Bezabeh, Barnaine APPLICANT: Bezabeh, Barnaine APPLICANT: Bezabeh, Barnaine TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF SEQ ID NOS: 377 SUPRARE: FastSEQ for Windows Version 4.0 SEQ ID NO 49 TYPE: PRT ORGANISM: home sapiens TYPE: PRT	Query Match Best Local Similarity	9; Conservative
Guence 49, Merah Incation Nobel Carlo No Nobel Carlo No Nobel Carlo No Nobel Carlo No Nobel Carlo No Nobel Carlo No Nobel Carlo No Nobel Carlo No No Nobel Carlo No No Nobel Carlo No No Nobel No No Nobel No No Nobel No No Nobel No No No Nobel No No No Nobel No No Nobel No No Nobel No No Nobel No No Nobel No No Nobel Nobel No No Nobel No No Nobel No No Nobel Nobel No No Nobel Nobel No Nobel Nobe	fatch	, G.
Sequence 49, My publication No GENERAL INFORMS APPLICANT: Co APPLICANT: V APPLICANT: V APPLICANT: V APPLICANT: CO APPLICANT: CO APPLICANT: B APPLICANT: B APPLICANT: B APPLICANT: B APPLICANT: B APPLICANT: B APPLICANT: B APPLICANT: B APPLICANT: B APPLICANT: B APPLICANT: CURRENT APPLIC CURRENT APPLIC CURRENT PILIN CURRENT PILIN CURRENT PILIN NUMBER OF SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	Query Match Best Local	Matches
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90 QOYGSSPCS 98

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RESULT 2 US-10-041-860-225 ; Sequence 225, Application US/10041860

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seq6.open.rapb
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US-10-104047-34

1. Sequence 3475, Application US/10104047

2. Sequence 3475, Application US/10104047

3. Publication No. US20030236392A1

3. APPLICANT: HELIX RESEARCH INSTITUTE

7. TILLE OF INVENTION: No. US2030236392A1e1 full length cDNA

7. FILE REFRENCE: H1-A0105

7. URRENT APPLICATION NUMBER: US/10/104,047

7. CURRENT APPLICATION NUMBER:

7. PRIOR APPLICATION NUMBER:

8. SOFTWARE: Petentin Ver: 2.1

8. SOFTWARE: Petentin Ver: 2.1

8. SOFTWARE: Petentin Ver: 2.1

8. SOFTWARE: Petentin Ver: 2.1

8. SOFTWARE: Petentin Ver: 3.1

8. SOFTWARE: Petentin Ver: 3.1

8. SOFTWARE: PRI Homo sapiens

9. US-10-104-047-3475
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Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Binyam
ITILE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
ITILE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
ITILE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
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ITILE OF INVENTION: ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 375
LENGTH: 108
ITYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
INCHARTED
US-10-041-860-375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10013310; Publication No. US20020192216A1; GENERAL INFORMATION: APPLICANT: Hamb, Jonathon Robert; APPLICANT: Hamb, Jonathon Robert; APPLICANT: Ballman, Margaret Jane; TITLE OF INVENTION: Therapeutic Use; TITLE OF INVENTION: Therapeutic Use; TITLE REPERBNCE: 674525-2003; CURRENT FILING DATE: 2001-12-07; PRIOR APPLICATION NUMBER: PCT/GB00/02191; PRIOR APPLICATION NUMBER: UK 9913350.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 00YGSSPCS 98
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US-10-104-047-3475
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US-10-013-310-3
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; Sequence 259, Application US/10041860
; Publication No. US2030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
APPLICANT: Fond, Xiao-Chi
; APPLICANT: Fond, Xiao-Chi
; APPLICANT: Fond, Xiao-Chi
; APPLICANT: Gazit, Gadi
; APPLICANT: Bezabeh, Binyam
; APPLICANT: Weber, Richard
; APPLICANT: Weber, Richard
; APPLICANT: Weber, Richard
; APPLICANT: Weber, Richard
; APPLICANT: Weber, Richard
; APPLICANT: Weber, Richard
; APPLICANT: Weber, Richard
; APPLICANT: Weber, Richard
; APPLICANT: ANTIBODES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE FERREREER ABGENIX.051A
; CURRENT PILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 108
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Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Score 51; DB 14; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.25;

Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                             GENERAL INCORVATION:
GENERAL INCORVATION:
APPLICANT: CORVAINION:
APPLICANT: Fergy Xiao-Chi
APPLICANT: Fergy Xiao-Chi
APPLICANT: Fergy Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
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Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
                                 Publication No. US20030157109A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-259
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US-10-041-860-225
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US-10-041-860-375
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PRIOR FILING DATE: 1999-06-08 PRIOR PEDLICATION NUMBER: UK 9921953.7 PRIOR FILING DATE: 1999-09-16 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin version 3.1 SEQ ID NO 3 LENGTH: 695

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Gaps

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Score 39; DB 13; Length 695; Pred. No. 1.7e+02; 2; Mismatches 0; Indels

Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative 2

; TYPE: PRT ; ORGANISM: House Mouse US-10-013-310-3

:||:|||| 376 RYGTSPCS 383

2 OYGSSPCS 9

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RESULT 7
US-09-903-248-5
Sequence 5, Application US/09903248
Sequence 5, Application US/09903248
Sequence 5, Application US/09903248
Sequence 5, Application US2002010226341
Setent No. US2002010226341
Setent No. US2002010226341
Septicant: UNFORMATION:
APPLICANT: Ince, Nedim
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
TITLE OF INVENTION: UNBER: US/09/903,248
CURRENT APPLICATION NUMBER: US/09/903,248
CURRENT FILING DATE: 2001-07-11
PRIOR PELING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIN Ver: 2.1
SEQ ID NO 5
LENGTH: 1242

Gaps Score 39; DB 9; Length 1242; Pred. No. 3e+02; 1; Mismatches 76.5%; Query Match
Best Local Similarity 85.7
Matches 6; Conservative

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2 QYGSSPC 8

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76.5%; Score 39; DB 9; Length 1242; 85.7%; Pred. No. 3e+02;

Best Local Similarity 85.7 Matches 6; Conservative

Query Match

430 EYGSSPC 436

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2 OYGSSPC 8

TYPE: PRT CNGANISM: Homo sapiens US-09-903-248-5

RESULT 10
US-09-903-216-5
; Sequence 5, Application US/09903216
; Sequence 5, Application US/09903216
; Sequence 5, Application US/09903216
; Sequence 5, Application US/09903216
; Patent No. US20020114811A1
; GARRAL Mands, Jack R.
; APPLICANT: Wends, Jack R.
; APPLICANT: Carlson, Rolf I.
; TILE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; TILE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; CURRENT APPLICATION NUMBER: US/09/903,216
; CURRENT FILING DATE: 2001-07-11
; PRIOR PEDLICATION NUMBER: 09/426,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5

TYPE: PRT
CORGANISM: Homo sapiens
US-09-903-216-5

76.5%; Score 39; DB 9; Length 1242; 85.7%; Pred. No. 3e+02; ive 1; Mismatches 0; Indels Query Match 76.5 Best Local Similarity 85.7 Matches 6; Conservative

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Gaps

430 EYGSSPC 436

US-09-859-604-5

seq6.open.rapb

430 EYGSSPC 436

RESULT 8
US-09-859-604-5
US-09-859-604-5
; Sequence 5, Application US/09859604
; Patent No. US20020110559A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzame M
; APPLICANT: Deutch, Alan H
; APPLICANT: Ghanbari, Hossein A
; TITLE OF INVENTYON: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; TITLE REFERENCE: 2146-032 CIP
; CURRENT APPLICATION NUMBER: US/09/859,604
; CURRENT FILING DATE: 2001-05-17
; PRIOR PELING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO S:
: LENGTH: 1242

2 OYGSSPC 8

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TYPE: PRT ORGANISM: Homo sapiens

Gaps

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US-10-334-143-10

US-10-334-143-10

Sequence 10, Application US/10334143

Publication No. US20040009549A1

GENERAL INFORMATION:

APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH

APPLICANT: SUDARSANAM, SUCHA

TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL

TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD

FILE REFERENCE: 038602/1543

CURRENT APPLICATION NUMBER: US/10/334,143

CURRENT PILING DATE: 2002-12-31

PRIOR FILING DATE: 2001-12-31
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS FILE REFERENCE: R.I. Hosp. - Malignant Neoplasms
CURRENT APPLICATION NUMBER: US/09/436,184
CURRENT FILING DATE: 1939-11-08
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 1242
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Pred. No. 3e+02;
1; Mismatches 0; Indels
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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CRGANISM: Homo sapiens
US-10-085-027-1
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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430 EYGSSPC 436
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; Sequence 5, Application US/09903023
; Patent No. US20020146421A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV1
; CURRENT APPLICATION NUMBER: US/09/903,023
; CURRENT FILING DATE: 1999-11-08
; PRIOR PILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1242
                                                                    Sequence 5, Application US/09903199
Sequence 5, Application US/09903199
Patent No. US20020122802A1
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: Ince, Nedim
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REFERENCE: 21486-032 DIV4
CURRENT APPLICATION NUMBER: US/09/903,199
CURRENT FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 5
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85.7%; Pred. No. 3e+02;
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Pred. No. 3e+02;
1; Mismatches 0; Indels
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US-09-436-184-5
; Sequence 5, Application US/09436184
; Publication No. US20030031670A1
; GENERAL INFORMATION
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo sapiens
US-09-903-199-5
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US-09-903-023-5
                                                         -09-903-199-5
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0; Gaps
                                                                                                                                                        Query Match 76.5%; Score 39; DB 15; Length 1316; Best Local Similarity 85.7%; Pred. No. 3.1e+02; Matches 6; Conservative 1; Mismatches 0; Indels 0
; NUMBER OF SEQ ID NOS: 207; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 10; LENGTH: 1316; TYPE: PRT ORCANISM: Homo sapiens US-10-334-143-10
                                                                                                                                                                                                                                    2 QYGSSPC 8
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504 EYGSSPC 510
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Search completed: April 21, 2004, 18:02:07 Job time: 27.1304 secs

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seq5.open.rai

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Sequence 1, Appli
Sequence 25325, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                            April 21, 2004, 17:28:28 ; Search time 8.42029 Seconds (without alignments) 42.918 Million cell updates/sec
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  /cgn2 6/ptodata2/jaa/5A_COMB.pep:*
  /cgn2 6/ptodata2/jaa/5B_COMB.pep:*
  /cgn2 6/ptodata2/jaa/6A_COMB.pep:*
  /cgn2 6/ptodata2/jaa/6B_COMB.pep:*
  /cgn2 6/ptodata2/jaa/PCTUS_COMB.pep:*
  /cgn2 6/ptodata2/jaa/PCTUS_COMB.pep:*
  /cgn2 6/ptodata2/jaa/PCTUS_COMB.pep:*
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  /cgn2 6/ptodata2/jaa/PCTUS_COMB.pep:*
  /cgn2 6/ptodata2/jaa/backfiles1.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-11444
US-09-252-991A-11910
US-09-252-991A-11910
US-09-252-991A-11910
US-09-252-991A-1910
US-09-252-991A-19612
US-08-613-552-6
US-09-252-991A-19612
US-09-252-991A-19612
US-09-252-991A-19656
US-09-252-991A-19656
US-08-974-59A-112
US-08-974-59A-112
US-09-971-112
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US-09-126-109-12
US-09-126-109-12
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US-08-126-126-12
US-08-126-126-12
US-08-126-128-12
US-08-126-128-12
US-08-126-138-12
US-08-134-1401-2
US-08-138-1401-2
US-08-138-1401-2
US-08-138-1401-2
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                                                                                                                                                                                                                                 389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    OM protein - protein search, using sw model
                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                   Title: (SEQ5
Perfect score: 31
Sequence: 1 atssrat 7
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                                                                                                                                                                                        Scoring table:
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                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
No.
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ASQUENCE 17444, Application US/09252991A; Sequence 17444, Application US/09252991A; Sequence 17444, Application US/09252991A; Parent No. 6551795; GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: DERGENCE: 107196.136; TITLE OF INVENTION: DERGENCE: 107196.136; TITLE OF INVENTION: US ER: 1999-02-18; FILE REFERENCE: 197196.136; CURRENT FILING DATE: 1999-02-18; PRIOR FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 17444; LENGTH: 138; TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-28404

US-09-252-991A-28404

Sequence 28404, Application US/09252991A

Sequence 28404, Application US/09252991A

Sequence 28404, Application US/09252991A

Sequence 28404

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUMBER: US/09/252,991A

TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/00/74,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 155
Sequence 16783, A Sequence 31728, A Sequence 32376, A Sequence 32376, A Sequence 28282, A Sequence 20771, A Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17,
                                                                                                                                                                                                                                                                                                                                                           Sequence 101, App
Sequence 42, Appl
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Sequence 17821, A
Sequence 30362, A
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Pred. No. 22;
1; Mismatches 0; Indels
US-09-252-991A-16783
US-09-252-991A-31728
US-09-252-991A-32376
US-09-252-991A-32376
US-09-252-991A-328282
US-09-252-991A-28460
US-09-252-991A-28460
US-09-252-991A-32402
US-09-252-991A-33100
US-09-252-991A-30100
US-09-252-991A-30100
US-09-345-33100
US-08-491-920-17
US-08-491-920-17
US-08-431-17821
US-09-345-236B-101
US-09-345-236B-101
US-09-345-236B-101
US-09-345-236B-101
US-09-345-236B-101
US-09-345-236B-101
US-09-345-291A-17821
US-09-252-991A-17821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
        1148
11599
11599
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99 ATSARAT 105
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General Information US/09252991A

Patent No. 655195

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22477
LENGTH: 270
                                            Sequence 17126, Application US/09252991A

Sequence 17126, Application US/09252991A

Batent No. 6551795

GENERAL INFORMATION:
APPLICANT:
MATC J. Rubenfield et al.
APPLICANT:
MATC J. Rubenfield et al.
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOWONAS
TITLE OF INVENTION:
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17126

LENGTH: 262
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROGIONOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
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Pred. No. 57;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-22477
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATSSRAT 7
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US-09-252-991A-19612
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US-09-252-991A-22477
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Fatent No. 6551795
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31910
LENGTH: 155
                                                                                                                                                                                                                                                                                                                               Sequence 18631, Application US/09252991A

Sequence 18631, Application US/09252991A

Parent No. 6551795

GENERAL INFORMATION:
APPLICANT: MAKE J. Rubenfield et al.
APPLICANT: MAKE J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 1999-02-18
PRIOR PELICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18631

LENGTH: 141
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Pred. No. 31;
1; Mismatches 0; Indels
                                                                               Length 138;
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                                                                                                                              0; Indels
                                                                            Score 28; DB 4;
Pred. No. 27;
1; Mismatches
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Pred. No. 28;
1; Mismatches
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US-09-252-991A-31910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17444
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Best Local Similarity 85.77
Lag 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                            Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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80 ATSARAT 86
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US-09-252-991A-31910
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US-09-252-991A-18631
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1 ATSSRAT 7
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LOCATION: -16...1
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-621-976-4221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08063552
| Patent No. 5688936
| Patent No. 5688936
| GENERAL INFORMATION:
| APPLICANT: Edwards, Robert H
| TITLE OF INVENTION: Vesicle Membrane Transport Proteins
| NUMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS:
| ADDRESSE: Sheldon & Mak
| CITY: Pasadena | CITY: Pasadena | CITY: Pasadena | CITY: Pasadena | CITY: Dasadena | COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.1%; Score 27; DB 1; Length 203; 85.7%; Pred. No. 71; vative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                             Length 427;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/063,552
FILING DATE: 19930514
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERENCE/DOCKET NUMBER: 9067-1
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 796-5321
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
FENTAL 203 amino acids
                                                                                                                                                                                                                                                         Query Match 90.3%; Score 28; DB 4;
Best Local Similarity 85.7%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches (
CURRENT FILING DATE: 1999-02-18
PRICR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 19612
LENGTH: 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Streptomyces plasmid US-08-063-552-6
                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 203 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       420 STSSRAT 426
                                                                                                                                                                                                                                                                                                                                               1 ATSSRAT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                    US-09-252-991A-19612
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-08-063-552-6
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PUT-1953-05704.

PUT-1953-05704.

APRICONTY ROBARIA. Robert H
TIMES OF SEQUENCES. 17
CORRESPONDENCE ADDRESS:

ADDRESSES: Standon & Mac
CORRESPONDENCE ADDRESS:

ADDRESSES: Standon & Mac
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APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Abamara, Tori
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 988;
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC Compatible
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION 1936
PRIOR APPLICATION DATE: US/08/974,549A
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.1%; Score 27; DB 3; I
85.7%; Pred. No. 4.2e+02;
:ive 0; Mismatches 1;
                                                               FILING DATE: 06-MAY-L99/
CLIASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLIASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLIASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLIASSIFICATION:
APPLICATION NUMBER: 36,429
REGISTRATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
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REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
        UMBER: US/08/851,843A
06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-974-549A-112
; Sequence 112, Application US/08974549A
; Patent No. 6166178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 988 amino acida
amino acid
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Best Local Similarity 85.7
Matches 6; Conservative
CURRENT APPLICATION DATA:
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                              APPLICATION NUMBER:
FILING DATE: 06-MAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           626 ATSDRAT 632
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                                                                                                                                                                                  Query Match

87.1%; Score 27; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels
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APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Toru
APPLICANT: Cech, Trona
APPLICANT: Makamra, Toru
APPLICANT: Makamra, Toru
APPLICANT: Mariey, Calvin
APPLICANT: Mariey, Calvin
APPLICANT: Mariey, Calvin
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APPLICANT: Mariey, Calvin
APPLICANT: Maries
CONTRESPONDENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CONTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 9411
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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ORGANISM: Pseudomonas aeruginosa
     COTHER INFORMATION: Xaa = ABP,Gly
NAME/KEY: UNSURE
LOCATION: 58
OTHER INFORMATION: Xaa = Cys,Ser
US-09-621-976-4221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85...
Best Local 6; Conservative
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196 TSSRAT 201
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Pred. No. 4.2e+02;
0; Mismatches 1; Indels
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US-09-430-323-69
1 Sequence 69, Application US/09430323
2 Sequence 69, Application US/09430323
3 Fatent No. 6309867
3 GENERAL INFORMATION:
3 NAFALICANT: Cech, Thomas R.
4 Indiants, Toru
Chapman, Karen B.
4 Morin, Gregg B.
4 HATLEY, Calvin A.
5 HATLEY, Calvin A.
6 NUMBER OF SEQUENCES:
6 CORRESPONDENCE ADDRESS:
7 CRESPONDENCE ADDRESS:
7 STREET: Two Embarcadero Center, 8th Floor
8 CITY: San Francisco
7 STREET: San Francisco
7 STREET: San Francisco
7 STREET: San Francisco
7 STREET: San Francisco
7 STREET: San Francisco
7 STREET: San Francisco
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
PTILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
PTILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 18-APR-1997
CLASSIFICATION SATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
CLASSIFICATION: 536
ATTOREY/AGBNT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,620
TELEBRAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 69:
CONTINNO FOR SEQ ID NO: 69:
CONTINNO FOR SEQ ID NO: 69:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 988 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: protein US-08-854-050-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                626 ATSDRAT 632
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85.7%; Pred. No. 4.2e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-854-050-69
US-08-854-050-69
Sequence 69, Application US/08854050
Patent No. 6251836
GENERAL INFORMATION
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Harley, Galvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco CITY: California COUNTRY: United States of America
         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419
FILING APPLICATION NUMBER: US 08/846,017
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING APPLICATION NUMBER: US 08/911,312
FILING APPLICATION NUMBER: US 08/912,951
FILING APPLICATION NUMBER: US 08/915,503
FILING APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION NUMBER: 36,429
FRIENG APPLICATION NUMBER: 36,429
FRIENG APPLICATION NUMBER: 36,429
FRIENG APPLICATION NUMBER: 36,429
FRIENGENCE/DOCKET NUMBER: 36,429
FRIENGENCE/DOCKET NUMBER: 36,429
FRIENGENCE/DOCKET NUMBER: 36,429
FRIENGENCE/DOCKET NUMBER: 36,429
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
) MOLECULE TYPE: protein
US-08-974-549A-112
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Gaps

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: CURADOWN
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/24,643
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/24,643
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/24,643
FILING DATE: 18-APR-1097
APPLICATION NUMBER: US 08/24,643
FILING DATE: 18-APR-1097
APPLICATION NUMBER: US 08/24,643
FILING DATE: 18-APR-1097
APPLICATION NUMBER: US 08/24,643
FILING DATE: 18-APR-1097
APPLICATION NUMBER: US 08/24,643
FILING APPLICATION NUMBER: US 08/24,643
FILING APPLICATION NUMBER: US 08/24,643
ATTORNATION TORORATION: US 08:
APPLICATION NO: 69:
APPLICATION FOR SEQ ID NO: 69:
APPLICATION FOR SEQ ID NO: 69:
APPLICATION FOR SEQ ID NO: 69:
APPLICATION FOR SEQ ID NO: 69:
APPLICATION: SEQ ID NO: 4.2e-02;
APPLICATION: APPLICATION: SEQ ID NO: 4.2e-02;
APPLICATION FOR PROPERIED OF THE APPLICATION: APPLICATION FOR THE APPLICATION: APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FOR THE APPLICATION FO
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Search completed: April 21, 2004, 17:40:05 Job time: 9.42029 secs

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Gaps . 0

Query Match Best Local Similarity 85.7%; Pred. No. 4.2e+02; Matches 6; Conservative 0; Mismatches 1; Indels

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein April 21, 2004, 17:25:48; Search time 4.56522 Seconds (without alignments) 102.653 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

Scoring table: BLOSUM62

141681 seqs, 52070155 residues Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	04		_	ratti	_	gallı	omod .	homod		homo	рошоц	homo	omod.	рошоч	DOMO!	chlan						mus m	homo		rattus	_	4	מו	ш С	_	_	P03383 human t-cel
QI	mΈ	DVL1 RAT	IRS1 MOUSE	IRS1_RAT	IRS1 HUMAN	LRP1 CHICK	KV3A HUMAN	KV3B_HUMAN	KV3D HUMAN	KV3M HUMAN	S107 HUMAN	S115 HUMAN	KV3L HUMAN	Z440 HUMAN	ZCH2 HUMAN	RNH2 CHLPN	MYO1 ONCMY	TDG HUMAN	PHLD MYCTU	PHLC MYCTU	TAI2 HUMAN	DLL1 MOUSE	CO7 HUMAN	AAC3 HUMAN	AK11 RAT	TSP2 CHICK	CO8B_RAT	T257 STAAU	T431_STAAM	FDS DROME	SYGA HELPJ	ENV_HTLV2
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% Query Match	76.5	76.5		9	•	ø			4	•			68.6	68.6	68.6	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	vo	4	4	64.7	. 4	64.7	4
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096017 homo sapien P07358 homo sapien P43354 homo sapien Q06219 mus musculu Q07917 rattus norv Q0925 schizosacch P53443 oryza sativ P97303 mus musculu Q9byv9 homo sapien Q9tuq3 sus scrofa P40528 saccharomyc	Buteleostomi; Homo.
CHKZ HUMAN CO8B_HUMAN NR42_HUMAN NR42_RAT ICBZ SCHPO PALZ_ORYSA BACZ MUSE BACZ HUMAN CO7_FIG SYGI_YEAST	ALIGNMENTS  ARD; PRT; 109 AA. , Last sequence update) , Last sequence update) , region GOL (Rheumatoid factor). Chordata; Craniata; Vertebrata; Buteleostomi;
64.7 543 1 64.7 591 1 64.7 598 1 64.7 598 1 64.7 603 1 64.7 710 1 64.7 716 1 64.7 841 1 64.7 841 1 64.7 1075 1	O
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	KESULT 1 KV3G HUMAN  ID KV3G HUMAN  STAND,  P04206,  DT 20-MAR-1987 (Rel. 04  DT 15-UUL-1999 (Rel. 38  DE IS KADPA chain V-III  OS HOMO Sapiens (Human)  OC EUKAIYOEA, Metazoa;  OC Maumalia; Eutheria;  OX NCBI_TAXID=9606;
	ООООВВВВЕНИЯ

The second of a sequence of a light chain variable region of a human acid sequence of a light chain variable region of a human acid sequence of a light chain variable region of a human are themseroid factor of the Wa idiotypic group, in part predicted by its reactivity with antipeptide antibodies.";

Mol. Immunol. 23:239-244(1986).

PIR, A0183; K31400.

PIR, A0183; K31400.

RSP, P80362; IWTL.

GO; GO:0005576; G:extracellular; NAS.

GO; GO:0005576; G:extracellular; NAS.

GO; GO:000523; F:antigen binding; NAS.

RO; GO:0006955; P:immune response; NAS.

RO; GO:00047; ig. 1.

PRAMI, PROSITE; PS50835; IG LIKE; 1.

KW Immunoglobulin V region.

FT DISULEID

SEQUENCE 109 AA; 11830 WW; 9349ASBID93588B6 CRC64; 

Gaps ö Query Match
Best Local Similarity 88.9%; Pred. No. 0.95;
Matches 8; Conservative 0; Mismatches 1; Indels

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90 QQYGSSPRS 98 1 QOYGSSPCS 9 g ઠે

RESULT 2
DV1.1 MOUSE
DV1.1 MOUSE
DV1.1 MOUSE
DV1.1 MOUSE
STANDARD; PRT; 695 AA.

C P51.4; 060868;
DT 01-0CT-1996 (Rel. 34, Created)
DT 01-0CT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 31, Last annotation update)
DT Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)
DE Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)
DE (DSH homolog 1).
GN DVL1 OR DVL.
GN DVL1 OR DVL.
OS Mus musculus (Mouse).
OS Hus musculus (Mouse).
OS Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Memmilia; Butheria; Rodentia; Sciurognathi, Muridae, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, Musine, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-Wistar Kyoto;

MEDLINE-21254118; bubMed=11354832;

MEDLINE-21254118; bubMed=11354832;

A de Lange R.P.J.; bubmed=11354832;

A st Clair D.M.; Dominiczak A.F.; Shaw D.J.;

A st Clair D.M.; Dominiczak A.F.; Shaw D.J.;

T expeping and sequencing rat dishevelled-1: a candidate gene for cerebral ischaemici insult in a rat model of stroke.";

C erebral ischaemici insult in a rat model of stroke.";

L Neurogenetics 3:99-106(2001).

C -1- FUNCTION: May play a role in the signal transduction pathway mediated by multiple Whr genes.

C -1- FUNCTION: May play a role in the signal transduction pathway containes to the DSH family.

C -1- SIMILARITY: Contains 1 DEP domain.

C -1- SIMILARITY: Contains 1 DEP domain.

C -1- SIMILARITY: Contains 1 DIX domain.
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVL1_RAT STANDARD, PRT; 695 AA.

30-WTG9, Q9VUG5, Q9WTB9;
30-WAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
5-FEB-2004 (Rel. 43, Last annotation update)
5-Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)
(DSH homolog 1).
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PROSITE; PS50186; DEP;

R PROSITE; PS50106; PDZ; 1.

RW Wnt signaling pathway; Developmental p..

FT DOMAIN 251 323 PDZ.

FT DOMAIN 425 499 PDLY-SER.

FT DOMAIN 390 393 POLY-SER.

TOT 122 125 MISSING (IN REF. 2).

TOT 122 125 MISSING (IN REF. 2).

Total 121 T -> N (IN REF. 2).

Total 211 T -> N (IN REF. 2).

Total 211 T -> N (IN REF. 2).

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Total 211 T -> N (IN REF. 2).

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Total 211 T -> N (IN REF. 2).

Total 211 T -> N (IN REF. 2).

Total 211 T -> N (IN REF. 2).

Total 211 T -> N (IN REF. 2).
                                                            DEP; 1.
DIX; 1.
PD2, 1.
hway; Developmental protein; 3D-structure.
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InterPro; IPR000839; Dishevell.
InterPro; IPR008331; Dishevelled.
InterPro; IPR001340; Dishevelled.
InterPro; IPR001158; DIX.
InterPro; IPR001158; PDZ.
Fram; PP00610; DEP; 1.
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EMBL; AF143546; AAD33897.2; -.
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376 RYGTSPCS 383
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DVL1_RAT
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                                                                                                                                                                                                                                                                                                                                                            IRSI OR IRS-1.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-9319226; Pubmed=8448209;
Keller S.R., Abebersold R., Garner C.W., Lienhard G.E.;
"The insulin-elicited 160 kba phosphotyrosine protein in mouse adipocytes is an insulin receptor substrate 1: identification by
                                                                                                                                                                                                    ö
                                                                                                                                                                                Length 695;
                                                                                                                                                                                                    0; Indels
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                                                      SMART; SM00021; DAX; 1.
SMART; SM00029; DEP; 1.
SMART; SM00209; DEP; 1.
PROSITE; PS50841; DIX; 1.
PROSITE; PS50841; DIX; 1.
PROSITE; PS50106; PDZ; 1.
Wht signaling pathway; Developmental protein.
DOMAIN 251 323 PDZ.
                                                                                                                                                                               Query Match 76.5%; Score 39; DB 1; Best Local Similarity 75.0%; Pred. No. 6.6; Matches 6; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                             01-UUN-1994 (Rel. 29, Created)
01-UUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                             PRT; 1233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=94220494; PubMed=8167159;
                                                                                                                                                             695 AA; 75447 MW;
                           PRINTS; PRO1760; DISHEVELLED.
PRINTS; PRO1761; DISHEVELLED1.
ProDom; PD003639; DIX; 1.
Pfam; PF02377; Dishevelled; 1.
                                                                                                                                                                                                                                                                                                                                            Insulin receptor substrate-1.
IRS1 OR IRS-1.
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                                                                                                                                                                                                                                                                                             STANDARD;
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376 RYGTSPCS 383
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                                                                                                                                                                                                                                                                                             MOUSE
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P35569;
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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.5%; Score 39; DB 1; Length 1233; 85.7%; Pred. No. 12; 0; Indels iive 1; Mismatches 0; Indels
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1233 AA; 130723 MW; COE9B2D890DADD87 CRC64;
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PHOSPHORYLATION (BY INSR)
(BY SIMILARITY).
(BY SIMILARITY).
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PHOSPHORYLATION (BY INSR)
(BY SIMILARITY).
PHOSPHORYLATION (BY INSR)
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MISSING (IN REF. 2)
H -> R (IN REF. 2).
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01-JUN-1994 (Rel. 29, Last sequence update)
110-CCT-2003 (Rel. 42, Last annotation update)
Insulin receptor substrate-1.
IRS1 OR IRS-1.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-Sprague-Dawley, TISSUE-Liver;
MEDLINE-91287824; PubMed-1648180;
PDB; 1AYB; 31-AUG-94.
MGD; MGI:9945; Irs1.
InterPro; IPR0001404; InBln_receptorS1.
InterPro; IPR001049; PH.
Ffam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
PALNTS; PR00628; INSULINESI.
SWART; SW00313; PH; 1.
SWART; SW0033; PH; 1.
SWART; SW00319; PTB; 1.
PROSITE; PS50003; PH DOWAIN; 1.
PROSITE; PS50003; PH DOWAIN; 1.
POWAIN 152 262
DOWAIN 1152 1262
DOWAIN 1194 1198 POLY-FRO.
MOD_RES 99 99 PHOSPHORYLA
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MEDLINE=94067102; PubMed=7504175;
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ID IRSI RAT
AC P35570;
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TISSUE-EPS;

XX MEDINE-2238257; PubMed=12477932;

XRELINE-2238257; PubMed=12477932;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,

And Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Heish F.K.,

And Hopkins R.F., Jordan H., Moore T., Marson T.L., Scheefer T.E.,

Rapleton M., Soares M.B., Bonaldo M.F., Carrinci P., Prange C.,

Rapleton M., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

Rapleton M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabask S.A., McKwan P.J., McKernan R.J., Malek J.A., Gunzarne P.H.,

Rapleton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Althalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rapleton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rapleton E., Ketteman M., Madan A., Rodrigues S.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rapletorfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rapletorfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

Ry Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
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MEDLINE-96303710; PubMed-8723689;
Esposito D.L., Mammarella S., Ranieri A., della Loggia F., Capani F., Consoli A., Mariani-Costantini R., Caramia F.G., Cama A., Battieta P.; "Deletion of Gly723 in the insulin receptor substrate-1 of a patient with noninsulin-dependent diabetes mellitus.";
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Mammarella S., Creati B., Esposito D.L., Arcuri P., della Loggia F.,

Capani F., Mariani-Costantini R., Caramia F.G., Battista P., Cama A.;

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non-conservative anino acid substitutions in a patient with
noninsulin-dependent diabetes mellitus.";

Hum. Mutat. 11:411-411 (1998).
                                                                                                                                                                                                                            TISSUE-Skeletal muscle;
MEDLINE-9292738; PubMed-8513971;
ARACHINE-9292738; PubMed-8513971;
ARACHI E., Sun X. V., Haag B.L. III, Chuang L.M., Zhang Y.,
Yang-Feng T.L., White M.F., Kahn C.R.;
"Human skeletal muscle insulin receptor substrate-1. Characterization of the cDNA, gene, and chromosomal localization.";
Diabetes 42:1041-1054(1993).
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        Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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MEDININE=96185461; PubMed=8599766;
MEDININE=96185461; PubMed=8599766;
Zhou M.-M., Huang B., Olejniczak E.T., Meadows R.P., Shuker S.B.
Miyazaki M., Trueb T., Shoelson S.E., Feeik S.W.;
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Lancet 342:828-832(1993).
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MEDLINE=92181456; PubMed=1311924;
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Sun X.J., Crimmins D.L., Myers M.G., Miralpeix M., White M.F.; "Pleiotropic insulin signals are engaged by multisite phosphorylation of IRS-1.";
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J. Biol. Chem. 268:18157-18166(1993).

-!-PUNCTION: May mediate the control of various cellular processes b insulin. When phosphorylated by the insulin receptor binds specifically to various cellular proteins containing SH2 domains ench as phosphatidylinositol 3-kinase p85 subunit or GRB2.
-!-SIMILARITY: Contains 1 PHB domain.
                                                                                                                                                                                                                                     MEDLINE=93352637; PubMed=8349691;
Tanasijevic M.J., Myers M.G., Thoma R.S., Crimmins D.L., White M.F.,
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IRS1 HUMAN STANDARD, PRT; 1242 AA.

AC P35569,
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
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PTR; S16948; S1648.
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InterPro; IPR002404; Insln_receptorS1.
InterPro; IPR01049; PH.
Pfan; PP02174; IRS; I.
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Pfan; PR01069; PH; I.
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SMART; SM00213; PH; I.
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DR EMBL; $15160; 136070.

PDB; 11R8; 15-MAV-97.

DR PDB; 11R8; 15-MAV-99.

DR Genew; HGNC:(4125; IRS1.

DR GO:00005737; C:cytoplasm; TAS.

GO; GO:0005737; C:cytoplasm; TAS.

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InterPro; IPR001849; FH.

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PRINTS; PR00169; PH: 1.

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"Structural basis for IL-4 receptor phosphopeptide recognition by the IRS-1 PTB domain..";
Nat. Struct. Biol. 3:388-393(1996).

**Attact. Biol. 3:388-393(1996).

**Institution: When phosphorylated by the insulin receptor binds specifically to various cellular proteins containing SH2 domains such as phosphatidylinositol 3-kinase p85 subunit or GRB2.

**Institution: When phosphatidylinositol 3-kinase p85 subunit or GRB2.

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(BY SIMILARITY).  P -> R (in dbsNP:1801108).  / FIId=VAR (11 dbsNP:1801118).  / FIId=VAR (14854.  A -> P (in dbsNP:180118).  / FIId=VAR (05299.).  MISSING (IN NIDDM).  / FIId=VAR (11 dbsNP:180120).  / FIId=VAR (14855.).  / FIId=VAR (14855.).  / FIId=VAR (14855.).  / FIId=VAR (14855.).  / FIId=VAR (14856.).  G (in dbsNP:180127).  / FIId=VAR (11 dbsNP:1801279).  G -> R (in dbsNP:1801279).	/FTTd=VAR 005500.  5 - y (IN NIDDM).  7 - Y (IN NIDDM).  7 - y (IN NIDDM).  7 - y (IN NIDDM).  6 - y (IN REF. 2).  7 - R (IN REF. 2).  9 - > R (IN REF. 2).	f; Score 39; DB 1; Length 1242; f; Pred. No. 12; O; Indels O; Gaps 1; Mismatches O; Indels O; Gaps PRT; 4543 AA.	nce updat ation upd -related (A2MR). aniata; V alliforme er, and C ., Schnei ensity li nship to
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CALCIUM-BINDING (POTENTIAL)
EGF-LIKE 6.

EGF-LIKE 7.

EGF-LIKE 8.

EGF-LIKE 9.

EGF-LIKE 10.

LDL-RECEPTOR CLASS A 11.

LDL-RECEPTOR CLASS A 12.

LDL-RECEPTOR CLASS A 13.

LDL-RECEPTOR CLASS A 13.

LDL-RECEPTOR CLASS A 14.

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LDL-RECEPTOR CLASS A 17.

LDL-RECEPTOR CLASS A 19.

LDL-RECEPTOR CLASS A 19.

LDL-RECEPTOR CLASS A 19.

LDL-RECEPTOR CLASS A 20.

EGF-LIKE 13.

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EGF-LIKE 14.

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LDL-RECEPTOR CLASS A 22.

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            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
          and activated alpha 2-macroglobulin, as well as the local
and activated alpha 2-macroglobulin, as well as the local
merabolism of complexes between plasminogen activators and their
endogenous inhibitors. Binds vitellogenin, calcium and alpha 2-
calcade and activators and their
endogenous inhibitors. Binds vitellogenin, calcium and alpha 2-
calcade acceptance of macroglobulin.

ALTERNATURE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
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DR PIR; A33102; ASX DAX MYGNOXYLS.

DR INCEPPO; IPRO00152; ASX MYGNOXYLS.

DR INCEPPO; IPRO00152; LDL receptor A.

DR INCEPPO; IPRO0003; Ldl receptor A.

DR PRINTS; PRO00051; Ldl receptor A; 31.

DR PRINTS; PRO00051; LDLARCEPTOR.

DR SWART; SM00192; LDLA; 31.

DR SWART; SM00192; LDLA; 31.

DR SWART; SM00192; LDLA; 31.

DR SWART; SM00192; LDLA; 31.

DR SWART; PS00101; ASX HYDROXYL; 3.

DR PROSITE; PS01010; ASX HYDROXYL; 3.

DR PROSITE; PS01010; ASX HYDROXYL; 3.

DR PROSITE; PS01010; ASX HYDROXYL; 3.

DR PROSITE; PS01010; ASX HYDROXYL; 3.

DR PROSITE; PS01016; EGF 3; 8.

DR PROSITE; PS0106; EGF 3; 8.

DR PROSITE; PS0106; EGF 3; 8.

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DR PROSITE; PS0106; EGF
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LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN.
EXTRACELULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
LDL.RECEPTOR CLASS A 1.
LDL.RECEPTOR CLASS A 2.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3.
EGF-LIKE 3.
EGF-LIKE 3.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 6.
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LDL-RECEPTOR CLASS A 9.
LDL-RECEPTOR CLASS A 10.
EGF-LIKE 5.
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Andrews D.W., Capra J.D.;
"Amdrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains from two idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
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MEDLINE=7188439; PubMed=5027703;
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 sappa chain VIII region SIE.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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              74.5%; Score 38; DB 1; Length 108; 100.0%; Pred. No. 1.5; 1. ndels :ive 0; Mismatches 0; Indels
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15 Appa chain V-III region Ti.
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NCBI_TaxID=9606;
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15-UU1-1999 (Rel. 38, Last annotation update)
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Homo sapiens (Human)
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BY SIMILARITY

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immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein RT Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";

L HOPPE-Seyler's Z. Physiol. Chem. 333:189-208 (1972).

C -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-!- MISCELLANEOUS: This is a Bence-Jones protein.

PIR, A01895, K3HUTI.

R HSSP, P80362; 1WTL.

R HSSP, P80362; 1WTL.

R GO, GO:0005576; C:extracellular, NAS.

R GO, GO:0005576; C:extracellular, NAS.

R GO, GO:0005576; P:immune response; NAS.

R GO, GO:000595; P:immune response; NAS.

R InterPro; IRR003596; Ig-V.

R InterPro; IRR003596; Ig-V.

R Fami, PR00477; ig; 1.

R PROSITE; PS50835; IG ILKE; 1.

R PROSITE; PS50835; IG ILKE; 1.

R INMUNOGLOBULIN V region, Bence-Jones protein.

PROSITE; PS50835; IG ILKE; 1.

R DISULEID 23 89; BSY SIMILARITY.
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MEDLINE-88171307; PubMed=3127527;

Kipps T.J. Tomhave E., Chen P.P., Carson D.A.;

Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukenia with little or no somatic mutation. Implications for etiology and immunotherapy.";

J. Exp. Med. 1677-1840-852(1988).

-1. DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-III region HIC precursor.
Homo sapplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteris; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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HSSP; PR0362; INTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005555; F:antigen binding; NAS.
GO; GO:000555; F:immune response; NAS.
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig-v.
FMAR; SM04406; IGv.
PROSITE; PS50835; IG_LIKE; I.
Immunoglobulin V region; Signal.
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A TISSUB-22388257; PubMed=12477932;

A Tausmer R.D., Collins P.S., Wagner L., Schemen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buctow K.H., Schemen C.M., Schuler G.D.,

A Lischul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Erownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Hiting M., Madan P., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences ";

R Proc. Nall. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Keratinocytes;
MEDLINE=92043866; PubMed=1940442;
MAdden P., Rasmussen H.H., Lefters H., Honore B., Dejgaard K.,
Olsen B., Kiil J., Malbum B., Andersen A.H., Basse B., Lauridsen J.B.,
Ratz G.P., Celis A., Vandekerckhove J., Celis J.E.;
"Molecular cloning, occurrence, and expression of a novel partially secreted protein 'psoriasin' that is highly up-regulated in psoriatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Paoriatic skin,
MEDLINE-960566; PubMed-8526920,
MEDLINE-9605665, PubMed-8526920,
Burgisser D.M., Siegenthaler G., Kuster T., Hellman U., Hunziker P.,
Birchler N., Heizmann C.W.;
"Amino acid sequence analysis of human S100A7 (psoriasin) by tandem
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                       74.5%; Score 38; DB 1; Length 129; 100.0%; Pred. No. 1.8; tive 0; Mismatches 0; Indels
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Glaeser R., Harder J., Christophers E., Schroeder J.M.,
                    129
14070 MW; 7395528EA2BB74D6 CRC64;
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Biochem. Biophys. Res. Commun. 217:257-263(1995).
                                                                                                                                                                                                                                                                                             P31151; Q9H1E2;
01-JUL-1993 (Rel. 26, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
8100 calcium-binding protein A7 (Psoriasin).
8100A7 OR PSORI.
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                                                     Query Match
Best Local Similarity 100.v
Loca 7; Conservative
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                                                                                                                                                                                                       "Bladder squamous cell carcinomas express psoriasin and externalize it
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99152356; FubMed=10026247;

Brodersen D.E., Nyborg J., Kjeldgaard M.;

Brodersen D.E., Nyborg J., Kjeldgaard M.;

Brodersen D.E., Nyborg J., Kjeldgaard M.;

Brodersen D.E., Nyborg J., Kjeldgaard M.;

Brodersen Ga2+-bound human psoriasin (S100A7) in the Zn2+-loaded and Zn2+-free states.";

Blochemistry 38:1695-1704 (1999).

Blochemistry 38:1695-1704 (1999).

Classical secretory pathway.

-!- SUBCELDILITY: Fetal ear, skin, and tongue and human cell lines. Highly up-regulated in psoriatic epidermis. Also highly expressed in the urine of bladder squamous cell carcinoma (SCC)
                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.05 ANGSTROMS).
MEDLINE=98220746; PubMed=9562557;
Brodersen D.E., Etzerodt M., Madsen P., Celis J.E., Thoegersen H.C., Nyborg J., Kjeldgaard M.;
Nyborg J., Kjeldgaard M.;
"EF-hands at atomic resolution: the structure of human psoriasin (5100A7) solved by MAD phasing.";
                                                                                                                                                   TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
MEDLINE=96212542; PubMed=8618345;
Cells J.E., Rasmussen H.H., Vorum H., Madsen P., Honore B., Wolf H.,
Orntoft T.F.;
                                                    TISSUE=Keratinocytes;

MEDLINE=3162043; PubMed=1286667;

Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,

Vandekerckhove J.;

Vandekerckhove J.;

Vandekerckhose of 145 proteins recorded in the two-dimensional gel

protein database of normal human epidermal keratinocytes.";

Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bearing patients. MW=11365; MW_ERR=0.7; METHOD=Electrospray. MASS SPECTROMETRY: Belongs to the S-100 family. SIMILARITY: Belongs to the S-nod calcium-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00036; efhand; 1.
Pfam; PF01023; S_100; 1.
ProDom; PD003407; CaSP S100; 1.
PROSITE; PS00108; EF HAND; 1.
PROSITE; PS00303; S100 CASP; 1.
Calcium-binding; Zinc; Metal-binding; Acetylation; 3D-structure.
"Genomic organization of human psoriasin (S100A7) gene."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                 K-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
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EMBL; AJ012825; CAC20409.1; --
PIR; A54327; A54327.
PDB; 1PSR; 13-JAN-99.
PDB; 2PSR; 15-JUN-99.
PDB; 3PSR; 15-JUN-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aarhus/Ghent-2DPAGE; 3002; IEF.
Genew; HGNC:10497; S100A7.
MIM; 600353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M86757; AAA60210.1; -.
                                                                                                                                                                                                                          to the urine.";
J. Urol. 155:2105-2112(1996).
[7]
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FASEB J. 17:1969-1971(2003).
-!- FUNCTION: May. be involved in epidermal differentiation and
-!- FUNCTION: May. be involved in epidermal differentiation and
-!- fullammation and might therefore be important for the pathogenesis
of psoriasis and other diseases.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBLIBARITY: Overexpressed in psoriasis.
-!- SIMILARITY: Belongs to the S-100 family.
-!- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-22881852; PubMed=12923069; Molf R., Mirnohammadsadegh A., Malz M., Lysa B., Tartler U., Remus R., Hengep U., Mirhel G., Ruzicka T.; Hengep U., Michel G., Ruzicka T.; Hongep U. Molecular cloning and characterization of alternatively spliced mRNA isoforms from psoriatic skin encoding a novel member of the S100
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                             EF-HAND 2 (HIGH AFFINITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 1;
Pred. No. 5.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
S100 calcium-binding protein A15.
                ACETYLATION
                                                                  ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AY189117; AAO40032.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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88 QSHGAAPCS 96
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TISSUE=Epidermis;
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   S115 HUMAN
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MOD RES
CA BIND
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HELIX
TURN
HELIX
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129 AA; 14073 MW; D3C55292772774D0 CRC64;

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Matches
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                          | EMBL; AX189118; AA040033.1; | EMBL; AX189118; AA040033.1; | Genew; HGNC:21657; S100A15. | Genew; HGNC:21657; S100A15. | InterPro; IPR0012048; EF-hand. | InterPro; IPR0012048; EF-hand. | Embl.; AD003407; CaBP $100; 1. | Embl.; PS00103; EP HAND; 1. | EMBL.; PS00103; EP HAND; 1. | EMBL.; PS00103; EP HAND; 1. | EMBL.; PS00103; S100, CABP; 1. | EMBL.; PS00103; S100, CABP; 1. | EMBL.; PS00103; S100, CABP; 1. | EMBL.; PS00103; S100, CABP; 1. | EMBL.; PS00103; S100, CABP; 1. | EMBL.; PS00103; S100, CABP; 1. | EMBL.; PS00103; S100, CABP; 1. | EMBL.; PS00103; S100, CABP; 1. | InterPro; PS00103; S100, CABP; 1. | InterPro; PS00103; S100, CABP; 1. | InterPro; PS00103; S100, CABP; 1. | InterPro; PS00103; S100, CABP; INTERPRITY) | EMBL.; PS00103; S100, CABP; INTERPRITY) | EMBL.; PS00103; S100, CABP; INTERPRITY | EMBL.; PS00103; S100, CABP; INTERPRITY | EMBL.; PS00103; S100, CABP; INTERPRITY | EMBL.; PS00103; S100, CABP; INTERPRITY | EMBL.; PS00103; S100, CABP; INTERPRITY | EMBL.; PS00103; S100, CABP; INTERPRITY | EMBL.; PS00103; S100, CABP; INTERPRITY | EMBL.; PS00103; S100, CABP; EMBL.; PS00103; S100, CABP; EMBL.; PS00103; S100, CABP; EMBL.; PS00103; S100, CABP; EMBL.; PS00103; S100, CABP; EMBL.; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS00103; PS001
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MEDLINE=88771307; PubMed=3127527;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Matcoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-i. DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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PRAMENDKK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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JKI SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 1; Length 100;
Pred. No. 5.2;
3; Mismatches 1; Indels
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Appa chain V-III region HAH precursor.
Homo sapiens (Human)
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PIR; PL0022; K3HUHA.

HSSP; P80362; INTL.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:000555; F:antigen binding; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; IG-like.

InterPro; IPR00110; IG-like.

SMART; SMO0406; IGv; 1.

PROSTIE; PS50835; IG_LIKE; 1.

Immunoglobulin V region; Signal.
              EMBL; AY189118; AAO40033.1; -. EMBL; AY189119; AAO40034.1; -.
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Local Similarity 55.6%;
les 5; Conservative
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88 QSHGAAPCS 96
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KV31_HUMAN

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DT 01-NOV

DT 01-NOV

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-!- SIMILARITY: Contains 1 KRAB domain.
-!- SIMILARITY: Contains 12 C2H2-type zinc fingers.
-!- SIMILARITY: Contains 12 C2H2-type zinc fingers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Tongue;
Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Tashiro H., Yamazaki M., Komiyama M., Sugiyama T., Irie R.,
Chuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Salto K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kimuchi H., Kanda K.,
Murakawa K., Kanehori K., Takahashi-Pujii A., Oshima A., Sugiyama A.,
Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                         ..
Length 129,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "NETO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
Score 35; DB 1;
Pred. No. 6.8;
1; Mismatches
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Last annotation update)
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10-0CT-2003 (Rel. 42, Last seq
10-0CT-2003 (Rel. 42, Last anno
2inc finger protein 440.
  Similarity 85.7%; 6; Conservative
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC cor send an email to licensesisb-sib.ch).

DR EMBL, BACOSTSC1 AAR35760.1; -
DR EMBL, BACOSTSC1 BACOSTSC1 AAR35760.1; -
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Search completed: April 21, 2004, 17:34:02 Job time : 5.56522 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 21, 2004, 17:26:23 ; Search time 24 Seconds (without alignments) 118.319 Million cell updates/sec Run on:

Title:
Perfect score! 51
Sequence: ' 1 qqygsspcs 9

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

1017041 seqs, 315518202 residues Searched:

1017041

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL Database :

sp\_unclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\* sp\_archea:\*
sp\_bacteria:\*
sp\_human:\*
sp\_human:\*
sp\_nnvertebrate:\*
sp\_mammal:\*
sp\_mnc:\*
sp\_organelle:\*
sp\_phage:\*
sp\_plant:\* sp\_rodent:\*
sp\_virus:\*
sp\_vertebrate:\*

Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Q8na39 homo sapien	Q91615 xenopus lae	P79773 gallus gall	Q28224 cercopithec	Q9ul78 homo sapien	Q7ufh0 rhodopirell	Q91gx9 oryza sativ	Q8rd12 thermoanaer	Q8cb29 mus musculu	Q9afd0 rhizobium m	Q92tg3 rhizobium m	O9pua5 xenopus lae	Q9nxf6 homo sapien	Q8k340 mus musculu	Q8c0d3 mus musculu	Q8bl43 mus musculu	
Ω	Q8NA39	291615	P79773	Q28224	Q9UL78	Q7UFH0	6X9T6Ö	Q8RD12	Q8CB29	Q9AFD0	Q92TG3	Q9PUA5	Q9NXF6	Q8K340	QBC0D3	Q8BL43	
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* Query Match Length DB	412	882	1240	1251	109	517	524	591	151	174	174	267	298	347	362	584	
% Query Match	76.5	76.5	76.5	76.5	74.5	70.6	70.6	70.6	68.6	68.6	68.6	9.89	68.6	68.6	68.6	9.89	
Score	39	30	39	39	38	36	36	36	35	35	35	35	35	35	35	35	
Result No.	н	7	٣	4	Ŋ	9	7	œ	σ'n	10	11	12	13	14	15	16	

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## ALIGNMENTS

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Istibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Ishibashi T., Kanehori K., Takiquchi S., Kusano J., Hizoka S., Muzakawa K., Takiquchi S., Kusano J., Hizoka S., Muzakawa K., Takiquchi S., Kusano J., Rumanbita H., Ishida M., Yamashita H., Chiba Y., A ugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito M., Nikuchi H., Kanda K., Yamamoto J., Isono Y., Kawai-Hio Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; T., Submitted (Jul.-2002) to the EmBL/GenBank/DDBJ databases.

EmBL; AK091189; BAC04089.1; ---
CO; GO:0007275; P:Gevelopment; IEA.

GO; GO:0007225; P:frizzled signaling pathway; IEA.

GO; GO:0007222; P:frizzled signaling cascade; IEA.
                                                                                                                                                         Eukaryota, Metazza, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                   Q8NA39;
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2003 (TrEMBLrel. 22, Last sequence update)
Hypochetical protein FLJ35870.
Homo sapiens (Human)
                                    412 AA
                                    PRT;
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InterPro; IPR000591; DEP.
InterPro; IPR008340; Dishevell.
InterPro; IPR001478; PDZ.
Pfam; PF00610; DEP; 1.
Pfam; PF006595; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01760; DISHEVELLED.
PRINTS; PR01761; DISHEVELLED1
SMART; SM00049; DEP; 1.
                                    PRELIMINARY;
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                                                                                                                                                                                             NCBI_TaxID=9606;
                                Q8NA39
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"Cloning of the chicken insulin receptor substrate 1 gene.";

Gene 178:51-55(1996).

C -!- SIMILARITY: CONTAINS 1 PH DOMAIN.

R EMBL; U43502; AAC60550.1; -.

R PIR; U55209; JG5209.

R PSP; P35568; IRS.

R GO; GO:0005158; F:insulin receptor binding; IEA.

R InterPro; IPR002404; Insln_receptorS1.

R InterPro; IPR001849; PH.

R PFAMTY: PR00169; PH; 1.

R PFAMTY: PR00169; PH; 1.

R RFMTYS; PR00628; INSULINRSI.

R SMART; SM00233; PH; 1.

R PROSITE; PS50003; PH; 1.
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Did J. S. Sorisky A., Zhu L., Pawson T.;

"Molecular Cloning of an Amphibian Insulin Receptor Substrate-1-Like
"Molecular Cloning of an Amphibian Insulin Receptor Substrate-1-Like
DNA and Involvement of Phosphatidylinositol 3-Kinase in Insulin-
Induced Xenopus Oocyte Maturation.";

Mol. Cell. Biol. 15:0-0 (1995).

HSSP; P35569; LIRS.

GO; GO:0004872; F:receptor binding; IEA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR002404; Insul. receptorisl.

Pfam; PR0174; IRS.

FRINTS; PR00628; INSULINESI.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
10-OCT-2003 (TrEMBLrel. 01, Last sequence update)
11-NOV-1996 (TrEMBLrel. 01, Last sequence update)
11-NOV-1996 (TrEMBLrel. 01, Last sequence update)
12-NOV-1996 (TrEMBLrel. 01, Last sequence update)
13-NOV-1996 (TrEMBLrel. 01, Last sequence update)
14-NOV-1996 (TrEMBLrel. 01, Last sequence update)
15-NOV-1996 (TrEMBLrel. 01, Nov-1996)
15-NOV-1996 (TrEMBLrel. 01, Nov-1996)
15-NOV-1996 (TrEMBLrel. 01, Nov-1996)
15-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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                                                                                                                                                                                                      Query Match 76.5%; Score 39; DB 4; Length 412; Best Local Similarity 75.0%; Pred. No. 13; Matches 6; Conservative 2; Mismatches 0; Indels
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                           PROSITE; PS50186; DEP; 1.
PROSITE; PS50106; PDZ; 1.
Hypothetical protein.
SEQUENCE 412 AA; 43743 MW; 93C3ABB1BF01C207 CRC64;
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P79773;
01-MAY-1997 (TrEMELrel. 03, Created)
01-OCT-2003 (TrEMELrel. 03, Last sequence update)
01-OCT-2003 (TrEMELrel. 25, Last annotation update)
Ingulin receptor substrate 1.
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STRAIN=Leghorn;
MEDLINE=97080546; PubMed=8921891;
Taouis M., Taylor S.I., Reitman M.;
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Best Local Similarity 85.7;
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Gallus gallus (Chicken).
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223 EYGSSPC 229
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MEDLINE=96067568; PubMed=7488107;
MEDLINE=96067568; PubMed=7488107;
MEDLINE=96067568; PubMed=7488107;
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                                                                                              Score 39; DB 13; Length 1240;
Pred. No. 39;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Pinmates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
1240 AA; 131813 MW; 7FDEB2CEADECA7B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
IRS-1(COS).
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01-OCT-2000 (TrEVBLrel. 15, Last sequence update)
01-OCT-2003 (TrEVBLrel. 25, Last annotation update)
Hypothetical protein.
0ryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lilliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                         вb.
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Gramene; O9LGX9; -.

GO: CO:0003677; F:DNA binding; IEA.

GO: CO:0006357; F:PNA binding; IEA.

InterPro; IPR003340; TF_B3.

InterPro; IPR003340; TF_B3.

Hypothetical protein:

EQUENCE 524 Aa; S8677 MW; 9F75AC5DC94C3E95 CRC64;
                                                            Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schleener H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula strain 1.";
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STRAINscv. Nipponbare;
STRAINscv. Nipponbare;
SGREAKI T.. Matsumocto T., Yamamocto K.;
GOTYZE SELIVE MIPPONDARE(GA3) GENOMIC DNA, Chromosome 1, PAC
clone:P0707253.";
Submitted (JUNN 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002481; BAA96595.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 10; Length 524;
Pred. No. 66;
1; Mismatches 1; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Beta-glucosidase-related glycosidases.
BGLX2 OR TTE0241.
Thermoanaerobacter tengcongensis.
Thermoanaerobacteriaces, Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaces, Thermoanaerobacteriales;
                                                                                                                                                                                                                                            Score 36; DB 16; Length 517;
Pred. No. 66; 1; Indels
0; Mismatches 1; Indels
                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).

EMBL, BX294147; CADP812.1, -

Hypothetical protein; Complete proteome.

SEQUENCE. 517 AA; 58112 MW; 8P8A047FBC7133D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591 AA
                                     STRAIN=1;
MEDLINE=22735913; PubMed=12835416;
                                                                                                                                                                                                                                                70.6%;
Local Similarity 87.5%;
Los 7; Conservative 0
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Best Local Similarity 75.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                               273 OYGSSPIS 280
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[1]
SEQUENCE FROM N.A.
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QARD12
ID QARD
AC QARD
DT 01-J
DT 01-J
DT 01-J
DT BELA
GN BGLX
OC BACT
                                                                                                                                                                                                                                                                                           Matches
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Q9LGX9
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                                                                                                                                                      Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria, Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                              Myosin-reactive autoantibodies in rheumatic carditis and normal
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Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
NCBI_TaxID=117;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 74.5%; Score 38; DB 4; Length 109; Best Local Similarity 100.0%; Fred. No. 5.2; Matches 7; Conservative 0; Mismatches 0; Indels
                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
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Last annotation update)
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EMBL; AF035036; AAD56272.1; -.
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                       109 AA.
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                       PRT;
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SMART; SM00406; IGy; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON TER 109 109
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HSSP; P80362; IWTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig.v.
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                       PRELIMINARY;
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PH0965; PH0965.
S34096; S34096.
                                                                                                                                (Fragment).
Homo sapiens (Human)
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Q7UFHO; Q7UFH0

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2707FH0
AC 270F
AC 270F
DT 01-0
DT 01-0
DT 01-0
DT RBB5
OS RHOd
OC PLAN
OC PLAN
OX NCBI

Gaps

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STRAIN=1021;
MEDDINE=1136508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Finan T.M., Weidner S., Wong K., Buhrmester J., Cowie A., Gouzy J.,
Golding B., Puehler A.; Ernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
fixing endosymbiont Sinorhizobium mellioti.";
Fixing endosymbiont Sinorhizobium mellioti.";
EMBL, Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                                                                                     SEQUENCE FROM N.A.
Del Papa M.F., Balague L.J., Lagares A.;
Del Papa M.F., Balague L.J., Lagares A.;
dertative Sinorhizobium meliloti gene cluster for phenylacetic acid
degradation.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PLATO OR REBIST OR SMB21637.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymb (megaplasmid 2).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Rhizobiaceae, Sinorhizobium/Ensifer group; Sinorhizobium.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                        Query Match 68.6%; Score 35; DB 2; Length 174; Best Local Similarity 71.4%; Pred. No. 35; Matches 5; Conservative 2; Mismatches 0; Indels
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GO; GO:0046821; C:extrachromosomal DNA; IEA.
InterPro; IPR002744; DUF59.
Pfam; PF01883; DUF59; 1.
ProDom; PD005595; DUF59; 1.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 174 AA; 19029 MW; ABE64850182DD83C CRC64;
                                                                                                                                                                                                                            EMBL, AFFS0436, AAK29442.1; -.
InterPro, IPR002744; DUF59.
Pfam, PF01883; DUF59; 1.
SEQUENCE 174 AA; 18973 MW; 349FF670182ADF2E CRC64;
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Q9PUA5;
01-MAY-2000 (TFEMBLrel. 13, Created)
01-MAY-2001 (TFEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 AA
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Q9PUA5
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MEDLINE=2236681; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the Manupais of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; ARO3691; ARO36031; --
Hypothetical protein.
SEQUENCE 151 AA; 16328 MW; C54CBC212D283BAF CRC64;
                                                                                                  MEDLINE=21992816; PubMed=11997336;

A REDLINE=21992816; PubMed=11997336;

Bao Q., Tian Y., Iu Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

A Tan H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

EMBL; AB012996; AAM23337.1;

RO; GO:0009575; P:carbohydrate metabolism; IEA.

InterPro; IPR002772; Glyco.hydro_30.

R InterPro; IPR001764; Glyco.hydro_31.

R Fam; PR01915; Glyco.hydro_31.

R Fam; PR01915; Glyco.hydro_31.

R Fam; PR01915; Glyco.hydro_31.

R Fam; PR01915; Glyco.hydro_32.

R PRINTS; PR01913; Glyco.hydro_32.

R PRINTS; PR01913; Glyco.hydro_32.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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68.6%; Score 35; DB 11; Length 151;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        591 AA; 64817 MW; EBF5A938DEA54101 CRC64;
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Last sequence update)
Last annotation update)
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(TrEMBLrel. 17,
(TrEMBLrel. 18,
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Matches 6; Conservative
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                       NCBI_TaxID=119072;
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01-JUN-2001
01-JUN-2001
01-OCT-2001
PaaD.
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Q9AFD0
ID Q9AFD
AC Q9AFD
DT 01-JU
DT 01-C
DT 01-G
GN PAAD.
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RESULT 9 **Q8CB29** 

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

MEDINE-22354683; PubMed=12466851;

The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

Analysis of the mouse transcriptome based on functional annotation of a nature 420:563-573(2002).

REMEL, AKO314660; BAC274981; 1. -.

REMEL, AKO314660; BAC274981; 1. -.

ROJ, GO:0007218; Pineuropeptide signaling pathway; IEA.

InterPro; IPR00159; RA_domain.

PROSITE; PSS0200; RA; 1.

RM Hypothetical protein.

SQUENCE 362 AA; 40933 MW; 32BI047ACC07B987 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
class-II containing protein.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                      Q8K340;

Q8K340;

Q1-CCT-2002 (TEMBLrel. 22, Last sequence update)

O1-CCT-2003 (TEMBLrel. 24, Last annotation update)

O1-JUN-2003 (TEMBLrel. 24, Last annotation update)

Hypothetical protein (Fragment).

Hypothetical protein (Fragment).

Hypothetical (Fragment).

Hypothetical protein (Fragment).

Hypothetical protein; Conradata, Vertebrata, Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Straubberg R.;
Submitted (WAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020818; PAH28854.1; -.
GO; GO:0007218; Peneuropeptide signaling pathway; IEA.
InterPro; IPR000159; RA_domain.
PROSITE; PSS0200; RA; 1.
Hypothetical protein.
NOW TER
SEQUENCE 347 AA; 39160 MW; 306E40D38A14B3DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 AA.
                                                                         347 AA
                                                                         PRT;
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RESULT 14
Q8K340
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I. Submitteed (FEB-2000) to the EMBL/GenBank/DDBJ databases.

R. Chillian AKO00288; BAA91057.1; T. CHC.

R. Pfan, PF00098; zf-CCHC; I.

R. PRINTS; PR0098; zf-CCHC; I.

R. PRINTS; RN00343; zn-CCHC; I.

R. PRART; SN00343; zn-CCHC; I.

R. PRART; SN00343; zn-CCHC; I.

R. PROSITE; PS50158; zg-CCHC; I.

R. PROSITE; PS50158; zg-CCHC; I.

R. PROSITE; PS50158; zg-CCHC; I.
                                                                                                                                                                                                                                                                                                                                                                DEPLINE_21152895; PubMed=11231068;

Thibbash S., Yasuda K.;

Ishibashi S., Yasuda K.;

Ishibashi S., Yasuda K.;

"Distinct roles of maf genes during Xenopus lens development.";

"Distinct roles of maf genes during Xenopus lens development.";

"Distinct roles of maf genes during Xenopus lens development.";

"Distinct roles of maf genes during Xenopus lens development.";

"Distinct Poologies of March 10.";

"Red; GO:00003677; F.DNA binding; IEA.

"Red; GO:00003677; F.DNA binding; IEA.

"Red; GO:00003677; F.DNA binding; IEA.

"Red; GO:00003677; F.DNA binding; IEA.

"Red; FROOGS F. TEALP."

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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 15, Last annotation update)
Hypothetical protein FLJ20281.
Hymos spiens (Human).
Eukaryota; Mctazoa; Chordata; Craniata, Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                 Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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68.6%; Score 35; DB 4; Length 298;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 2; Indels
        01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
bZIP transcription factor L-Maf.
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Best Local Similarity 66...
6, Conservative
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Copyright (c) 1993 - 2004 Compugen Ltd.
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SEO6 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 ффудварсв 9 Scoring table: Sequence:

1586107 seqs, 282547505 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\* geneseqp20028;\* geneseqp2003as;\* geneseqp2003bs;\* geneseqp2004s;\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp20018:\* 4.0.0 6 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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#### ALIGNMENTS

Propionibacterium acnes immunogenic protein #4729. AAU43833 standard; protein; 87 AA. (first entry) 13-FEB-2002 AAU43833; 

SAPHO syndrome, synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes.

WO200181581-A2. 01-NOV-2001. 20-APR-2001; 2001WO-US012865

21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P.

(CORI-) CORIXA CORP.

Bhatia Wang SS, Mitcham JL, Wang S, Jen S, Carter D; Persing DH, M e J, Zhang Y, L'maisonneuve J, Skeiky YAW,

WPI; 2001-616774/71. N-PSDB; AAS59521. Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.

Example 1; SEQ ID NO 5028; 1069pp; English.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by p. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory

presence or absence of P. acnes in a partient comprises contacting the presence or absence of P. acnes in a partient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used adapostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formatt directly from WIPO at 

Sequence 87 AA;

Gaps . Query Match 78.4%; Score 40; DB 4; Length 87; Best Local Similarity 87.5%; Pred. No. 17; Matches 7; Conservative 0; Mismatches 1; Indels

1 QQYGSSPC 8

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55 QGYGSSPC 62

ABM40352 standard; protein; 87 AA.

ABM40352;

(first entry) 20-OCT-2003 Propionibacterium acnes predicted ORF-encoded polypeptide #5028.

Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.

Propionibacterium acnes

WO2003033515-A1

24-APR-2003

11-OCT-2002; 2002WO-US032727

15-OCT-2001; 2001US-00978825

(CORI-) CORIXA CORP.

Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Barth B, Vallieve-Douglass J;

Maisonneuve JL; Jones R, Carter D;

WPI; 2003-381789/36. N-PSDB; ACF64450.

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Example 1; SEQ ID NO 5028; 1481pp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; antibodies against polypeptides of the invention; encompassed to an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides.) 

polymucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymucleotides of the reading frame) contained within the P. acnes polymucleotides of the reading frame) to but was obtained in electronic form a directly the printed specification, but was obtained in electronic format directly from WIPO at ftp. WiPo.int/published\_pot\_sequences \$

Sequence 87 AA;

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Gaps ö Score 40; DB 6; Length 87; Pred. No. 17; 0; Mismatches 1; Indels 78.48; 87.58; Ouery Match
Best Local Similarity 87.5.
Local 7, Conservative

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62 œ 1 QOYGSSPC

ઠે g RESULT 3 ADB65321

ADB65321 standard; protein; 412 AA.

ADB65321;

(first entry) 04-DEC-2003 Human protein encoded by clone TESTI20079980.

Human, pharmaceutical, diagnostic, gene therapy, tissue regeneration, cell regeneration, membrane protein, signal transduction-related protein, transcription-related protein, osteoporosis, neurological disease, cancer; tumour. 

Homo sapiens

EP1308459-A2

07-MAY-2003.

28-MAR-2002; 2002EP-00007401.

05-NOV-2001; 2001JP-00379298. 25-JAN-2002; 2002US-00350978.

(HELI-) HELIX RES INST. (REAS-) RES ASSOC BIOTECHNOLOGY.

Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S; Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I; Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

WPI; 2003-450961/43. N-PSDB; ADB63351.

New polynuclectides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.

Claim 1; Page; 222pp; English

The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel

Use of an inhibitor of a Hedgehog signaling pathway in preparation of a medicament for treating epithelial cell hyperplasia, inflammation, cancer or an immune disorder.

Disclosure; Page 71; 78pp; English

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CC polypeptides. Also claimed is a polypeptide encoded by the polymucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polymucleotide, immunologically assaying the polypeptide or peptide of the polymucleotide by contacting the polypeptide or peptide of the polymucleotide by contacting the polypeptide or peptide or with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polymucleotide in an expressible manner and an antisense polymucleotide. The oligonucleotide is useful as a primer for synthesising the polymucleotide, or as a probe for detecting the polymucleotide. The oligonucleotide contacting are useful as a primer for synthesising the polymucleotide, or as a probe for detecting the polymucleotide and many disease-related proteins are useful as pharmaceutical agents and many disease-related contacts and many disease-related contacts and proteins, signal transduction-related proteins, signal transduction-related proteins, contacting them can be used as indicators for diseases (e.g. ostcoporosis, the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention, Note: Some of the content of the polymucleoting them encoded protein of the polymucleotide in the printed content of the content of the protein of the protein of the printed content of the protein of the printed content of the protein of the printed content of the protein of the protein of the printed content of the protein of the printed content of the protein of the protein of the printed content of the printed content of the protein of the preference information supplied by the
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Sequence 412 AA;

ö ; 0 Score 39;. DB 7; Length 412; Pred. No. 1.2e+02; 2; Mismatches 0; Indels 76.5%; 75.0%; 6; Conservative Query Match Best Local Similarity Matches 6; Conserv

:||:|||| 93 RYGTSPCS 100 2 OYGSSPCS 9

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AAY97560 standard; protein; 695 AA. AAY97560;

05-APR-2001 (first entry)

Mouse Dishevelled-1 protein sequence.

Mouse, Hedgehog signalling pathway; inhibitor; autoimmune disorder; epithelial cell hyperplasia; fibrosis; inflammation; adenocarcinoma; immune disorder; cancer; thyroiditis; insulitis; multiple sclerosis; iridocyclitis; uveitis; orchitis; hadiaon's disease; asthma; myasthenia gravis; rheumatoid arthritis; hubus erythematosus; emphysema; adult respiratory distress syndrome; chronic bronchitis; acelectasis; silicosis; hypersensitivity pneomonitis; idiopathic pulmonary fibrosis; silicosis; paternal fibrosis; atherosclerosis; myocardial infarction; gastrointestinal tract disorder; hepatic disease; Alzheimer's disease; Wnt signalling pathway; BMP signalling pathway; sonic hedgehog; bishevelled-1; Dv1-1. AAN 97560
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AAN 97

Mus musculus.

WO200074706-A1.

14-DEC-2000.

05-JUN-2000; 2000WO-GB002191

99GB-00013350. 99GB-00021953. 08-JUN-1999; 16-SEP-1999;

(LORA-) LORANTIS LTD

Lamb JR, Hoyne GF, Dallman MJ;

09-APR-2001; 2001GB-00008872. 09-APR-2001; 2001GB-00008873.

(LORA-) LORANTIS LTD

WPI; 2001-061652/07. N-PSDB; AAA37898.

```
This sequence is mouse dishevelled-1 (DV1-1), and is part of the Hedgehog signalling pathway. The invention relates to the use of an inhibitor of a fight ling pathway. The invention relates to the use of an inhibitor of a Hedgehog signalling pathway, in the preparation of a medicament for treating epithelial cell hyperplasia, fibrosis of tissue, inflammation, cancer (especially adenocarcinoma) or an immune disorder. The immune of usorder can be an autoimmune disorder. The immune of usorder can be an autoimmune disorder such as thyroiditis, insultis, multiple sclerosis, iridocyclitis, veeitis, orchitis, hepatitis, addisor's disease, wysathenia gravis, rheumatoid arthritis or lupus carcinome, chronic obstructive airway disorders including aslou useful for treating lung or kidney diseases such as adult respiratory distress synthmache, chronic obstructive airway disorders including aslou useful for treating lung or kidney diseases such as adult respiratory diseases including alloosis, hypersensitivity diseases of lung such as including allicosis, hypersensitivity diseases of lung such as idiopathic pulmonary fibrosis, pneumonia including interstitial preumonia and acute interstitial preumonia, and pleural fibrosis. pneumonia including interstitial preumonia including interstitial preumonia, and pleural fibrosis. They can also be used in the trearment of infarmation associated with atherocalerosis, e.g. wyocardial infarction, diseases of the central nervous system e.g. Alzheimer's disease and diseases of the defendence pathway is that of Sonic hedgehog signalling pathway is that or Bobbert hedgehog signalling pathway is were the BMP signalling pathway.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; Hedgehog signalling pathway; T-cell mediated disease; T-cell apoptosis; Notch signalling pathway; cancer; breast; prostate; ovary; T-cell activation; T-cell proliferation; lymphoma; carcinoma; autoinmune disease; inflammatory disease; proliferative disorder; viral infection; syndrome; immunodeficiency; neurodegenerative disease; wasting disease; dishevelled-1; DvI-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.5%; Score 39; DB 4; Length 695; 75.0%; Pred, No. 2e+02; cive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse dishevelled-1 (Dvl-1) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG71359 standard; protein; 695 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-2002; 2002WO-GB001666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JAN-2003 (first entry)
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pathway or a modulator of a target of the pathway in the preparation of medicament for treating T-cell mediated disease or infection or a disease or disorder associated with increased or decreased T-cell apoptosis and cor modification of (peripheral) T-cell activation or proliferation or T-cell apoptosis, and for modulation of the Notch signalling pathway in immune cells. The modulator is useful for treating cancer of the breast, prostem or ovary, lymphomas and carcinomas, autoimmune diseases such as systemic lupus erythematosus, multiple sclerosis and diseases such as stherosis and diseases.

Inflammatory diseases such as atherosis and psoriasis, viral inflections such as AlDS and herpesviruses, genetic immunodeficiencies, neurodegenerative diseases such as Alzheimer's disease and Parkinson's disease, myelodysplastic syndromes such as albastic anaemia, ischaemic injuries such as myocardial infarction, toxin-induced diseases such as carkoas and wasting diseases such as cachexia. This sequence represents the mouse dishevelled-1 (DVI-1) protein
                                                                                        Use of a modulator of Hedgehog signaling pathways for treating T-cell mediated disease or infection and diseases associated with increased or decreased T-cell apoptosis and T-cell proliferation.
                                                                                                                                                                                       The invention relates to use of a modulator of a Hedgehog signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Purified nucleic acid encoding Insulin Receptor Substrate - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insulin receptor substrate-1; IRS-1; probe; vector; transform; IRS-1 metabolism; insulin related disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 6;
Pred. No. 2e+02;
2; Mismatches
             Champion BR
                                                                                                                                                           Disclosure; Page 150; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR28047 standard; protein; 1155 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JOSL-) JOSLIN DIABETES CENT INC.
               Dallman MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92WO-US000437
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Best Local Similarity 75.0
Matches 6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 RYGTSPCS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kahn CR, White MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-365881/44.
N-PSDB; AAQ29703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 OYGSSPCS 9
             Hoyne GF,
                                           2003-058470/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 695 AA;
                                                              N-PSDB; ABS55984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRS-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9213083-A1
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17-MAR-1993
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               Lamb JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
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                                                                           The sequence given is the rat insulin receptor substrate-1 (IRS-1). The IRS-1 gene was isolated using the probe sequences given in AAQ29701-02. The IRS-1 sequence can be inserted into a vector and used to transform cells to produce IRS-1. The level of IRS-1 metabolism can then be studied and abnormal levels may be seen to be indicative of insulin related disease. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the IRSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises the amino acid and coding sequence of the IRSA protein which functions to modify insulin physiological activity and control the intake of saccharides into cells. The DNA and protein sequences of the invention are useful in gene diagnosis and screening (e.g. drug candidates for type II diabetes). The present amino acid sequence represents a rat IRSAL-related protein
prepare IRS-1, for diagnosis and treatment of insulin related diseases and abnormal cellular proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat; IRSAL; insulin activity modification; saccharide intake;
gene diagnosis; screening; type II diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.5%; Score 39; DB 6; Length 1235; 85.7%; Pred. No. 3.6e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                             Length 1155;
                                                                                                                                                                                                                             76.5%; Score 39; DB 2; Length 115
85.7%; Pred. No. 3.4e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takahashi S, Hakuno F, Kurihara S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 40-48; 58pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                            AA016354 standard; protein; 1235 AA
                                                     Disclosure, Fig 12; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-APR-2002; 2002WO-JP003579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat IRSAL-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                                                                                                                             385 EYĞSSPC 391
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                   Sequence 1155 AA;
                                                                                                                                                                                                                                                                                              2 QYGSSPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200283730-A1.
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Length 695 0; Indels 2 QYGSSPC 8

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The invention relates to modulators that affect the interaction of a polypeptide defining a PI (phosphotyrosine interaction) domain, or its conserved variants or fragments, with APP (amyloid precursor protein). The polypeptide defining a PI domain binds to the cytoplasmic domain of APP, regulating the secretion of APP fragments. By modulating this interaction, the modulator can inhibit or prevent APP processing and trafficioning, and thus progress or onset of Alzheimer's disease. The modulators are used to treat and/or prevent neurodegenerative diseases in mammals, particularly Alzheimer's disease and dementia. Sequences AAY13448-461 represent examples of polypeptides defining a PI domain
                                                                                                                                Phosphotyrosine interaction domain; PI domain; modulator; APP; amyloid precursor protein; cytoplasmic domain; Alzheimer's disease; neurodegenerative disease; dementia; IRS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                           Cell line for screening agents that inhibit processing of amyloid precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 2; Length 1242;
Pred. No. 3.7e+02;
1; Mismatches 0; Indels
                                                                                                         Amino acid sequence of human IRS-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW93972 standard; protein; 1242 AA
                          AAY13461 standard; protein; 1242 AA.
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                                                                                                                                                                                                                                                                                                     97US-00957660.
98US-00062085.
                                                                             26-JUL-1999 (first entry)
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430 EYGSSPC 436
                                                                                                                                                                                                                                                                                                                                                                        Buxbaum J,
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-326703/27
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Best Local Similarity
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                                                                                                                                                                                                                    WO9921995-A1
                                                                                                                                                                                                                                                                          23-OCT-1998;
                                                                                                                                                                                                                                                                                                     24-OCT-1997;
                                                                                                                                                                                                                                                                                                                   17-APR-1998;
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                06-MAY-1999
                                                   AAY13461;
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This invention describes a method for the treatment of diseases involving insulin resistance using a substance which inhibits the binding of insulin receptor substrate to 14-3-3 protein, identified by screening potential inhibitors for their ability to inhibit this binding. The composition described in the invention for the treatment of diseases involving insulin resistance contains as active component, an inhibitor of the binding of all or part of insulin receptor substrate 1 or 2 (IRS-1) to all or part of insulin receptor substrate 1 or 2 (IRS-1) to all or part of 14-3-3 protein. Disorders involving insulin resistance include diaberes, diabetic retinopathy, diabetic neuropathy, impaired glucose tolerance, diabetic nephropathy, hyperinsullnaemia, hyperlipemia, arteriossclerosis, hypertenaion, obestry, ischaemic heart disease, ischaemic brain disease and peripheral embolism
                                                                                                                                                                                                                                                                                                                                      Treatment of insulin resistance using insulin receptor substrate binding inhibitor.
insulin resistance; 14-3-3 protein; inhibitor; screening; diabetes; diabetic retinopathy; diabetic neuropachy; glucose tolerance; diabetic nephropathy; hyperinsulinaemia; hyperlipemia; arteriosclerosis; hypercension; ischaemic heart disease; ischaemic brain disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Epidermal growth factor-like domain; EGF-like domain; cancer;
human aspartyl beta-hydroxylage; HAAH; malignant neoplasm; tumour;
insulin receptor substrate; IRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a human insulin receptor substrate (IRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 3.7e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 16-22; 30pp; Japanese.
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                                                                                                                                                                                                                                                                                          Kanda
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                                                                                                                                                                                                                          97JP-00263719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.5%;
                                                                                                                                                                                                                                                        (DAUC ) DAIICHI PHARM CO LID.
                                                                                                                                                                                                                                                                                         Kubo H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 85...
6; Conservative
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                                                                                                                                                                                                                                                                                          ABano T,
                                                                                                                                                                                                                                                                                                                       WPI; 1999-254929/21
                                                 hypertension; ischaperipheral embolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 OYGSSPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200135102-A2
                                                                                                                                                                                                                             29-SEP-1997;
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                                                                                                                                                                                             25-SEP-1998;
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                                                                                                                                WO9916462-A1
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                                                                                                                                                                08-APR-1999
                                                                                                                                                                                                                                                                                       Yazaki Y,
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Insulin receptor substrate; IRS-1; IRS-2; inhibitor; disease; obesity;

Human IRS-1 and IRS-2 binding inhibitor protein.

(first entry)

30-JUN-1999

AAW93972;

Al-Mahmood S;

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The present sequence represents a human insulin receptor substrate (IRS).

Compounds which inhibit IRS also inhibit growth of tumours which

coverexpress human asparty1 (asparaginy1) beta-hydroxylase (HAAH) enzyme.

Epidermal growth factor (EGF) like domains of polypeptides are

hydroxylated by HAAH enzymes. HAAH is used in the method of the

invention. The specification describes a method for diagnosing a

malignant neoplasm in a mammal. The method comprises contacting a body

fluid with an antibody which binds to HAAH polypeptide under complex

forming conditions, and detecting the antigen-antibody complex. The

method is useful for diagnosing and prognosing a malignant neoplasm in a

conjuly fluid e.g. central nervous system (CNS) derived body fluid, blood

serum, urine, saliva, sputum, lung effusion, and ascites fluid of mammal,

where the neoplasm is derived from endodermal lissue and is salected from

colon cancer, breast cancer, pancretic cancer, liver cancer, cancer, one

colon cancer, breast cancer, pancretic cancer, liver cancer, or

section, are useful for killing tumour cells
                                                                                                                                                                        Diagnosing malignant neoplasm in a mammal, involves contacting mammalian sample with antibody that binds to human aspartyl beta-hydroxylase polypeptide to form antigen-antibody complex and detecting the complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRS-1; insulin receptor substrate-1; angiogenesis; capillary tube; endothelial cell; retinopathy; rheumatoid arthritis; Crohn's disease; atheroscleroscis; ovarian hyperstimulation; psoriasis; endometriosis; restencesis; wound healing; peripheral vascular disease; hypertenation; vascular inflammation; Raynaud disease; aneurysm; arterial restencesis; thrombophlebitis; lymphodema; isohemia; angina; myocardial infarction; chronic heart disease; macular degeneration; osteoporosis; cell multiplication; antitumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.5%; Score 39; DB 4; Length 1242; 85.7%; Pred. No. 3.7e+02; 1ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of human insulin receptor substrate-1.
                                                                         Carlson RI;
                                     (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB99797 standard; protein; 1242 AA.
                                                                           De La Monte SM, Ince N,
                                                                                                                                                                                                                                                          Example 7; Page 52; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-2002; 2002WO-FR002067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUN-2001; 2001FR-00007805.
99US-00436184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             430 EYGSSPC 436
                                                                                                                 2001-329171/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QYGSSPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1242 AA;
                                                                                                                                      N-PSDB; AAF89816
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  08-NOV-1999;
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                                                                               Wands JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB99797;
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The present sequence represents IRS-1 (insulin receptor substrate-1) polypeptide. IRS-1 is used to produce the compositions of the invention. The specification describes an angiogenesis-andifying composition. Containing at least one a nucleic acid selected from the gene encoding IRS-1 or a molecule that inhibits expression of that nucleic acid. The composition inhibits the formation of capillary tubes by endothelial composition inhibits the formation of capillary tubes by endothelial composition is used to treat and diagnose diseases associated with angiogenesis, particularly retinopathy, rheumatoid arthritis, crown sidease, atherosclerosis, ovarian hyperstimulation, psoriasis, cendometriosis, restenosis after ablloon angioplasty, overproduction of tissue during wound healing, peripheral vascular diseases, hypertension, vascular inflammation, Raymand disease, aneurysm, arterial restenosis, thrombophlebitis, lymphagitis, lymphodema, ischemia, angina, mycoardial infarction, chronic heart disease, (congestive) cardiac insufficiency, age-related macular desentation and osteoporosis.
                                                                                                         Angiogenesis-modifying composition, useful for treatment or diagnosis of e.g. retinopathy, comprises inhibitor of expression of the insulin receptor substrate-1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevent cell multiplication, especially as antitumor agents, and as research reagents for in vitro or in vivo studies on signalling pathways
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; aspartyl (asparaginyl) beta-hydoxylase; HAAH; cytostatic; immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B; brain tumour; glioma; glioblastcma; astrocytoma; haemangloma; pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer; liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm; metastatic CNS neoplasm; IRS-1; insulin receptor substrate-1; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.5%; Score 39; DB 6; Length 1242; 85.7%; Pred. No. 3.7e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild-type Tyr substituted by Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Insulin-receptor substrate-1, IRS-1, Y896F mutant.
                                                                                                                                                                                           Disclosure; Page 49-52; 52pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG72369 standard; protein; 1242 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-2001; 2001US-00859604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00436184
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Best Local Similarity 85.7
Matches 6; Conservative
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(WAND/) WANDS J R.
(DMON/) DE LA MONTE S M.
(DEUT/) DEUTCH A H.
(GHAN/) GHANBARI H A.
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Ghanbari HA;
 Deutch AH,
De La Monte SM,
 Wands JR,
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WPI; 2003-066676/06

Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of mammal with detectably-labeled antibody which binds to human aspartyl (asparaginyl) beta-hydroxylase.

Example 7; Page; 34pp; English

The invention relates to diagnosing a neoplasm and inhibiting tumour congrowth in a mammal, using an antibody that binds to human asparty desparability) beta-hydroxylase (ERAM). Diagnosing a neoplasm comprises contacting a tissue with a decerably labelled antibody where an increase in level of attibody binding at tissue site. Compared to the level of binding to normal non-neoplastic tissue indicates the presence of a composition in ammanal involves administering the antibody conjugated to a cytoroxic agent to a mammal. Also manned involves administering the antibody of conferring an immune response to a tumour cell in a mammal, by administering the antibody and ammal, by administering the antibody and ammal, by administering the antibody and the mammal into the mammal into HAAH-specific immune response in a mammal, by administering to the mammal cell in a mammal, by administering to the mammal cell in a mammal, by administering to the mammal cell and laterage of the composition encoding the artibody and HAAH poperising an extracellular domain and lacking a cytoplasmic fomain of HAAH, an extracellular domain and lacking a cytoplasmic form hybridoma FBSO, continued and HAAH which lacks enzymatic activity or alpha-kecogluterate binding domain and epidermal growth factor (EGF) like domain. The methods are useful for diagnosing neoplasm of activity or abrain tumour cell (e.g. glioma, glioblascoma, astrocyroma contractic carcinoma cell and for inducing a HAAH-specific immune ceponse in a mammal. The method is useful for diagnosing malignant concert, pancreatic carcinoma cell and for inducing a HAAH-specific immune ceponse in a mammal. The method is useful for diagnosing malignant concert, pancreatic carcinoma cell and for inducing a HAAH-specific immune cell oright and metastatic CNS neoplasms of both neuronal and glial concert, lavaression when activated by the IRS-1 signal transduction caecade. Cumours e.g. glioma, glioblastoma, astrocytoma and conferent sequence represence and concert of the present sequence is no

Sequence 1242 AA;

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76.5%; Score 39; DB 6; Length 1242;
85.7%; Pred. No. 3.7e+02;
cive 1; Mismatches 0; Indels
                   Best Local Similarity 85.7
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ABG72372 standard; protein; 1242 AA RESULT 13
ABG72372
ID ABG72
XX
AC ABG72
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ABG72372;

Human Insulin-receptor substrate-1, IRS-1, Y612F/Y941F mutant

Human, aspartyl (asparaginyl) beta-hydoxylase; HAAH; cytostatic; immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B; brain tumour; glioma; glioblastoma; astrocytoma; haemangioma; pancreatic carcinoma; colon cancer; braest cancer; pancreatic cancer; liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm; metastatic CNS neoplasm; neceptor substrate-1; mutant; mutein.

Ното варіелв Synthetic

/note= "Wild-type Tyr substituted by Phe" Location/Qualifiers Misc-difference 612 Misc-difference 941 

/note= "Wild-type Tyr substituted by Phe"

JS2002110559-A1

15-AUG-2002.

17-MAY-2001; 2001US-00859604.

08-NOV-1999; 99US-00436184

(WAND/) WANDS J.R. (DMON/) DE LA MONTE S M. (DEUT/) DEUTCH A H. (GHAN/) GHANBARI H A.

Deutch AH, Ghanbari HA; De La Monte SM, Wands JR,

WPI; 2003-066676/06.

Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue mammal with detectably labeled antibody which binds to human aspartyl (asparaginyl) beta-hydroxylase.

Example 7; Page; 34pp; English.

The invention relates to diagnosing a neoplasm and inhibiting tumour CC growth in a mammal, using an antibody that binds to human aspartyl growth in a mammal, using an antibody that binds to human aspartyl carboar-hydroxylase (HAAH). Diagnosing a neoplasm comprises contacting a tissue with a detectably-labelled antibody where an increase to lare to comman in non-neoplastic tissue side compared to the presence of a binding to normal non-neoplastic tissue indicates the presence of a complasm at the tissue site. Inhibiting tumour growth in mammal involves administering the antibody conjugated to a cytocoxic agent to a tumour call in a mammal, by administering to the mammal. HAAH-specific immune response in a mammal, by administering to the mammal. The polypeptide (or a polymocleotide composition encoding the artibody or its fragment which binds to HAAH (where the antibody is FBSO, extracellular domain and lacking a cytoplasmic domain of HAAH conprising an extracellular domain and lacking a cytoplasmic domain of HAAH conprising an extracellular domain and lacking a cytoplasmic domain of HAAH which lacks enzymatic artibody or its fragment which binds to HAAH which lacks enzymatic catcivity or 1989, and alforman call line chosen from hybridoma FBSO, HABSO, HABSO, HABSO, and HAA19B, and a fragment of HAAH which lacks enzymatic activity or alpha-ketoglutarate binding domain and epidermal growth factor (ESP)-like domain. The methods are useful for diagnosing menions or namemal, inhibiting tumour cell (e.g. glioma, glioblastoma, astrocytoma or haemangioma) in a mammal, for conferring immune concer, pancreatic cancer, liver cancer and cancer of the bile ducts. The response to a mammal, for conferring immune concer, pancreatic cancer, liver cancer and cancer of the bile ducts. The method is also useful for diagnosing neoplasms of colon cancer, breast cancer, pancreatic cancer, liver cancer and cancer of the bile ducts. The method is also useful for diagnosing neoplasms of colon cancer, breast cuencer, liver cancer and canc

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The invention relates to diagnosing a neoplasm and inhibiting tumour growth in a mammal, using an antibody that binds to human aspartyl (asparaginyl) betea-hydroxylase (HAAH). Diagnosing a neoplasm comprises contacting a tissue with a detectably-labelled antibody where an increase in level of antibody binding at tissue site compared to the level of binding to normal non-neoplastic tissue indicates the presence of a neoplasm at the tissue site. Inhibiting tumour growth in mammal involves administering the antibody conjugated to a cytotoxic agent to a mammal. Also included are a method of conferring an immune response to a tumour
HAAH expression when activated by the IRS-1 signal transduction cascade. Note: The present sequence is not shown in the specification but was created by the indexer using the IRS-1 sequence appearing as ABG72368 and the information in Example 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; aspartyl (asparaginyl) beta-hydoxylase; HAAH; cytostatic; immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B; brain tumour; glicma; glioblastoma; astrocytoma; haemangicma; apparereatic carcinoma; colon cancer; breast cancer; pancreatic cancer; liver cancer; cancer of the bile ducts; primary malignant CNS neoplasm; metastatic CNS neoplasm; IRS-1; insulin receptor substrate-1; mutant;
                                                                                                                                                                                                                                                        Length 1242;
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(DMON/) DE LA MONTE S M.
(DEUT/) DEUTCH A H.
(GHAN/) GHANBARI H A.
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CC cell in a mammal, by administering the antibody, a method of inducing an HAAH-specific immune response in a mammal, by administering to the mammal of HAAH-specific immune response in a mammal, by administering to the mammal composition encoding the colypeptide, or its degenerate variant), a fragment of HAAH comprising and extracellular domain and lacking a cytoplasmic domain of HAAH, an FBSO, extracellular domain and lacking a cytoplasmic domain of HAAH, an FBSO, extivity or alpha-ketoglutarate binding domain and epidermal growth that mammal, inhibiting tumour growth in a mammal, conferring an immune cresponse to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma or haemangioma) in a mammal, for conferring immune response to a brain tumour cell (e.g. glioma, glioblastoma, astrocytoma or haemangioma) in a mammal. For moducing a HAAH-specific immune cresponse in a mammal. The method is useful for diagnosing malignant conferring immune response to a mammal. The method is useful for diagnosing malignant conferring immune response to a mammal. The method is useful for diagnosing malignant concer, liver cancer and cancer of the bile ducts. The method is also useful for diagnosing malignant concer, pancreatic cancer, liver cancer and cancer of the bile ducts. The method is also useful for diagnosing malignant concer, liver cancer and cancer of the bile ducts of cumours e.g. glioma, glioblastoma, astrocytoma or haemandiona conference represents a mutant human IRS-1 (insulin receptor substrate-1). IRS-1 mutants were used to elucidate the upregnlation of substrate-1). IRS-1 mutants were used to elucidate the upregnlation concerted by the indexer using the IRS-1 sequence appearing as ABG72368 and the information in Example 7 ö Human, aspartyl (asparaginyl) beta-hydoxylase, HAAH, cytostatic; immunostimulant; antibody; neoplasm; tumour; FB50; 86A; 5C7; 19B; brain tumour; glioma; glioblastcoma; astrocytoma; haemangioma; pancreatic carcinoma; colon cancer; breast cancer; pancreatic cancer; liver cancer; cancer of the blle ducts; primary malignant CNS neoplasm; metastatic CNS neoplasm; IRS-1; insulin receptor substrate-1; mutant; ö Human Insulin-receptor substrate-1, IRS-1, Y896F/Y1179F mutant. Query Match 76.5%; Score 39; DB 6; Length 1242; Best Local Similarity 85.7%; Pred. No. 3.7e+02; Matches 6; Conservative 1; Mismatches 0; Indels /note= "Wild-type Tyr substituted by Phe" /note= "Wild-type Tyr substituted by Phe" ABG72371 standard; protein; 1242 AA. Location/Qualifiers 17-MAY-2001; 2001US-00859604 99US-00436184 06-FEB-2003 (first entry) Φ Sequence 1242 AA; 2 OYGSSPC Misc-difference Misc-difference US2002110559-A1 Homo sapiens. Synthetic. 38-NOV-1999; ABG72371; RESULT 15 RXPXEXBXBXBXBXBXBXBXBXBXBXBXBXBXBX \$ ò

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(WAND/) WANDS J R.
(DMON/) DE LA MONTE S M.
(DEUT/) DEUTCH A H.
(GHAN/) GHANBARI H A. Wands JR,

Ghanbari HA; Deutch AH, De La Monte SM,

WPI; 2003-066676/06

Diagnosing neoplasm and inhibiting tumor growth, by contacting tissue of mammal with detectably-labeled antibody which binds to human aspartyl (asparaginyl) beta-hydroxylase.

Example 7; Page; 34pp; English

The invention relates to diagnosing a neoplasm and inhibiting tumour cycowth in a mammal, using an antibody that binds to human aspartyl (asparaginyl) beta hydroxylase (HAAM). Diagnosing a neoplasm comprises contacting a tissue with a detectably labelled antibody where an increase in level of antibody binding at tissue site compared to the level of binding to normal non-neoplastic tissue indicates the presence of a administering the antibody conjugated to a cytocoxic agent to a mammal. Also included are a method of conferring an immune response to a tumour cell in a mammal, by administering the antibody, a method of inducing an HAAH-specific immune response in a mammal, by administering the antibody is method of inducing an extracellular domain and lacking a cytoplasmic domain of HAAH, and lacking a cytoplasmic domain of HAAH comprising an extracellular domain and lacking a cytoplasmic domain of HAAH, conferring to the mammal conferring and induced are a method of conferring a cytoplasmic domain of HAAH, conferring to the mammal extracellular domain. The methods are useful for diagnosing neoplasm of artibody or its fragment of a tragment of HAAH (where the antibody is FBSO, 684, 5C7 or 198), a hybridoma call line chosen from hybridoma FBSO, HA186A, HA15CA and HA2199, and a fragment of HAAH (where the antibody is FBSO, 684, 5C7 or 198), a hybridoma call line chosen from hybridoma response to a brain tumour call line chosen from hybridoma servivity or alpha-ketoglutarate binding domain and epidermal growth factor (EGF)-like domain. The methods are useful for diagnosing method cancer. Conferring immune response to a brain tumour call inference and cancer of the bile duces. The method is useful for diagnosing malignant complasms derived from endodermal tissue, e.g. colon cancer, breast carcinoma cell and for inducing a HAAH-specific immune cell origin and metastatic Carcinoma cell and for inducing a diagnosing malignant cell origin and metastatic carcinoma cell and cancer, live response to a gent proplasms of centr 

Sequence 1242 AA;

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Best Local Similarity 85.7
Matches 6; Conservative

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Search completed: April 21, 2004, 17:33:16 Job time : 37 secs

Scoring table:

Searched:

Minimum DB E Maximum DB E

Database :

Title: Perfect score:

Sequence:

OM protein

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JOHNSTAIL INFORMATION:
APPLICANT: ABGENIX, INC.
APPLICANT: CORVALAN, Jose, R.F.
APPLICANT: CORVALAN, Jose, R.F.
APPLICANT: GAIA, Xiao-Chi
APPLICANT: YANG, Xiao
APPLICANT: YANG, Xiao
APPLICANT: WEBER, Richard
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APPLICANT: WINDER PRINGER
CURRENT APPLICATION WUNBER: PCT/US03/00398
CURRENT FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 377
SOFTWARE FRAESEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 108
PCT-US03-00398-49
PCT-US03-00398-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 49, Application PC/TUS0300398 GENERAL INFORMATION:
      TYPE: PRT
ORGANISM: homo sapiens
      -US03-00398-49
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40.5
                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                  April 21, 2004, 17:33:24; Search time 133.826 Seconds (Without alignments) 65.641 Million cell updates/sec
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2: (cgn2 6/ptodata/2/paa/USO8_COMB.pep:*

3: (cgn2 6/ptodata/2/paa/USO9_COMB.pep:*

3:
                                                                                                                                                                                                                                                                                           6019581
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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51
1 qqygsspcs 9
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Score

Result No.

Sequence 3972, Ap Sequence 885, App Sequence 3973, Ap Sequence 71531, A

Sequence 255, App Sequence 255, App Sequence 257, App Sequence 49, Appli Sequence 47, Appli Sequence 259, App Sequence 259, App Sequence 259, App Sequence 31779, A Sequence 11863, A Sequence 5028, Ap Sequence 5028, Ap Sequence 5028, Ap Sequence 5028, Ap Sequence 5028, Ap Sequence 36707, A Sequence 36707, A Sequence 2544, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 2546, Ap Sequence 264, App Sequence 264, App Sequence 264, App Sequence 2673, Ap Sequence 2674, Ap Sequence 2

PCT-US03-00398-49

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Gaps
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APPLICANT: FENG, Xiao-Dong
APPLICANT: CHEN, Francine
APPLICANT: GAZIT, Gad;
APPLICANT: GAZIT, Gad;
APPLICANT: BERZAEH, Binad
APPLICANT: BERZAEH, Binad
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
FILE REPERENCE: ABGENIX. 051VPC
CURRENT PILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 375
LENGTH: 108
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GENERAL INFORMATION:
APPLICANT: ABGENIX, INC.
APPLICANT: FLOEGE, Juergen
APPLICANT: GAZIT, Gad;
APPLICANT: GAZIT, Gad;
APPLICANT: LAROCHELLE, William, J.
APPLICANT: LICHENTERN, WILLIAM.
TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEW TREATMENT OF NEW TREATMENT OF NEW TREATMENT OF NEW TREATMENT OF NEW TREATMENT OF NEW TREATMENT FILIAM DATE: 2003-09-16
CURRENT FILIAM DATE: 2003-09-16
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 4
LENTH: 108
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100.0%; Score 51; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                           Sequence 375, Application PC/TUS0300398 GENERAL INFORMATION:
                                                                                                                                                                                                           CORVALAN, Jose, R.F.
JIA, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: homo sapiens
PCT-US03-00398-375
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                                         90 COYGSSPCS 98
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1 OOYGSSPCS 9
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                                                                    Gaps
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APPLICANT: GAZIT, Gadi
APPLICANT: WEBER, Richard
APPLICANT: BEZABER, Richard
APPLICANT: BEZABER, BINYAM
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
FILE REFERENCE: ABGENIX.051VPC
CURRENT APPLICATION NUMBER: PCT/US03/00398
CURRENT FILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 225
LENGTH: 108
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TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF
CURRENT APPLICATION WUMBER: PCT/US03/00398
CURRENT APPLING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 377
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 259
LENGTH: 108
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100.0%; Score 51; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels
                      Query Match
100.0%; Score 51; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                           Sequence 225, Application PC/TUS0300398
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORVALAN, JOSE, R.F.
JIA, Xiao-Chi
FENG, Xiao
YANG, Xiao-Dong
CHEN, Francine
                                                                                                                                                                                                                                                                                                  ABGENIX, INC.
CORVALAN, JOSE, R.F.
JIA, Xiao-Chi
FENG, Xiao
YANG, Xiao-Dong
CHEN, Francine
GAZIT, Gadi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAZIT, Gadi
WEBER, Richard
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CRGANISM: homo sapiens
PCT-US03-00398-259
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; ORGANISM: homo sapiens
PCT-US03-00398-225
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APPLICANT: Dia, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yang, Xiao-Dong
APPLICANT: Ang, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 375
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 108;
                                   APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICAN: Weber, Richard
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REPREMENTS: ABGSNIX: 051A
CURRENT APPLICATION NOBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 259
LENGTH: 108
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100.0%; Pred. No. 1.1
:ive 0; Mismatches
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Corvalan, Jose R.F.
Jia, Xiao-Chi
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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CRGANISM: homo sapiens
US-10-041-860-375
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: homo sapiens
US-10-041-860-259
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US-10-665-383-4
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GENERAL INCORVATION:
GENERAL INCORVATION:
APPLICANT: Carvalan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGRNIX.051A
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FREESE FOR WINDOWS Version 4.0
SEQ ID NO 225
LENGTH: 108
                                                                                                                                              APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
FILE REPREMENTE: ABGRIX.051A
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Mismatches
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Best Local Similarity 100.0%; Pred. No. : Matches 9; Conservative 0; Mismatch
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Best Local Similarity 100.0%; Pred. No. 1
Matches 9; Conservative 0; Mismatche
                                                       Sequence 49, Application US/10041860
GENERAL INFORMATION:
APPLICANT: Orralan, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
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US-10-041-860-259
Sequence 259, Application US/10041860
; GENERAL INFORMATION:
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US-10-041-860-225
Sequence 225, Application US/10041860
; GENERAL INFORMATION:
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US-10-041-860-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT;
CRGANISM: homo sapiens
US-10-041-860-49
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Sequence 11863, Application US/09791537
Sequence 11863, Application US/09791537
Sequence 11863, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Benomix, Inc.
APPLICANT: Denser, Joseph
APPLICANT: Denser, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT FAPILICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 11863
LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 97444
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Score 45; DB 22; Length 109;
Pred. No. 13;
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                                                                                    0; Indels
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90.0%; Pred. No. 75;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 97444, Application US/09791537 GENERAL INFORMATION:
        88.2%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
        Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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CRGANISM: Homo sapiens
US-09-791-537-97444
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US-09-791-537-11863
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Dereck
APPLICANT: Debe, Dereck
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
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        TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
FILE REFERENCE: ABGENIX.052A
CURRENT APPLICATION NUMBER: 0210/665,383
CURRENT ELLING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/411,137
PRIOR FILING DATE: 2002-09-16
SRIGHT OF SEQ ID NOS: 97
SOFTWARE: FASELSEQ FOR WINDOWS VERSION 4.0
SQOTWARE: FASELSEQ FOR WINDOWS VERSION 4.0
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88.9%; Pred. No. 3.5;
tive 1; Mismatches
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
US-09-791-537-11779
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CORGANISM: Homo sapiens
US-09-791-537-82003
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ORGANISM: homo sapiens
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US-09-791-537-82003
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 36703
LENGTH: 81
TYPE: PRT
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-36703
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Rest Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels
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425 EYGSSPC 431
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PCT-US03-34861-1
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PCT-US03-34861-3
                  Sequence 1, Appli
Sequence 52, Appl
Sequence 57, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 123, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 14, Appli
Sequence 64, Appli
Sequence 64, Appli
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                                                                                                         April 21, 2004, 17:34:09; Search time 6.3913 Seconds (without alignments) 39.310 Million cell updates/sec
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'cgn2_6/ptodata/2/paa/VCG_NEW_COMB.pep: *

'cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep: *

'cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep: *

'cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep: *

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'cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep: *

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'cgn2_6/ptodata/2/paa/USO0_NEW_COMB.pep: *
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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PCT-US03-34861-1

US-10-630-009-52

US-10-630-009-56

US-10-630-009-56

US-10-630-009-7

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PCT-US03-36894-123

US-10-63-244-9

PCT-US03-3834A-27

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PCT-US03-38234A-16

PCT-US03-38234A-18

US-10-275-027A-807

US-10-275-027A-807

US-10-275-027A-807

US-10-275-027A-807
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Maximum Match 100%
Listing first 45 summaries
                                                                            - protein search, using sw model
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Sequence 3. Application PC/TUS0334861
; Sequence 3. Application PC/TUS0334861
; GRENERAL INFORMATION:
; APPLICANT: CELL SIGNALING TECHNOLOGY, INC.
; APPLICANT: POLAXIEWICZ, Roberto
; APPLICANT: HI, Yu
; APPLICANT: WU, Jiong
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REPERBUGE: CST-209 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/34861
; FILE REPERBUGE: CST-209 PCT
; CURRENT APPLICATION NUMBER: US 60/422,409
; PRIOR PILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 3
; LENGTH: 1231
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| GENERAL INFORMATION |
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                                    Sequence 7250, Ap Sequence 4272, Ap Sequence 132, Appl Sequence 1150, Appl Sequence 6, Appl Sequence 19, Appl Sequence 19, Appl Sequence 14, Appl Sequence 11, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 34251, Appl Sequence 34251, Appl Sequence 34251, Appl Sequence 32361, Appl Sequence 34251, Appl Sequence 32361, Appl Sequence 32361, Appl Sequence 32361, Appl Sequence 32361, Appl Sequence 32361, Appl Sequence 32361, Appl Sequence 32361, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequence 118, Appl Sequ
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US-10-800-250-38

US-60-556-841-4272

US-10-630-009-55

US-10-630-009-55

PCT-US03-3384A-132

PCT-US04-02881.150

US-10-630-009-6

US-10-612-497A-88

US-10-612-497A-19

US-10-612-497A-14

US-10-612-497A-14

US-10-612-497A-14

US-10-612-497A-65

US-10-612-497A-65

US-10-612-497A-65

US-10-612-497A-65

US-10-768-952-24

US-10-768-952-24

US-10-768-952-24

US-10-768-952-24

US-10-767-701-34251

US-10-767-701-34251

US-10-767-701-34251
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85.7%; Pred. No. 25;
cive 1; Mismatches
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Best Local Similarity 85.7
Matches 6; Conservative
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CRGANISM: Mus musculus
PCT-US03-34861-3
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APPLICANT: Ditzel, H.
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their participartic of invention: autoimmune disease
FITLE OF INVENTION: autoimmune disease
FITLE OF INVENTION: autoimmune disease
FILE REFERENCE: 1361.005052
CURRENT APPLICATION NUMBER: US/10/630,009
FILE REFERENCE: 2001-04-06
FILE APPLICATION NUMBER: US 09/828,708
PRIOR FILING DATE: 2001-04-06
FILE REFERENCE: AND MOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
ILENGTH: 9
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: NEVEU, MARK J.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/10/612,497A
CURRENT FILING DATE: 2003-07-01
PRIOR PILING DATE: 1999-12-23
PRIOR PILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 87
LENGTH: 96
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100.0%; Pred. No. 2.8;
ive 0; Mismatches 0; Indels
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       Mismatches
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
           7; Conservative
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; ORGANISM: Homo sapiens
US-10-612-497A-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Homo sapiens
US-10-630-009-56
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               Matches
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Sequence 52, Application US/10630009
GENERAL INFORMATION:
APPLICANT: Burton, D.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
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Pred. No. 26;
1; Mismatches 0; Indels
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; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/10663244
; Sequence 32, Application US/10663244
; GENERAL INFORMATION:
APPLICANT: Rondon, Isaac J.
APPLICANT: Rondon, Isaac J.
TITLE OF INVENTION: CD44 LIGANDS
TITLE OF INVENTION: CD44 LIGANDS
CURRENT FILING DATE: 2003-09-15
CURRENT FILING DATE: 2003-09-15
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PRIJES APPLICATION NUMBER: US 60/469,123
SOFTWARE: PRIJES APPLICATION NUMBER: US 60/469,123
SOFTWARE: PRIJES APPLICATION NUMBER: US 60/469,123
SOFTWARE: PRIJES APPLICATION NUMBER: US 60/469,123
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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CRGANISM: Homo sapiens
US-10-630-009-52
                   ; SEQ ID NO 1
; LENGTH: 1242
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-34861-1
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Best Local Similarity
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74.5%; Score 38; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
JAPPLICANT: ABGENIX, INC.
APPLICANT: CARROL, Frank, I.
APPLICANT: ABRAHA, Philip
APPLICANT: HRAHA, Philip
APPLICANT: HARK-FRENDSCHO, Mary
APPLICANT: HARK-FRENDSCHO, Mary
APPLICANT: FENG, Xiao
TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
FILE REFERENCE: ABGENIX.071VPC
                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: artificial sequence
PEATURE:
OTHER INFORMATION: antibody light chain variable region
PCT-US03-36894-123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
74.5%; Score 38; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches
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US-10-663-244-9
Sequence 9, Application US/10663244
Sequence 9, Application US/10663244
GENERAL INFORMATION:
APPLICANT: Rondon, leaac J.
APPLICANT: Rondon, leaac J.
APPLICANT: Rent, Rachel Baribault
TITLE OF INVENTION: CD44 LICANDS
FILE REFERENCE: 10280-063001
CURRENT APPLICATION NUMBER: US/10/663,244
CURRENT FILING DATE: 2003-09-15
PRIOR PILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2003-05
NUMBER OF SEQ ID NOS: 165
SOFTWARE: FEALSEQ for Windows Version 4.0
SENGIN 108
CURRENT FILING DATE: 2003-11-17
PRICR APPLICATION NUMBER: US 60/251,448
PRICR FILING DATE: 2000-12-05
PRICR APPLICATION NUMBER: US 10/006,593
PRICR FILING DATE: 2001-12-05
PRICR APPLICATION NUMBER: US 10/307,724
PRICR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PATENTIN VERSION 3.2
LENGTH: 108
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PCT-US03-38384A-27
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US-10-630-009-7

Sequence 7, Application US/1063009

GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Butron, D.
APPLICANT: Butron, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particil
FILE REFERENCE: 136.06502

CURRENT APPLICATION NUMBER: US/10/630,009

CURRENT FILING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 105

TENGTH: 105

TENGTH: 105

CRGANISM: Homo sapiens
                                                               US-10-630-009-3

Sequence 3, Application US/10630009

Sequence 3, Application US/10630009

Sequence 3, Application US/10630009

Sequence 3, Application US/10630009

APPLICANT: Ditzel, H.

APPLICANT: Burton, D.

APPLICANT: Schaller, M.

TITLE OF INVENTION: autoimmune disease

TITLE OF INVENTION: autoimmune disease

TITLE OF INVENTION: autoimmune disease

TITLE OF INVENTION: autoimmune disease

TITLE OF INVENTION: autoimmune disease

TITLE OF INVENTION: autoimmune disease

TITLE OF INVENTION: autoimmune disease

TITLE OF INVENTION UNMERR: US/10/630,009

CORRENT FILING DATE: 2003-07-29

PRIOR APPLICATION NUMBER: US 09/828,708

PRIOR APPLICATION UNMERR: US 09/828,708

PRIOR FILING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSEQ for Mindows Version 4.0
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74.5%; Score 38; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REPRENCE: 54 CIP PCT (1087-2 CIP PCT)
CURRENT APPLICATION NUMBER: PCT/US03/36894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo sapiens
US-10-630-009-3
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LENGTH: 105
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74.5%; Score 38; DB 1;
100.0%; Pred. No. 3.2;
:ive 0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US03/38234
PRIOR FILING DATE: 2003-12-02
NUMBER OF SEQ ID NOS: 222
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US03-38234A-4
                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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CRGANISM: Homo sapiens
PCT-US03-38234A-6
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APPLICANT: ABGENIX.
APPLICANT: LEXICON GENETICS INCORPORATED
APPLICANT: Gregory M. Landes
APPLICANT: Gregory M. Landes
APPLICANT: APPLANT MARY Haak-Frendscho
APPLICANT: Ling Chen
APPLICANT: APPLANT MARY MARY R. Lee
APPLICANT: Xiao-Chi Jian
APPLICANT: Xiao-Chi Jian
APPLICANT: Xiao-Chi Jia
APPLICANT: Mark R. Nocerini
TITLE OF INVENTION: ANTIBODIES
PILE REPERENCE: ABGENIX.072PC
CURRENT APPLICANION NUMBER: PCT/US03/38234A
CURRENT FILING DATE: 2003-02-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application PC/TUS0338384A
; Sequence 28, Application PC/TUS0338384A
; GENERAL INFORMATION:
    APPLICANT: ABCENIX, INC.
    APPLICANT: ABCHIA, Philip
    APPLICANT: ARRAN, Philip
    APPLICANT: HAAK-FRENDSCHO, Mary
    APPLICANT: FRANCARION: ANTIBODIES AGAINST DRUGS OF ABUSE
    TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
    TITLE REFERENCE: ABGENIX: 011VPC
    CURRENT APPLICATION NUMBER: PCT/US03/38384A
    CURRENT APPLICATION NUMBER: 60/430717
    PRIOR FILING DATE: 2003-12-02
    PRIOR FILING DATE: 2002-12-02
    PRIOR FILING DATE: 2002-12-02
    NUMBER OF SEQ ID NOS: 141
    SOFTWARE: FASTSEQ for Windows Version 4.0
    SERVANT: 100
       CURRENT APPLICATION NUMBER: PCT/US03/38384A
CURRENT FILING DATE: 2003-12-02
PRIOR PAPLICATION NUMBER: 60/430717
PRIOR PILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 141
SOGTWARE: FABTESQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 109
TYPE: PRT
COGGANISM: Mus musculus
PCT-US03-38384A-27
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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TYPE: PRT
ORGANISM: Mus musculus
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Sequence 6, Application PC/TUS0338234A

Sequence 6, Application PC/TUS0338234A

GENERAL INFORMATION:
APPLICANT ABGENIX, INC.
APPLICANT: Gregory M. Landes
APPLICANT: Mark-Frendscho
APPLICANT: Ling Chen
APPLICANT: Mark-Frendscho
APPLICANT: Main Ling
APPLICANT: Main Ling
APPLICANT: Alao-Chi Jia
APPLICANT: Xiao-Chi Jia
APPLICANT: Xiao-Chi Jia
APPLICANT: Mare Beerini
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE AZ AND USES THEREOF
FILE REFERENCE: ABGENIX: 072VPC
CURRENT FAPLICATION NUMBER: PCT/US03/38234
PRIOR FILING DATE: 2003-02-19
PRIOR FILING DATE: 2003-12-02
PRIOR FELING DATE: 2003-12-02
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 109
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GENERAL INFORMATION:
APPLICANT: ABGENIX, INC.
APPLICANT: BESTON GENETICS INCORPORATED
APPLICANT: Gregory M. Landes
APPLICANT: Ling Chen
APPLICANT: Ling Chen
APPLICANT: Meina Ling
APPLICANT: Meina Ling
APPLICANT: Xiao Peng
APPLICANT: Xiao Peng
APPLICANT: Xiao Peng
APPLICANT: Xiao Peng
APPLICANT: And R. Nocerini
APPLICANT: Mark R. Nocerini
APPLICANT: MARK R. Nocerini
APPLICANT: MARK R. Nocerini
APPLICANT: MARK R. NOCERINI
APPLICANT: MARK R. NOCERINI
APPLICANT: MARK R. NOCERINI
APPLICANT: MARK R. NOCERINI
APPLICANT: MARK R. NOCERINI
APPLICANT: MARK R. NOCERINI
APPLICANT: MARK R. NOCERINI
APPLICANT: MARK R. NOCERINI
APPLICANT: MARK R. NOCERINI
APPLICANT: MARK R. NOCERINI
APPLICATION NUMBER: PCT/US03/38234A
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Length 109,
                                                           0; Indels
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Thu Apr 22 05:59:23 2004
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Search completed: April 21, 2004, 17:58:26 Job time : 6.3913 secs

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RESULT 1
US-08-094-948A-29
Sequence 15, Appl
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Sequence 2, Appli
Sequence 503, App
Sequence 310, App
Sequence 310, App
Sequence 11, Appl
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Sequence 14, Appl
Sequence 14, Appl
Sequence 150, Appl
Sequence 150, Appl
Sequence 150, Appl
Sequence 150, Appl
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Sequence 29, Appl
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                                                                                              April 21, 2004, 17:28:28 ; Search time 10.8261 Seconds (without alignments) 42.918 Million cell updates/sec
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. /cgn2 / cybcdata/2/iaa/5B COMB.pep:*
. /cgn2 = 6/ptodata/2/iaa/6A COMB.pep:*
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. /cgn2 = 6/ptodata/2/iaa/PCTUS COMB.pep:*
. /cgn2 = 6/ptodata/2/iaa/PCTUS COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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PCT-US95-0319-29
US-08-317-310A-15
US-08-317-310A-15
US-08-357-139-2
US-08-357-139-2
US-08-357-139-2
US-08-357-139-2
US-08-357-139-2
US-08-357-139-2
US-08-477-887-14
US-08-477-531B-14
US-08-477-531B-14
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US-08-437-484B-150
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US-09-246-274-178
US-09-246-274-178
US-09-218-150
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Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Perfect score:
Sequence:
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Sequence 29 Application US/08094948A

Fatent No. 5621075

GENERAL INFORMATION:

APPLICANT: Wahn, C. Ronald
APPLICANT: Withe, Morris F.

APPLICANT: Wither, Morris F.

APPLICANT: Wither, Morris F.

APPLICANT: Wither Sequences, 29

CORRESPONDERS: 29

CORRESPONDERS: 129

CORRESPONDERS: Lahive & Cockfield
STREE: 60 State Street, Suite 510

CITY: Boston
STATE: Massachusetts

COMPUTRY: U.S.A.

ZIP: 02109

COMPUTRY: U.S.A.

ZIP: 02109

COMPUTRY: BEADABLE FORM:

MEDILOTION TYPE: THOUS OF SEQUENCES OF SECTION WINGER: Patentin Release #1.0, Version #1.25

COMPUTRY: DATE: 21-UULY-1993

PRIGNARY APPLICATION DATA:

APPLICATION NUMBER: US 07/643,982

FILING DATE: 18-JAN-1991

RECESTRATION NUMBER: US 07/643,982

FILING DATE: 18-JAN-1991

REFERENCE CHARACTER: NUMBER: JDP-013DV

TELECOMMUNICATION NUMBER: JS,965

REFERENCE CHARACTERISTICS:

LENGARTH: 1155 amino acids

TYPE: amino acids

TYPE: amino acids
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US-08-899-575-151

US-08-899-575-151

US-08-085-108743-151

US-08-085-131-183

US-08-085-131-183

US-09-042-333-46

US-09-758-417A-311

US-09-456-090A-38

US-09-456-090A-50

US-09-456-090A-74

US-09-456-090A-80

US-09-456-090A-80

US-09-456-090A-80

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Pred. No. 80;
1; Mismatches
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Best Local Similarity 85.7
Matches 6; Conservative
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MOLECULE TYPE: protein
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Query Match 76.5%; Score 39; DB 2; Length 1234; Best Local Similarity 85.7%; Pred. No. 86; Matches 6; Conservative 1; Mismatches 0; Indels
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SCEQUENCE 15, Application PC/TUS9513041

GENERAL INFORMATION:

APPLICANT: WHITE, Morris F.

APPLICANT: PIERCE, Jacalyn H.

TITLE OF INVENTION: THE IRS FAMILY OF GENES

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/317,310

FILING DATE: 03-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: LOUIS MYSTEM: 35,965

REGISTRATION NUMBER: 35,965

REGISTRATION NUMBER: 35,965

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REGISTRATION NUMBER: 35,965

REGISTRATION NUMBER: 35,965

REGISTRATION NUMBER: 35,965

REGISTRATION NUMBER: 35,
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,310A
FILING DATE: 03-0CT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT TWORNATION:
NAME: LOUIS Myers
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: UPP-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (17)227-5941
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1234 amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-317-310A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425 EYGSSPC 431
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                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White, Morris F.
APPLICANT: White, Morris F.
APPLICANT: Rothenberg, Paul Louis
TITLE OF INVENTION: INSUIN RECEPTOR SUBSTRATE
TITLE OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
CORRESPONDENCE LAMIVE & COCKfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER PROCOMPATION:
COMPUTER PROCOMPATION:
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US96/09319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15.7.

Sequence 15. Application US/08317310A

Setent No. 5858701

GENERAL INFORMATION:

APPLICANT: WHITE, Morris F.

APPLICANT: PIERCE, Jacalyn H.

TITLE OF INVENTION: THE IRS FAMILY OF GENES

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: BOSTON

STATE: Massachusetts

COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 5
Pred. No. 80;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/094,948
FILING DATE: 21-JULY-1993
APPLICATION NUMBER: US 07/643,982
FILING DATE: 18-JAN-1991
ATTORNEY, AGENT INFORMATION:
NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE, DOCKET NUMBER: JDP-013DV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 29:
SQUENCE TRANSFERSISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.5
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein PCT-US96-09319-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 EYGSSPC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 OYGSSPC 8
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ZIF: 02109 COMPUTER READABLE FORM:

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ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-557-139-2
                                                                                                                                                                                                                                                                                                                                                                                        :||||||
431 EYGSSPC 437
                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                              2 OYGSSPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-350-260A-503
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US-09-508-691-1

| Sequence | Application US/09508691
| Patent No. 6498139
| GENERAL INFORMATION:
| APPLICANT: YAZALY, YOSHIO
| APPLICANT: YAZALY, YOSHIO
| APPLICANT: KANDO, HIDBO
| APPLICANT: KANDO, AKIRA
| TILLE OF INVENTION: REMEDIES FOR DISEASES CAUSED BY INSULIN RESISTANCE
| CURRENT FALLON NUMBER: US/09/508,691
| CURRENT FILING DATE: 1998-09-25
| PRIOR FILING DATE: 1998-09-25
| PRIOR FILING DATE: 1998-09-25
| PRIOR FILING DATE: 1997-09-29
| NOWINGER OF SEQ ID NOS: 5
| SEQ ID NO 1
| LENGTH: 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INCORNATION:
APPLICANT: Pedersen, Oluf
APPLICANT: Pedersen, Christian
APPLICANT: Frederiksen, Kathrine A.
TITLE OF INVENTION: MUTANT DNA ENCODING INSULIN RECEPTOR
TITLE OF INVENTION: SUBSTRATE 1
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58277300 No. 5827730disk of No. 5827730th America
STREET: 405 Lexington Avenue
                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                        Score 39; DB 5; Length 1234;
Pred. No. 86;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 4; Length 1242;
Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compartible
OPPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
#PPLICATION NUMBER: US/08/557,139
FILING DATE: 12-FEB-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6

US-08-557-139-2

; Sequence 2, Application US/08557139

; Patent No. 5827730
                                                            76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                          Query Match
Best Local Similarity 85.7
Matches 6; Conservative
; FRAGMENT TYPE: internal PCT-US95-13041-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-508-691-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 EYGSSPC 436
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425 EYGSSPC 431
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                                                                                                                                    2 OYGSSPC 8
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US-08-758-417A-210
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                                                                                                                                                                 Gaps
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                                                                                                                                              Score 38; DB 2; Length 9;
Pred. No. 3e+05;
0; Mismatches 0; Indels
PRILING DATE: 31-WAR-1994

PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECHONE: 312-474-6300
INFORMATION FOR EG. DI NO: 503:
SEQUENCE CHARACTERISCICS:
LENGTH: 9 amino acids
                                                                                                                                               Query Match 74.5%; Sc
Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-350-260A-503
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PRILING MARE: A. 1970.

PRICE APPLIANCE AND ALL B. 68165.639
PRILING APPLIANCE AND ALL B. 68165.639
PRILING APPLIANCE AND ALL B. 68165.639
PRILING APPLIANCE AND ALL B. 68165.639
PRILING APPLIANCE AND ALL B. 68165.639
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PRILING APPLIANCE AND ALL B. 68165.639
PRILING APPLIANCE AND ALL B. 68165.631
PRICE APPLIANCE ON WORRE B. 89 6914.404
PRILING APPLIANCE ON TO ALL B. 68165.633
PRILING APPLIANCE AND ALL B. 69178.463
PRILING APPLIANCE AND ALL B. 69178.463
PRILING APPLIANCE AND ALL B. 69178.463
PRILING APPLIANCE AND ALL B. 69178.417
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PREPRESENCE AND ALL B. 69178.417
PREPRESENCE AND ALL B. 69178.417
PREPRESENCE AND ALL B. 69178.417
PREPRESENCE AND ALL B. 69178.417
PREPRESENCE AND ALL B. 69178.617
PROPROCETTE AND ALL B. 69178.617
PROPROCE AND ALL B. 69178.617
PROPROCE AND ALL B. 69178.617
PROPROCE AND ALL B. 69178.617
PROPROCE AND ALL B. 69178.617
PROPROCE AND ALL B. 69178.617
PROPROCE AND ALL B. 69178.617
PROPROCE AND ALL B. 69178.617
PROPROCE AND ALL B. 69178.617
PROPROCE AND ALL B. 69178.617
PROPROCE AND ALL B. 69178.617
PROPROCE AND ALL B. 69178.617
PROPROCE AND ALL B. 691
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Gaps
                                                                                                      MEDIUM TIPE: Floppy disk
COMPUTER: BEACHINE
COMPUTER: BATONINE
SOFTWARE: PETENTIN Release #1.0, Version #1.25 (EPO)
SOFTWARE: PETENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
PRILING DATE: 25-Jun-1998
PRIOR APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 2206318.9
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 24-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 16-SEP-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTONBEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, MARK J.
APPLICANT: HANNE, JEFREY H.
APPLICANT: HANNE, JEFREY H.
APPLICANT: HANNE, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENT APPLICATION NUMBER: US/09/472,087
CURRENT APPLICATION NUMBER: 1999-12-23
PRIOR PILLING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: BALLING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PALENTH: Ver. 2.1
SEQ ID NO 8 7
LENDERTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 4;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.5%; Sco. 100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 503: US-09-104-337A-503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 503:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 87, Application US/09472087
Patent No. 6682736
                              ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Nissim, Ahuva
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSE: Audrey L. Bartnicki
STREET: Marshall, Geretein & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

74.5%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
                      : Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION **CURROWN-
PRIOR APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/52,322
FILING DATE: 10-OCT-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,731
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/155,331
FILING DATE: 28-DW-1993
APPLICATION NUMBER: US 08/056,762
FILING DATE: 28-NOV-1993
APPLICATION NUMBER: US 08/055,331
FILING DATE: 28-AUL-1993
APPLICATION NUMBER: US 08/055,331
FILING DATE: 28-AUL-1993
APPLICATION NUMBER: US 08/055,331
FILING DATE: 28-AUL-1993
APPLICATION NUMBER: US 08/055,131
FILING DATE: 16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 210:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 503, Application US/09104337A Patent No. 6492160 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-
INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-758-417A-210
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US-09-104-337A-503
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Sequence 14, Application US/08477531B
; Sequence 14, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studinicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; VUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER REDABLE FORM:
; MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
; COMPUTER: IBM PC compatible
; COMPUTER: IBM PC compatible
; COMPUTER: OF STREET: PC-DOS/MS-DOS
; COMPUTER: PLOSSEE: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 1; Length 107;
Pred. No. 10;
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLOPPY disk
COMPUTER: ENDOPY disk
COMPUTER: IMP DC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGFWARE: Patentin Release #1.0, Version #1.25
SOGFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/472,788A
FILING DATE: 0'-JUN-1995
RIGN APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
PRIOR APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 33,851
RELEPHONE: 202/371-2600
TELEPHONE: 202/371-2600
TELEPHONE: 202/371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.5%; Scor.
100.0%; Pred. No. 10.
... 0; Mismatches
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SEQUENCE CHARACTERICTICS:
LENGTH: 107 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.5
Best Local Similarity 100.
Matches 7; Conservative
TUMBER OF SEQUENCES: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 QQYGSSP 95
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U.S.08-107-669D-14
U.Sequence 14, Application US/08107669D
Parent No. 576686
GENERAL INFORMATION:
MAPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SECUENCES:
ADDRESSES: Sterme, Kessler, Goldstein and Fox P.L.L.G.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STRIE: 10005-3934
COUNTYS: United States of America
STRIE: DOMOTORS: TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBW FC Compatible
COMPUTER: IBW FC Compatible
COMPUTER: 13-10-10-19-3
CLASSIFICATION NUMBER: US/08/107,669D
FRING DATE: 13-DEC-1991
ATTORNEY/ABERT 13-DEC-1991
ATTORNEY/ABERT 13-DEC-1991
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ATTORNEY/ABERT 13-DEC-1991
ATTORNEY/ABERT 13-DEC-1991
ATTORNEY/ABERT 13-DEC-199
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                                                                                      Query Match

74.5%; Score 38; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 0; Indels
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US-08-472-788A-14
Sequence 14, Application US/08472788A
Patent No. 5770196
Patent No. 5770196
SEMPLAL INFORMATION:
TITLE OF INVENTION:
Modified Antibody Variable Domains
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
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   ; ORGANISM: Homo sapiens US-09-472-087-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 QQYGSSP 95
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0; Gaps
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Sequence 4-95

Batent No. 5861155

GENERAL INFORMATION:

TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES

TITLE OF INVENTION: HIREROF

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF

STREET: 75 STATE STREET, 23RD FLOOR

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIPP: 02109

CONPUTER: LIM PC compatible

COMPUTER: BADADE

COMPUTER: PREADABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: PREADABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: LIM PC compatible

COMPUTER: LIM PC compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRATION NUMBER: PC/1894/00387

FILING DATE: UNVEMBER 21, 1994

ATTORIC APPLICATION DATA:

APPLICATION NUMBER: PC/1894/00387

FILING DATE: NOVEMBER 21, 1994

ATTORIC APPLICATION INFORMATION:

NAME: YANKWATCH, LEON R.

REGISTRATION NUMBER: 30,237

REBERRENCE/DOCKET NUMBER: 30,237

REBERRENCE/DOCKET NUMBER: 95,497-L

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                    PILING DATE:

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

PRING APPLICATION DATA:

PRING APPLICATION DATA:

APPLICATION NUMBER: 08/107,669

FILING DATE: 13-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 100 07/808,464

FILING DATE: 13-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 33,551

ATORNEY/AGENT INFORMATION:

NAME: MIChele A. Chabala

REFERENCE/DOCKET NUMBER: 30 010.100004/MAC

TELEPHONE: 202/371-2540

INPORMATION FOR EAG ID NO: 14:

TELEPACE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TOTAL: 107 amino acids

TYPE: mino acid

TOTAL: 107 amino acids

TOTAL: 107 amino acids
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INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-5318-14
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FILING DATE:
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US-08-652-558-49
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74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             Search completed: April 21, 2004, 17:40:06 Job time: 11.8261 secs
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-558-49
                                                                                                                                                                                                                    88 QQYGSSP 94
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Ig kappa chain V-I
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insulin receptor s
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insulin receptor s
alpha-2-macroglobu
Ig kappa chain V r
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Ig kappa chain V r April 21, 2004, 17:27:33 ; Search time 8.21739 Seconds (without alignments) 105.353 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM protein - protein search, using sw model F30601 K3HUGO S30185 S16948 JC5209 JS0670 A53102 A25521 S37520 S37520 S37519 S37519 S37510 S37510 S37510 S37510 K3HUB6 K3HUB6 K3HUB6 K3HUB6 K3HUB6 K3HUB6 K3HUB6 K3HUB1 K3 BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Query Match Length DB SEQ6 51 1 qqygsspcs 9 PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Title: Perfect score: Sequence: Scoring table: Score Database : Searched: Result No. Run on: 

30 38 74.5 109 2 A30608 31 38 74.5 109 2 D30601 32 38 74.5 109 2 C30601 33 38 74.5 109 2 G30601 34 38 74.5 109 2 H30601 35 38 74.5 109 2 F44151 36 38 74.5 109 2 F44151 37 74.5 119 2 S47181 39 74.5 116 2 B27594 41 38 74.5 116 2 B27594 41 38 74.5 112 2 S40327 42 38 74.5 129 1 K3HUHI 43 38 74.5 129 2 S49532 44 3 74.5 129 2 S49532 44 3 74.5 129 2 S49532	Ig kappa chain V-I	rappa	cappa	cappa	карра	cappa	tappa	cappa	cappa	kappa	kappa	kappa	kappa	anti-Sm antibody V	IG light chain var	kappa chain
38 74.5 109 38 74.5 109 38 74.5 109 38 74.5 109 38 74.5 109 38 74.5 109 38 74.5 109 38 74.5 101 38 74.5 116 38 74.5 116 38 74.5 116 38 74.5 129																
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	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	38	38	38	38	38	38	38	38	38	38	38	38	38	33	80	38
	30	31	32	33	34	35	36	37	38	6 6	40	41	42	4.3	4 4	45

## ALIGNMENTS

RESULT 1 F30601 Ig kappa chain V-III region (Neu) - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: F30601 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solor R; Car, Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solor R; Reference number: A30601, MUID:89215279; PMID:2496160 A;Accession: F30601 A;Accession: F30601 A;Accession: P30601 A;Accession: F30601 A;Accession: F30601 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin, A;Mc, A	Query Match 88.2%; Score 45; DB 2; Length 109;  Best Local Similarity 77.8%; Pred. No. 0.2;  Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  Qy 1 QQYGSSPCS 9              90 QQYGASSPCT 98	RESULT 2 K3HUGO IG Kappa chain V-III region (Gol) - human N;Alternate names: rheumatoid factor C;Species: Homo sapiens (man) C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000 C;Accession: A01893 R;NewKirk, M.; Chen, P.P.; Carson, D.; Posnett, D.; Capra, J.D. R;NewKirk, M.; Chen, P.P.; Carson, D.; Posnett, D.; Capra, J.D. A;Title: Amino acid sequence of a light chain variable region of a human rheumatoid factor A;Reference number: A01893; MUID:86230578; PMID:3086710 A;Accession: A01893 A;Molecule type: protein	A; Residues: 1-109 <new> C; Genetics: A; Genetics: A; Genetics: C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp C; Complex: An immunoglobulin heterotetramer; immunoglobulin heterotetramer; immunoglobulin bomology C; Superfamily: immunoglobulin heterotetramer; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin homology c! MM&gt; F; 16-91/Domain: immunoglobulin homology c! MM&gt; F; 23-89/Disulfide bonds: #status predicted</new>
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Gaps

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Length 1235

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insulin receptor substrate 1 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 16-Jul-1999
C;Accession: JC5209; PC4305
R;Taouis, M: Taylor, S.I.; Reitman, M.
Gene 178, S1-55, 1996
A;Tatle: Cloning of the chicken insulin receptor substrate 1 gene.
A;Reference number: JC5209; MUID:97080546; PMID:8921891
A;Accession: JC5209
A;Status: preliminary; nucleic acid sequence not shown
A;Accession: PC4305
A;Cross-references: GB:U43502; NID:g1685084; PIDN:AAC60050.1; PID:g1685085
A;Accession: PC4305
A;Accession: PC4305
A;Accession: PC4305
C;Comment: This protein
A;Residues: 1-5 < TAZ>
C;Comment: This protein acts as a docking protein and mediates multiple interactions amo C;Genetics:
A;Genetics:
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: 
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A;Residues: 1-1242 <RES>
A;Cross-references: GB:S62539; NID:g386256; PIDN:AAB27175.1; PID:g386257
A;Cross-references: GB:S62539; NID:g386256; PIDN:AAB27175.1; PID:g386257
B;Nishiyama, M.; Wands, J.R.
B;Ochem. Biophys. Res. Commun. 183, 280-285, 1992
A;Title: Cloning and increased expression of an insulin receptor substrate-1-like gene in A;Reference number: JS0670; MUID:92181456; PMID:1311924
A;Reference number: JS0670; MUID:92181456; PMID:1311924
A;Residues: 1-134,/G',135-361,'R',363-383,'R',385-1242 <NIS>
A;Residues: 1-134,'G',135-361,'R',363-383,'R',385-1242 <NIS>
A;Residues: GSS9563; NID:g246465; PIDN:AAB21608:1; PID:g246466
A;Experimental source: hepatocellular carinoma cell line FOCUS
R;Smith, L.K.; Bradshaw, M.; Croall, D.E.; Garner, C.W.
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J80670; PN0678 (C) Accession: IS3160; J80670; PN0678 (C) Accession: IS3160; J80670; PN0678 (C) Accession: IS3160; J80670; PN0678 (C) Apart (C) Angology (C) Angology (C) Angology (C) Angology (C) Apart (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Angology (C) Ango
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C;Keywords: phosphoprotein
F;11-112/Domain: pleckstrin repeat homology <PLK>
F;11-112/Domain: pleckstrin repeat homology <PLK>
F;463,549,610,630,660,730,940,987,1010/Binding site: phosphate (Tyr) (covalent) #status
F;11-113/Domain: pleckstrin repeat homology <PLK>F;872-891/Region: glutamine-rich
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Pred. No. 30;
1; Mismatches
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A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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NiAlternate names: insulin receptor substrate pp185
C;Species Rattus norvegicus (Norway rat)
C;Species Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C;Accession: 185948; A39811
R;Sun, X.J; Rothenberg, P.; Kahn, C.R.; Backer, J.M.; Araki, E.; Wilden, P.A.; Cahill, Nature 352, 73-77, 1991
A;Title: Structure of the insulin receptor substrate IRS-1 defines a unique signal trans
A;Reference number: 816948; MUID:91287824; PMID:1648180
A;Accession: 516948
A;Molecule type: mRNA
A;Residues: 1-1235 <5UN>
A;Coss-references: EMBL:X58375; NID:956503; PIDN:CAA41264.1; PID:956504
A;Residues: 1-1235 <5UN>
A;Coss-references: EMBL:X58375; NID:956503; PIDN:CAA41264.1; PID:956504
A;Reference number: A302-8311, 1991
A;Title: Purification and partial sequence analysis of pp185, the major cellular substrate A;Accession: A39811; MUID:91217066; PMID:2022647
A;Reference number: A39811; MUID:91217066; PMID:2022647
A;Residues: 44-51;173-178;223-243;489-506;635-646;871-882,'I',884,'X',886-888;932-936,'X
A;Note: the phosphotyrosine residue was not identified
C;Comment: This protein and the beta chain of the insulin receptor itself are the major C;Comment: Phosphorylation of this protein in response to insulin is maximal at 30 secondical insulin is maximal at 30 secondical insulin in the property is an insulin in the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the p
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EGF homology <EG15>
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LDL receptor YWTD-containing repeat homology <YW41>
alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
85K chain extracellular #status predicted <EXT>
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                                           receptor ligand-binding repeat homology <LDL5>
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F; 934-929/Domain: LDL rece
F; 934-1009/Domain: LDL rec
F; 1003-10149/Domain: LDL rec
F; 1103-1049/Domain: LDL rec
F; 1103-1049/Domain: LDL rec
F; 1103-1049/Domain: LDL rec
F; 1103-1138/Domain: LDL rec
F; 1133-1139/Domain: LDL rec
F; 125-1259/Domain: LDL rec
F; 1257-1259/Domain: LDL rec
F; 1257-1259/Domain: LDL rec
F; 1341-1354/Domain:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F,2338-2232/Domain:
F,2348-2423/Domain:
F,2448-2447-2441
F,2448-2455/Domain:
F,2590-2234/Domain:
F,2560-2234/Domain:
F,2646-2662/Domain:
F,2646-2623/Domain:
F,2646-2633/Domain:
F,3184-334/Domain:
F,3410-3445/Domain:
F,3410-3445/Domain:
F,3410-3445/Domain:
F,3451-3405/Domain:
F,3451-3405/Domain:
F,3533-366/Domain:
F,3610-3644/Domain:
F,3610-3644/Domain:
F,3620-3728/Domain:
F,3620-3728
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F;3943-452/Domain: B;3953-4420/Domain: B
F;3969-4011/Domain: E;4012-4055/Domain: L
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Alpha-Z-macroglobulin receptor precursor - chicken

Alpha-Z-macroglobulin receptor precursor - chicken

NAlternate names: 1091; LDL receptor-related protein 1; low density lipoprotein receptor

Contes and Seps 1988 #sequence_revision 04-Sep-198 #text_change 22-Jun-1999

Cyaccession: AS3102

Nimpf, J. S. Stifani, S.; Bilous, P.T.; Schneider, W.J.

J. Biol. Chem. 269, 212-219, 1994

Altitle: The Somatic Cell-specific low density lipoprotein receptor-related protein of the Alternate number: AS3102; MUD:94103212; PMID:7506255

Altitle: The Somatic Cell-specific low density lipoprotein receptor-related protein of the Alternate preliminary

Altocession: AS3102

Altitle: The Somatic Cell-specific low density lipoprotein receptor-related protein of the Altocession: AS3102

Altitle: The Somatic Cell-specific low density lipoprotein receptor-related protein of the Altocession: AS3102

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Altocession: AS3102

Altocession: A
Biochem. Biophys. Res. Commun. 196, 767-772, 1993
A/Title: The insulin receptor substrate (IRS-1) is a PEST protein that is susceptible to A/Reference number: PN0678; MUID:94059102; PMID:8240352
A/Accession: PN0678; MUID:94059102; PMID:8240352
A/Accession: PN0678; MUID:94059102; PMID:8240352
A/Accession: PN0678
A/Molecule type: protein
A/Residues: 1-14,338-353,411-439;538-545, VV, 547-567,656-697;724-758;932-943;1028-1056;1
C;Comment: This protein appears to be the major substrate for insulin-stimulated tyrosin of dock various proteins containing the phosphotyrosine-binding Src-homology domain 2 (St Comment: This protein contains at least 11 PEST regions, which suggests rapid turnover C;Genetics:
A/Gene: GDB:IRS1
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C'Species: Homo sapiens (man)
C'Date: Oc-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: 837513
R;Klein, U.; Kueppers, R.; Rajewsky, K.
R;Klein, U.; Kueppers, R.; Rajewsky, K.
Bubmitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: 837501
                                                                                                                                                    Sylvapa chain V region, subgroup III (clone MH52) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Brown 1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C;Accession: S67940
R;Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Altoimmunity 12, 135-141, 1992
A;Reference number: S67940, MUID:92314301; PMID:1617110
A;Reference number: S67940
A;Retus: preliminary
A;Residues: 1-91 cHERA
A;Cross-references: EMBL:X73852
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 < KLE>
A;Cross-references: EMBL: 226598; NID:g405668; PIDN:CAA81352.1; PID:g405669
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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llarity 100.0%; Pred. No. 3.6;
Conservative 0; Mismatches 0; Indels
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C;Species: Homo sapiens (man)
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100.0%; Pred. No. 3.6;
ive 0; Mismatches 0
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Matches 7; Conservative
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73 QQYGSSP 79
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Matches 7, Conserv
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337520
Ig Asapa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: 837520
R;Kalein, U:; Kueppers, R.; Rajewsky, K.
R;Accession: Human IgM(+) IgD(+) cells, the major B cell subset in the peripheral blood A;Accession: 837520
A;Accession: 837520
A;Accession: 837520
A;Accession: S37520
A;Accession: Sanda
A;Accession: Sanda
A;Accession: Sanda
A;Accession: Sanda
C;Cspecial type: mRNA
A;Residues: 1-91 < KLE>
A;Accession: Sanda
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Ig Kappa chain V region (321) - human (fragment)

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Date: 21-May-1988 #sequence_revision 21-May-1990 #text_change 09-May-1997

C; Date: 21-May-1988 #sequence_revision 21-May-1990 #text_change 09-May-1997

C; Date: 21-May-1988 #sequence_revision 21-May-1990 #text_change 09-May-1997

R; Chen, P.P., Albrandt, K.; Orida, N.K.; Radoux, V.; Chen, B.Y.; Schrantz, R.; Liu, F.T.

Proc. Natl. Acad. Sci. U.S.A. 83, 8318-8322, 1986

A; Title: Genetic Dasis for the cross-reactive idiotypes on the light chains of human IgM

A; Reference number: A94135; MUID:87041448; PMID:3095834
                                                                                                                                                                                                                                                                                                            F;116,138,187,276,359,448,731,926,1048,1152,1153,1193,1216,1305,1509,1556,1573,1614,1643
3485,3659,7386,3837,3952,4074,4124,4178,4278/Binding site: carbohydrate (Asn) (covalent)
F;168,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;2855/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
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     VWTD-containing repeat homology <YW44>
YWTD-containing repeat homology <YW45>
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A;Residues: 1-54 «CHE»
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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  F;4056-4098/Domain: LDL receptor YWTD-cont. F;4150-4181/Domain: LDL receptor YWTD-cont. F;4150-4181/Domain: EGF homology <EG15- F;4235-4266/Domain: EGF homology <EG18- F;4231-4302/Domain: EGF homology <EG18- F;4271-4302/Domain: EGF homology <EG19- F;4307-4338/Domain: EGF homology <EG20- F;4343-4373/Domain: EGF homology <EG20- F;4343-4373/Domain: EGF homology <EG21- E;4376-4408/Domain: EGF homology <EG21-
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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Matches 7, Conservative
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A; Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood A; Reference number: 837501
A; Accession: 837510
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-92 «KLB»
A; Residues: 1-92 «KLB»
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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74.5%; Score 38; DB
Best Local Similarity 100.0%; Pred. No. 3.6
Matches 7; Conservative 0; Mismatches
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S37519
R;Klein, U:; Kueppers, R.; Rajewsky, K.
R;Klein, U:; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
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R;Klein, U.; Kueppers, R.; Rajewsky, K.
Rsubmitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood A;Reference number: S37501
A;Accession: S37517
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837510
19 kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: 837510
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C;Accession: 83751
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837517
19 kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
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A;Molecule type: mRNA
A;Residues: 1-92 <KLES
A;Cross-references: EMBL:Z26615; NID:g405676; PIDN:CAA81368.1; PID:g405677
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 «KLES
A;Cross-references: EMBL:226613; NID:9405680; PIDN:CAA81366.1; PID:9405681
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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100.0%; Pred. No. 3.6;
cive 0; Mismatches
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100.0%; Pred. No. 3.6;
:ive 0; Mismatches
                            C; Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 100...
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Matches 7; Conservative
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